

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118.845 Seconds
(without alignments) updates/sec
2085.165 Million cell

Title: US-10-691-079-1
Perfect score: 2863
Sequence: 1 MGSNKSXPDKASQRRRLSEP.....AFLEDYFTSTPQYQPGENTL 542

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp19808:*
- 2: geneseqp1908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*
- 9: geneseqp20068:*
- 10: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2863	100.0	542	5 ABB97339	Abp97339 Novel hum
2	2863	100.0	542	8 ADY84075	ADY84075 Human Src
3	2821	98.5	536	2 AAR39706	Aar39706 Human pp6
4	2821	98.5	536	5 ABG95123	Abg95123 Human V-b
5	2821	98.5	536	5 AAU78678	Aau78678 Human SH2
6	2821	98.5	536	6 ABP57260	Abp57260 Human src
7	2821	98.5	536	7 ADI20072	Adi20072 Human C-S
8	2821	98.5	536	8 ADL22904	Adl22904 Human MP2
9	2821	98.5	536	8 ADO88400	Adg88400 Human wil
10	2821	98.5	536	8 ADO97772	Adg97772 Human can
11	2821	98.5	536	8 ADU04517	Adu04517 Protein t
12	2821	98.5	536	8 ADY84076	ADY84076 Human Src
13	2821	98.5	536	9 ADY94834	ADY94834 Human wil
14	2821	98.5	536	9 AEA35914	Aea35914 Human Src
15	2821	98.5	541	8 ADY84080	ADY84080 Human Src
16	2820.5	98.5	541	8 ABB57261	Abp57261 Mouse Src
17	2820.5	98.5	541	8 ADY84077	ADY84077 Murine Sr
18	2816	98.4	535	7 ADF45087	Adf45087 Human kin
19	2816	98.4	535	9 AED21154	Aed21154 Human non
20	2788	97.4	530	8 ADO88402	ADY88402 Human mut
21	2788	97.4	530	9 ADY94836	ADY94836 Human mut
22	2650.5	92.6	533	3 AAU44447	AAU44447 Wild-type
23	2650.5	92.6	533	4 AAB84661	Aab84661 Amino aci

24	2650.5	92.6	533	9 AEB07192	Aeb07192 Chicken c
25	2646.5	92.4	533	3 AAY44449	Aay44449 Mutant ch
26	2645.5	92.4	533	2 AAR39705	Aar39705 Chicken p
27	2644.5	92.4	533	3 AAY44451	Aay44451 Mutant ch
28	2469	86.2	523	9 AEB07190	Aeb07190 Rous sarc
29	2396.5	83.7	565	4 ABG23778	Abg23778 Novel hum
30	2230	77.9	423	8 ADQ97769	Adq97769 Mouse can
31	2110.5	73.7	543	4 AAB84663	Aab84663 Amino aci
32	2110.5	73.7	543	4 ABG10302	Abg10302 Novel hum
33	2110.5	73.7	543	6 ADA00843	Ada00843 Human Src
34	2110.5	73.7	543	7 ADP45099	Adp45099 Human kin
35	2110.5	73.7	543	8 ADL22913	Adl22913 Human MP2
36	2110.5	73.7	543	8 ADO19329	Ado19329 Human PRO
37	2110.5	73.7	543	8 ADO19331	Ado19331 Human PRO
38	2110.5	73.7	543	8 ADQ26047	Adq26047 v-yes-1 y
39	2110.5	73.7	543	8 ADU06318	Adu06318 Novel bro
40	2110.5	73.7	543	9 ADW78761	Adw78761 Human Yam
41	2110.5	73.7	543	9 ADY19868	Ady19868 PRO polyP
42	2110.5	73.7	543	9 AEA23955	Aea23955 Human PRO
43	2110.5	73.7	543	9 AEA35915	Aea35915 Human Yes
44	2110.5	73.7	543	9 AED01122	Aed01122 Human C-X
45	2104.5	73.5	541	5 AAU74614	Aau74614 Perinucle

ALIGNMENTS

RESULT 1
ID ABB97339 standard; protein; 542 AA.

AC ABB97339;

DT 27-JUN-2002 (first entry)

XX Novel human protein SEQ ID NO: 607

XX Human; antiangiogenic; vulnary; antiinflammatory; immunomodulator;

XX antifertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;

KW neuroprotective; antiparkinsonian; protein therapy; EST;

KW expressed sequence tag.

XX Homo sapiens.

XX OS

XX PN MO200222660-A2.

XX PR 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US026015.

XX PR 11-SEP-2000; 2000US-00659671.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Zhou P, Auendi V, Zhang J, Zhao QA, Ren F;

XX PI Kue AT, Yang Y, Wehrman T, Dzmanac RT;

XX DR WPI: 2002-292408/33.

XX DR N-PSDB; ABRN32525.

XX PS Example 2; SEQ ID NO 607; 509pp; English.

XX CC The present invention provides the protein and coding sequences of 444

XX CC novel human proteins. These were isolated from expressed sequences tags

XX CC (ESTs). They can be used to stimulate cell growth, to regulate

XX CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

XX CC e.g. in burn treatment, to regulate the immune system e.g. to treat

XX CC multiple sclerosis, to regulate activin or inhibin e.g. to treat

XX CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke

XX CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

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CC rheumatoid arthritis, and to treat nervous system disorders e.g.
 XX Parkinson's disease. The present sequence is a protein of the invention
 SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 5; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPQKASQRRRLSEPAENVHAGAGAFPASQTPSPKASADGHRGPSAFAAPAAE 60
DB 1 MGSNKSXPQKASQRRRLSEPAENVHAGAGAFPASQTPSPKASADGHRGPSAFAAPAAE 60
QY 61 PKLFGGNSSDVTYSPOAGPLAGVTTFVALYDYESRTETDLSFKKGBRLQIVNNTKRY 120
DB 61 PKLFGGNSSDVTYSPOAGPLAGVTTFVALYDYESRTETDLSFKKGBRLQIVNNTKRY 120
QY 121 DVBEGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 180
DB 121 DVBEGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 180
QY 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYS 240
DB 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYS 240
QY 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVYLGCGCFGEVWMTNGTTR 300
DB 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVYLGCGCFGEVWMTNGTTR 300
QY 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
QY 361 GETGKTYLRLPOLVMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 361 GETGKTYLRLPOLVMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLI 420
QY 421 EDNEYTAPOGAKFPKWTAPRALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNREV 480
DB 421 EDNEYTAPOGAKFPKWTAPRALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNREV 480
QY 481 LDQVERGYRMPCEPCEPSLHDLMOCKMRKEPERPTEYLQAFLEDFYFSTEPYOYGE 540
DB 481 LDQVERGYRMPCEPCEPSLHDLMOCKMRKEPERPTEYLQAFLEDFYFSTEPYOYGE 540
QY 541 NL 542
DB 541 NL 542

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RESULT 2
 ADY84075
 ID ADY84075 standard; protein; 542 AA.

ADY84075;
 02-JUN-2005 (first entry)
 Human Src protein isoform 1 SEQ ID NO.1.
 pharmaaceutical; Alzhimers disease; neuroprotective; nootropic;
 Src tyrosine kinase.
 Homo sapiens.
 EP1413887-A1.
 28-APR-2004.
 22-OCT-2002; 2002EP-00292608.
 22-OCT-2002; 2002EP-00292608.

PA (AVET) AVENTIS PHARMA SA.
 XX Mercken L, Zambiano N, Russo T;
 XX WPI; 2004-332834/31.

PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT Involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.

PS Claim 4; SEQ ID NO 1; 45pp; English.

CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 1
 CC of human Src protein.

SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 8; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.5e-245;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPQKASQRRRLSEPAENVHAGAGAFPASQTPSPKASADGHRGPSAFAAPAAE 60
DB 1 MGSNKSXPQKASQRRRLSEPAENVHAGAGAFPASQTPSPKASADGHRGPSAFAAPAAE 60
QY 61 PKLFGGNSSDVTYSPOAGPLAGVTTFVALYDYESRTETDLSFKKGBRLQIVNNTKRY 120
DB 61 PKLFGGNSSDVTYSPOAGPLAGVTTFVALYDYESRTETDLSFKKGBRLQIVNNTKRY 120
QY 121 DVBEGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 180
DB 121 DVBEGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLINAEPRGT 180
QY 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYS 240
DB 181 FLVRESSTTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRTQFNSLQQLVAYYS 240
QY 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVYLGCGCFGEVWMTNGTTR 300
DB 241 KHADGLCHRLTYVCTSPKQTOGLAKDAWEIPRESLRLEVYLGCGCFGEVWMTNGTTR 300
QY 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
DB 301 VALKTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
QY 361 GETGKTYLRLPOLVMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 361 GETGKTYLRLPOLVMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLI 420
QY 421 EDNEYTAPOGAKFPKWTAPRALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNREV 480
DB 421 EDNEYTAPOGAKFPKWTAPRALYGRFTIKSDVMSFGILLTELTTKGRVYPGVNREV 480
QY 481 LDQVERGYRMPCEPCEPSLHDLMOCKMRKEPERPTEYLQAFLEDFYFSTEPYOYGE 540
DB 481 LDQVERGYRMPCEPCEPSLHDLMOCKMRKEPERPTEYLQAFLEDFYFSTEPYOYGE 540
QY 541 NL 542
DB 541 NL 542

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RESULT 3
 AAR39706
 ID AAR39706 standard; protein; 536 AA.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118.845 Seconds

(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXKMDASQRRRSLEP.....AFLEDFYFSTBPQYQGENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.8:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003s:*
7: geneeqp2004s:*
8: geneeqp2005s:*
9: geneeqp2006s:*
10: geneeqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2863	100.0	542	5	ABD97339 Novel hum
2	2863	100.0	542	8	ADY84075 Human Src
3	2821	98.5	536	2	AAR39706 Human pp6
4	2821	98.5	536	5	ABG95123 Human V-8
5	2821	98.5	536	5	AAU78678 Human SH2
6	2821	98.5	536	6	ABP57260 Human src
7	2821	98.5	536	7	AD120072 Human c-S
8	2821	98.5	536	8	AD122904 Human MP2
9	2821	98.5	536	8	ADG88400 Human will
10	2821	98.5	536	8	ADG97772 Human can
11	2821	98.5	536	8	ADU04517 Protein t
12	2821	98.5	536	8	ADY84076 Human Src
13	2821	98.5	536	9	ADY94834 Human w11
14	2821	98.5	536	9	AEA35914 Human Src
15	2821	98.5	541	6	ADY84080 Human Src
16	2820.5	98.5	541	6	ABP57261 Human Src
17	2820.5	98.5	541	8	ADY84077 Murine Sr
18	2816	98.4	535	7	ADY45087 Human kin
19	2816	98.4	535	7	ABD21154 Human non
20	2788	97.4	530	8	ADG88402 Human mut
21	2788	97.4	530	8	ADY94835 Human mut
22	2650.5	92.6	533	3	AAV44447 Wild-type
23	2650.5	92.6	533	4	ABD84661 Amino aci

24	2650.5	92.6	533	9	ABD07192 Chicken c
25	2646.5	92.4	533	3	AAV44449 Mutant ch
26	2645.5	92.4	533	3	AAR39705 Chicken p
27	2644.5	92.4	533	3	AAV44451 Mutant ch
28	2469	86.2	523	9	ABD07190 Rous sarc
29	2396.5	83.7	565	4	ABG23778 Novel hum
30	2230	77.9	423	8	ADG97769 Mouse can
31	2110.5	73.7	543	4	ABD84663 Amino aci
32	2110.5	73.7	543	4	ABG10302 Novel hum
33	2110.5	73.7	543	6	ADU00843 Human Src
34	2110.5	73.7	543	7	ADP45099 Human kin
35	2110.5	73.7	543	8	AD122913 Human MP2
36	2110.5	73.7	543	8	AD019329 Human PRO
37	2110.5	73.7	543	8	AD019331 Human PRO
38	2110.5	73.7	543	8	ADQ26047 v-yes-1 y
39	2110.5	73.7	543	8	ADU06318 Novel brc
40	2110.5	73.7	543	9	ADW78761 Human Yam
41	2110.5	73.7	543	9	ADY19868 PRO polyP
42	2110.5	73.7	543	9	AEA23955 Human PRO
43	2110.5	73.7	543	9	AEA35915 Human Yes
44	2110.5	73.7	543	9	AD011122 Human c-Y
45	2104.5	73.5	541	5	AAV74614 Perinucle

ALIGNMENTS

RESULT 1
ID ABD97339 standard; protein; 542 AA.

ABD97339;

27-JUN-2002 (first entry)

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Homo sapiens.
W0200222660-A2.
21-MAR-2002.
10-SEP-2001; 2001WO-US026015.
11-SEP-2000; 2000US-00659671.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F, Yang Y, Wehrman T, Drmanac RT, Yang Y.
WPI; 2002-292408/33.
N-PSDB; ABN32525.
An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
Example 2; SEQ ID NO 607; 509bp; English.
The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate actin or inhibit e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g.

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CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention
XX
SQ Sequence 542 AA;

Query Match	100.0%;	Score 2863;	DB 5;	Length 542;
Best Local Similarity	100.0%;	Pred. NO. 1.5e-245;		
Matches 542;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MSMNSKPKPDASORRSLSEPAENVHAGGGGAFPSQCPSPADNDGHRGSAAPAPAAE	60
Db	1	MSMNSKPKPDASORRSLSEPAENVHAGGGGAFPSQCPSPADNDGHRGSAAPAPAAE	60
QY	61	PKLFGGPNSSDVTYSPORAGPLAGVTFVALVDYESRTEJDSFPKGBELQIVNTRKY	120
Db	61	PKLFGGPNSSDVTYSPORAGPLAGVTFVALVDYESRTEJDSFPKGBELQIVNTRKY	120
QY	121	DVREGDWMLAHSISTQGTGYIPBNYVAPSDSIOAEEMYPFGKTRRESERLLNANERGT	180
Db	121	DVREGDWMLAHSISTQGTGYIPBNYVAPSDSIOAEEMYPFGKTRRESERLLNANERGT	180
QY	181	FLVRSSETTKGAYCJSVSPDNNAGLNVHXYTKRKLDGSGFYITSRQFNSIQOLVAYYS	240
Db	181	FLVRSSETTKGAYCJSVSPDNNAGLNVHXYTKRKLDGSGFYITSRQFNSIQOLVAYYS	240
QY	241	KHADGLCHRLTTCPTSPKOTOGLANDAMEIPRESLRLEKLGQCGFGEVWNGTNGTTR	300
Db	241	KHADGLCHRLTTCPTSPKOTOGLANDAMEIPRESLRLEKLGQCGFGEVWNGTNGTTR	300
QY	301	VAIKTLKPGTMSPEAFLOBAQVMKCLRHEKLVOLJAVVSBEPIYIVTEYMSKSLDPLK	360
Db	301	VAIKTLKPGTMSPEAFLOBAQVMKCLRHEKLVOLJAVVSBEPIYIVTEYMSKSLDPLK	360
QY	361	GRTGXYTLRLPOLVDMAAOIASGAYYERBNVYHRDLRANILYGENULYCKVADFGLABLI	420
Db	361	GRTGXYTLRLPOLVDMAAOIASGAYYERBNVYHRDLRANILYGENULYCKVADFGLABLI	420
QY	421	EDNETAAGACAFPIKMTAPBEAALYGRFTIKSDVMSFGILLTELTKGRVPVPGWNNREY	480
Db	421	EDNETAAGACAFPIKMTAPBEAALYGRFTIKSDVMSFGILLTELTKGRVPVPGWNNREY	480
QY	481	LDQVERGTRMPCBPBCEPSLHDLIMCQCMWKEPBERPTFEYLOAFLEDYFTSTEPQYQPE	540
Db	481	LDQVERGTRMPCBPBCEPSLHDLIMCQCMWKEPBERPTFEYLOAFLEDYFTSTEPQYQPE	540
QY	541	NTL 542	
Db	541	NTL 542	

XX	RESULT 2
XX	ADY84075
ID	ADY84075 standard; protein; 542 AA.
XX	
AC	ADY84075;
DT	02-JUN-2005 (first entry)
XX	
DE	Human Src protein isoform 1 SEQ ID NO:1.
XX	
KW	pharmaceutical; Alzheimers disease; neuroprotective; nootropic; Src tyrosine kinase.
XX	
OS	Homo sapiens.
XX	
PN	EPI413887-A1.
XX	
PD	26-APR-2004.
XX	
PF	22-OCT-2002; 2002EP-00292608.
XX	
PR	22-OCT-2002; 2002EP-00292608.
XX	

PA (AVET) AVENTIS PHARMA SA.
XX
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PI Mercken L, Zambrano N, Russo T;
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XX
DR WPI, 2004-332834/31.

PT Identifying therapeutic compound for treating Alzheimer's disease,
PT involves providing Src protein and determining inhibitory effect of
PT compound on Src activity.
XX

Claim 4; SEQ ID NO 1; 45pp; English.

CC The invention relates to a novel method for identifying (M1) a
CC therapeutic compound for the treatment of Alzheimer's disease, involving
CC providing a Src protein and determining the inhibitory effect of a
CC compound on the Src activity. The method optionally involves providing a
CC sequence which regulates Src expression and determining if a compound
CC inhibits the expression of Src protein. A compound of the invention has
CC neuroprotective and neurotropic activity. The compound identified by the
CC method of the invention is useful for preparing a pharmaceutical for
CC treating Alzheimer's disease. The present sequence represents isoform 1
CC of human Src protein.

SQ Sequence 542 AA;

Query Match	100.0%;	Score 2863;	DB 8;	Length 542;
Best Local Similarity	100.0%;	Pred. No. 1.5e-245;		
Matches 542;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible][illegible]

Qy 121 DVREGDWLASHLSSTGOTGYIPSNVVPAPSDSIQAEEWYFGKITRRESERLLNAENPRT 180
Dd 121 DVREGDWLASHLSSTGOTGYIPSNVVPAPSDSIQAEEWYFGKITRRESERLLNAENPRT 180			

Qy 181 FLVRESFTTKGAYCLSVSDFDNAGKGLNWKHYKTRKLDSSGFYITSRTQFNSLLOOLVAAYS 240
Db 181 FLVRESFTTKGAYCLSVSDFDNAGKGLNWKHYKTRKLDSSGFYITSRTQFNSLLOOLVAAYS 240	

241 KHADGICRLTTCPTSKPQTGGIAXDAWEIPBSLRLEVKLGCGCFGEYMGTTNGTTR 300
241 KHADGICRLTTCPTSKPQTGGIAXDAWEIPBSLRLEVKLGCGCFGEYMGTTNGTTR 300
241 KHADGICRLTTCPTSKPQTGGIAXDAWEIPBSLRLEVKLGCGCFGEYMGTTNGTTR 300

QY	QY
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361 GETGKRLRLPOLVDMAQIASGNAVVERMNYHARDLRANILYGENLVCKVADFGIARLI 420

DB 361 GETGKRLPLQVDMQAQIASGVAVERMNVYHRDLRAANIIVGENLVCKVADFGIARLI 420

DY 421 EDNETAROGAKFPIKWTAFEAALYGRFTIKSDVWSFGILLTELTTKGRVYPGCVNREV 480

Db 421 EDNETTAROGAKFPFKWTAPEALYGRFTIKSDVMSFGILTELTTKGRVPYPCMVNREV 480

Qy 481 LDQVERGYRMECPPECESLHDMCQCRKEEERPTFEYLQAFLEDYFTSTBEOYQPGC 540

Dd	481	LDQVERGRMPCPPECPESLHDMCQWKRKEBERPFYEYLQAFLEDFYFSTEBQYQPGE	540
Oy	541	NL 542	

RESULT 3
AAR39706
ID AAR39706 standard; protein; 536 AA

RESULT 3
AAR39706
ID AAR39706 standard; protein; 536 AA.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118,845 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MSNKSQKPKASQRRSLRP.....AFLEDYFTSTPEQYQENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq.8:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2863	100.0	542	5 ABB97339	Novel hum
2	2863	100.0	542	8 ADY84075	Human Src
3	2821	98.5	536	2 AAR39706	Human pp6
4	2821	98.5	536	5 ABG95123	Human v-8
5	2821	98.5	536	5 AAU78678	Human SH2
6	2821	98.5	536	6 ABP57260	Human Src
7	2821	98.5	536	7 ADI20072	Human C-S
8	2821	98.5	536	8 ADL22904	Human MP2
9	2821	98.5	536	8 ADQ88400	Human w1
10	2821	98.5	536	8 ADQ97772	Human can
11	2821	98.5	536	8 ADU04517	Protein t
12	2821	98.5	536	8 ADY84076	Human Src
13	2821	98.5	536	9 ADV94834	Human w1
14	2821	98.5	536	9 AEA35914	Human Src
15	2821	98.5	541	8 ADY84080	Human Src
16	2820.5	98.5	541	8 ABP57261	Mouse Src
17	2820.5	98.5	541	8 ADY84077	Murine Sr
18	2816	98.4	535	7 ADY45087	Human Kin
19	2788	97.4	530	8 AED21154	Human non
20	2788	97.4	530	8 ADQ88402	Human mut
21	2788	97.4	530	8 ADV94836	Human mut
22	2650.5	92.6	533	3 AAU44447	Wild-type
23	2650.5	92.6	533	4 AAB84661	Amino aci

ALIGNMENTS

RESULT 1
ABB97339
ID ABB97339 standard; protein; 542 AA.
XX
AC ABB97339;
XX
DT 27-JUN-2002 (first entry)
XX
DE Novel human protein SEQ ID NO: 607.
XX
KW Human; anti-neoplastic; anti-inflammatory; immunomodulator;
KW antileukemia; anti-infective; cytotoxic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.
XX
OS Homo sapiens.
XX
PN W0200222660-A2.
XX
PD 21-MAR-2002.
XX
PE 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
FI Tang YT, Liu C, Zhou P, Adundi V, Zhang J, Zhao QA, Ren F;
FI Xue AD, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
XX
DR An isolated polynucleotide for treating diseases associated with its
XX encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Example 2; SEQ ID NO 607; 509bp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to treat aplastic anaemia, to help tissue regrowth
CC haematopoietic e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAGPLAGVTTFVALYDYSRTEEDLSFKKGERLQIVNNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAGPLAGVTTFVALYDYSRTEEDLSFKKGERLQIVNNTRKY 120
QY 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180
DB 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
DB 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240

QY 241 KHADGLCHRLTTCPTSKPQTQGLAKDAWEIPRESRLRLEVKLGCGCFGEVMMGTWNGTTR 300
DB 241 KHADGLCHRLTTCPTSKPQTQGLAKDAWEIPRESRLRLEVKLGCGCFGEVMMGTWNGTTR 300
QY 301 VALKTLPKGTMSPEAFLOEAQVMMKLRHEKLVOLYAVVSEBPYIVTEYMSKSLDPLK 360
DB 301 VALKTLPKGTMSPEAFLOEAQVMMKLRHEKLVOLYAVVSEBPYIVTEYMSKSLDPLK 360
QY 361 GETGKTLRLPOLYDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGIARLI 420
DB 361 GETGKTLRLPOLYDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGIARLI 420
QY 421 EDNEYTARQAKFPFKWTAPBAALYGRFTIKSDVMSFGILTELTTGKRVPPGMVNRREV 480
DB 421 EDNEYTARQAKFPFKWTAPBAALYGRFTIKSDVMSFGILTELTTGKRVPPGMVNRREV 480
QY 481 LDQVERGYRMPCEPCBESLHDLMCQMKRKEPERPTEFYLOAFLEDYFTSTBPQYQPG 540
DB 481 LDQVERGYRMPCEPCBESLHDLMCQMKRKEPERPTEFYLOAFLEDYFTSTBPQYQPG 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
ADY84075
ID ADY84075 standard; protein; 542 AA.

XX ADY84075;

XX 02-JUN-2005 (first entry)

XX Human Src protein isoform 1 SEQ ID NO:1.

XX pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX Src tyrosine kinase.

XX Homo sapiens.

XX EP1413887-A1.

XX 26-APR-2004.

XX 22-OCT-2002; 2002EP-00292608.

XX 22-OCT-2002; 2002EP-00292608.

XX

PA (AVET) AVENTIS PHARMA SA.

XX Mercken L, Zambrano N, Rusco T;

XX WPI; 2004-332834/31.

XX Identifying therapeutic compound for treating Alzheimer's disease.

PT Involves providing Src protein and determining inhibitory effect of

PT compound on Src activity.

PS Claim 4; SEQ ID NO 1; 45dp; English.

CC The invention relates to a novel method for identifying (M) a
CC therapeutic compound for the treatment of Alzheimer's disease, involving
CC providing a Src protein and determining the inhibitory effect of a
CC compound on the Src activity. The method optionally involves providing a
CC sequence which regulates Src expression and determining if a compound
CC inhibits the expression of Src protein. A compound of the invention has
CC neuroprotective and nootropic activity. The compound identified by the
CC method of the invention is useful for preparing a pharmaceutical for
CC treating Alzheimer's disease. The present sequence represents isoform 1
CC of human Src protein.

SQ Sequence 542 AA;

Query Match 100.0%; Score 2863; DB 8; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60

DB 1 MGSNKSXPKASQRRSLRLEPAENVHAGGAFPPASQTPSPKASADGHRGSAAPAPAAE 60

QY 61 PKLFGFNSSDVTYSPQAGPLAGVTTFVALYDYSRTEEDLSFKKGERLQIVNNTRKY 120

DB 61 PKLFGFNSSDVTYSPQAGPLAGVTTFVALYDYSRTEEDLSFKKGERLQIVNNTRKY 120

QY 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180

DB 121 DVEBGDMWLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLNENPRGT 180

QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240

DB 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240

QY 241 KHADGLCHRLTTCPTSKPQTQGLAKDAWEIPRESRLRLEVKLGCGCFGEVMMGTWNGTTR 300

DB 241 KHADGLCHRLTTCPTSKPQTQGLAKDAWEIPRESRLRLEVKLGCGCFGEVMMGTWNGTTR 300

QY 301 VALKTLPKGTMSPEAFLOEAQVMMKLRHEKLVOLYAVVSEBPYIVTEYMSKSLDPLK 360

DB 301 VALKTLPKGTMSPEAFLOEAQVMMKLRHEKLVOLYAVVSEBPYIVTEYMSKSLDPLK 360

QY 361 GETGKTLRLPOLYDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGIARLI 420

DB 361 GETGKTLRLPOLYDMAAQIASGMAYYERNYVHRDLRANILVGENLVCKVADFGIARLI 420

QY 421 EDNEYTARQAKFPFKWTAPBAALYGRFTIKSDVMSFGILTELTTGKRVPPGMVNRREV 480

DB 421 EDNEYTARQAKFPFKWTAPBAALYGRFTIKSDVMSFGILTELTTGKRVPPGMVNRREV 480

QY 481 LDQVERGYRMPCEPCBESLHDLMCQMKRKEPERPTEFYLOAFLEDYFTSTBPQYQPG 540

DB 481 LDQVERGYRMPCEPCBESLHDLMCQMKRKEPERPTEFYLOAFLEDYFTSTBPQYQPG 540

QY 541 NL 542

DB 541 NL 542

RESULT 3
AAR39706
ID AAR39706 standard; protein; 536 AA.

XX AAR39706;
AC 25-MAR-2003 (revised)
DT 23-DEC-1993 (first entry)
XX Human pp60 c-src protein.
DE Human pp60 c-src protein.
KM Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX Homo sapiens.
OS MO9314193-A1.
XX 22-JUL-1993.
PD 05-JAN-1993; 93WO-US000445.
XX 06-JAN-1992; 92US-00820011.
PR (UYA) UNIV YALE.
PA Bell L, Madri JA, Warren SL, Luthringer DJ;
PI WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX Genetically engineered endothelial cells - which exhibit enhanced cell
PT migration, urokinase-type plasminogen activator activity, and reduced
PR mononuclear cell adhesion and fibronectin prodn.
XX Disclosure; Page 75-77; 91pp; English.
PS The DNA encoding a portion or (more preferably) the entire pp60 c-src
XX polypeptide (Given in AAQ46688) is used to transform endothelial cells.
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than non-
CC transformed counterparts; have an enhanced ability to inhibit the
CC formation of thrombi and/or dissolve thrombi once they have formed and
CC exhibit reduced mononuclear cell adhesion. They can also be used to
CC improve the success of surgical procedures such as coronary angioplasty,
CC heart bypass surgery, vessel graft and stent implantation. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 536 AA;
Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 MGSNKSFKDASQRRSLPEPAENVHAGAGAFPAQTPPSKPSADGHRGSAAPAPAAE 60
DB 1 MGSNKSFKDASQRRSLPEPAENVHAGAGAFPAQTPPSKPSADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSSTVTSPQAGPLAGCVTFVALIYESTETEDLSFKKGERLQYNNTRKV 120
DB 61 PKLFGGNSSTVTSPQAGPLAGCVTFVALIYESTETEDLSFKKGERLQYNNTRKV 117
QY 121 DVREGDMLHSLSTGOTGYPSNYVAPSDSIQAEWYFGITRRESERLLNENPQT 180
DB 118 ---EGDMMLHSLSTGOTGYPSNYVAPSDSIQAEWYFGITRRESERLLNENPQT 174
QY 181 FLVSESTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 175 FLVSESTTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTQFNSLQOLVAYYS 234
QY 241 KHAAGLCHRLTTCPTSPQOTQGLAKDAWEIPRESLRLEVLDGGCFEYVWNGTTR 300
DB 235 KHAAGLCHRLTTCPTSPQOTQGLAKDAWEIPRESLRLEVLDGGCFEYVWNGTTR 294
QY 301 VAIKTLKPGTSPAPFLOEAOVMKKLRHEKLVQYAVVSEEPYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTSPAPFLOEAOVMKKLRHEKLVQYAVVSEEPYIVTEYMSKSLDPLK 354

QY 361 GENGKYLRLPOLVMAAOIASGMAVVERMNVYHRDLRAANTLVGENLVCKYADFGIARLI 420
DB 355 GETGYLRLPOLVMAAOIASGMAVVERMNVYHRDLRAANTLVGENLVCKYADFGIARLI 414
QY 421 EDNEYTARQAKFPDKMTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPQVNVREV 480
DB 415 EDNEYTARQAKFPDKMTAPALYGRFTIKSDVMSFGILLTELTTKGRVVPQVNVREV 474
QY 481 LDQYRGYRMPCEPCESLHDLMCQCKRKEPERPFEYVQAPLEDYFTSTEPQYQGE 540
DB 475 LDQYRGYRMPCEPCESLHDLMCQCKRKEPERPFEYVQAPLEDYFTSTEPQYQGE 534
QY 541 NL 542
DB 535 NL 536
RESULT 4
ID ABG95123 standard; protein; 536 AA.
XX ABG95123;
AC 04-DEC-2002 (first entry)
XX Human v-src isoform.
DE Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX Homo sapiens.
OS WO200269900-A2.
XX 12-SEP-2002.
PD 01-MAR-2002; 2002WO-US006518.
XX 01-MAR-2001; 2001US-0272751P.
PR (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
PI WPI; 2002-698710/75.
XX N-PSDB; ABS73324.
DR Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX
PS Disclosure; Page 310-312; 389pp; English.
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular

CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein
 CC
 XX

SO Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 5; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```

QY 1 MGSNKSXPXASORRRSLRPAENVHAGGAFPSQTPSKPASADGHRGSAFAFAAAE 60
DB 1 MGSNKSXPXASORRRSLRPAENVHAGGAFPSQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLFGFNSSDVTYSPQRAGPLAGVTFVALYDYESTRTDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDVTYSPQRAGPLAGVTFVALYDYESTRTDLSFKKGERLQIVNTRKV 117
QY 121 DVEEGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 180
DB 121 DVEEGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 180
QY 118 ---EGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 174
DB 118 ---EGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 174
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 240
DB 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 234
QY 241 KHADGLCHRLTTYCPTSKPQTQGLADAWAIPRESRLRLEVLAGGCGFGEVWGMGTNGTTR 300
DB 235 KHADGLCHRLTTYCPTSKPQTQGLADAWAIPRESRLRLEVLAGGCGFGEVWGMGTNGTTR 294
QY 301 VAIKTKLPGTMSPEAFQEAQVNMKRLHEKLVQLYAVVSEPIYITERYMSKSLDLFLK 360
DB 295 VAIKTKLPGTMSPEAFQEAQVNMKRLHEKLVQLYAVVSEPIYITERYMSKSLDLFLK 354
QY 361 GEGKGYRLPOLYDMAQIASGMAVYERMYVHNDLPAANILVGENLVCVADPGLARLI 420
DB 355 GEGKGYRLPOLYDMAQIASGMAVYERMYVHNDLPAANILVGENLVCVADPGLARLI 414
QY 421 EDNEYTAROGAKFPKIKWTAPAAALYGRFTIKSDVMSFGILLTETLTGKRVYPMVMREV 480
DB 415 EDNEYTAROGAKFPKIKWTAPAAALYGRFTIKSDVMSFGILLTETLTGKRVYPMVMREV 474
QY 481 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPEERPTFEYLQAFLEDYFTSTEPQYQGE 540
DB 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPEERPTFEYLQAFLEDYFTSTEPQYQGE 534
QY 541 NL 542
DB 535 NL 536

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RESULT 5

ID AAU78678 standard; protein; 536 AA.

AC AAU78678;

DT 18-JUN-2002 (first entry)

DE Human SH2/SH3 domain containing protein, v-src.

XX Protein profiling; c-src; SH2; SH3; antibody microarray;

KM protein microarray; DNA microarray; expression profiling; immunology;

XX protein analysis; proteome analysis; human; protein expression profiling.

OS Homo sapiens.

PN WO200214867-A2.

PD 21-FEB-2002.

PF 13-AUG-2001; 2001MO-US041709.

XX 11-AUG-2000; 2000US-0224939P.

PR 12-APR-2001; 2001US-0283498P.

XX (AGIL-) AGILIX CORP.

PI Chait BT, Latimer DR, Lizardi PM, Keshnar ER, Morrow JS;

XX Rott ME, Maccossich MJ, McConnell KJ;

XX WPI; 2002-304072/34.

PT Detecting multiple analytes by separating a set of reporter signals
 PT having common property from molecules lacking common property; altering
 PT signal, detecting and distinguishing altered forms of signal from each
 PT other.

PS Disclosure; Page 224; 341pp; English.

CC The invention relates to detecting (M1) multiple analytes involving
 CC separating a set of reporter signals (RS), where each RS has a common
 CC property, from molecules lacking the common property, altering the RS,
 CC and detecting and distinguishing the altered forms of the RS from each
 CC other. The method (M1) is useful for detecting multiple analytes M1 is
 CC useful for detection of analytes and biomolecules, (such as proteins,
 CC peptides and protein fragments), preferably for multiplex detection and
 CC analysis of analytes and biomolecules. M1 is useful to detect a specific
 CC analyte (in a specific sample or in multiple samples) or multiple
 CC analytes (in a single sample or multiple samples), and to gather and
 CC catalogue information about unknown analytes. M1 is useful as a detection
 CC system in a number of fields, including antibody or protein microarrays,
 CC DNA microarrays, expression profiling, comparative genomics, immunology,
 CC diagnostic assay and quality control. M1 is useful as a detection and
 CC analysis system for protein analysis, proteome analysis, proteomic,
 CC protein expression profiling, de novo protein discovery, functional
 CC genomics and protein detection. M1 increases the sensitivity and accuracy
 CC of detection of analytes of interest, and allows a complex sample of
 CC analytes to be quickly and easily catalogued in a reproducible manner. M1
 CC is compatible with techniques involving cleavage, treatment or
 CC fragmentation of a bulk sample in order to simplify the sample prior to
 CC introduction into the first stage of a multistage detection system. M1 is
 CC also compatible with any desired sample, including raw extracts and
 CC fractionated samples. The present sequence is human c-src whose SH2/SH3
 CC domains are detected in a sample, using the method of the invention
 CC
 XX

SO Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 5; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 1 MGSNKSXPXASORRRSLRPAENVHAGGAFPSQTPSKPASADGHRGSAFAFAAAE 60
DB 1 MGSNKSXPXASORRRSLRPAENVHAGGAFPSQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLFGFNSSDVTYSPQRAGPLAGVTFVALYDYESTRTDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDVTYSPQRAGPLAGVTFVALYDYESTRTDLSFKKGERLQIVNTRKV 117
QY 121 DVEEGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 180
DB 118 ---EGDWMLAHSLSTGQGYIPSNYVAPSDSIQAEEMVFGKTRRSEERLLNAENPRGT 174
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 240
DB 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQQLVAYYS 234
QY 241 KHADGLCHRLTTYCPTSKPQTQGLADAWAIPRESRLRLEVLAGGCGFGEVWGMGTNGTTR 300
DB 235 KHADGLCHRLTTYCPTSKPQTQGLADAWAIPRESRLRLEVLAGGCGFGEVWGMGTNGTTR 294

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XX 27-DEC-2002; 2002MO-US041564.
PF
XX
XX 28-DEC-2001; 2001US-0345888P.
PR
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX
XX Schmitt JM, Stork PJS;
PI
XX
XX WPI, 2003-587076/55.
DR
XX
XX N-PSDB; ADI20071.
DR
XX
XX
XX New specific-binding agent which specifically binds to Src when Src is
PT phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
PT when Ser17 is not phosphorylated, useful for identifying abnormal cell
PT proliferation.
XX
XX Disclosure; SEQ ID NO 2; 40pp; English.
XX
XX
XX The present invention relates to a specific-binding agent which
XX specifically binds to Src when Src is phosphorylated at serine at
XX position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
XX phosphorylated. The specific-binding agent is useful as a diagnostic
XX agent. The agent and the methods may also be used for treating Src-
XX positive tumors or heart disease. The present sequence represents human c-
XX Src.
XX
XX Sequence 536 AA;
SQ
XX
XX
XX Query Match 98.5%; Score 2821; DB 7; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXKASQRRSLPEAEVNHGAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
QY
XX 1 MGSNKSXPXKASQRRSLPEAEVNHGAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
DB
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
QY
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
DB
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
QY
XX 121 DVREGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 180
DB
XX 118 ---EGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 174
QY
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKYIKRLDSDGFPYITTSRTQFNSLQQLVAYYS 240
DB
XX 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKYIKRLDSDGFPYITTSRTQFNSLQQLVAYYS 234
QY
XX 241 KHAHDGCHRLTTCYCPSPKSPKOTQGLADKAMEIPRESRLPEYKLGCGCGEYVMGTMNCTTR 300
DB
XX 235 KHAHDGCHRLTTCYCPSPKSPKOTQGLADKAMEIPRESRLPEYKLGCGCGEYVMGTMNCTTR 294
QY
XX 301 VAIKTLKPGTMSPEAFLOEAQVWKQLRHEKLVOLYAVVSEPTIYVTEYMSKSLDDFLK 360
DB
XX 295 VAIKTLKPGTMSPEAFLOEAQVWKQLRHEKLVOLYAVVSEPTIYVTEYMSKSLDDFLK 354
QY
XX 361 GETGKTLRLPQLVDMAAQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGARLI 420
DB
XX 355 GETGKTLRLPQLVDMAAQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGARLI 414
QY
XX 421 ENDEYVARQAGAKPIKMTAPEALYGRFTTKSDVMSFGILLTTLTKGRVPYGMNREV 480
DB
XX 415 ENDEYVARQAGAKPIKMTAPEALYGRFTTKSDVMSFGILLTTLTKGRVPYGMNREV 474
QY
XX 481 LDQVERGYRMPCEPCESESLHDLCCQWKEPERPFEEYLOAFLEDDYFTSTEPQVQGE 540
DB
XX 475 LDQVERGYRMPCEPCESESLHDLCCQWKEPERPFEEYLOAFLEDDYFTSTEPQVQGE 534
QY
XX 541 NL 542
XX
XX 535 NL 536
DB
```

```
RESULT 8
ADL22904
ID ADL22904 standard; protein, 536 AA.
XX
XX ADL22904;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human MP2153 polypeptide sequence SEQ ID NO: 24.
DE
XX
XX human; MP2153; p21; p53; cancer.
KM
XX
XX Homo sapiens.
OS
XX
XX WO2004015069-A2.
EN
XX
XX 19-FEB-2004.
PD
XX
XX 06-AUG-2003; 2003MO-US024505.
PF
XX
XX 07-AUG-2002; 2002US-0401701P.
PR
XX 16-SEP-2002; 2002US-0411017P.
PR
XX 30-DEC-2002; 2002US-0437107P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Francis-Liang H, Friedman L, Kidd T, Roche S, Belvin M;
XX Plozman GD, Lickteig K, Zhang H, Amundsen CD;
XX
XX WPI; 2004-180653/17.
DR
XX
XX N-PSDB; ADL22887.
DR
XX
XX
XX Identifying a candidate p21 or p53 pathway modulating agent using an
PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
PT breast cancer.
XX
XX Example 3; Page 87-90; 110pp; English.
XX
XX
XX The present invention relates to a method of identifying a candidate p21
XX or p53 pathway modulating agent. This comprises providing an assay system
XX comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
XX acid, contacting the assay system with a test agent, where in its
XX presence the system provides a reference activity, and detecting a test
XX agent-biased activity of the assay system, wherein a difference between
XX the test agent-biased activity and the reference activity identifies the
XX test agent as a candidate p21 or p53 pathway modulating agent. The
XX methods and compositions of the present invention are useful for the
XX diagnosis and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the p21 or p53 pathway, such as
XX cancer, preferably colon or head and neck cancer. The present sequence is
XX a human MP2153 protein sequence of the invention.
XX
XX Sequence 536 AA;
SQ
XX
XX
XX Query Match 98.5%; Score 2821; DB 8; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXKASQRRSLPEAEVNHGAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
QY
XX 1 MGSNKSXPXKASQRRSLPEAEVNHGAGGAPASQTPSPKASADGHRGSAAPAPAAE 60
DB
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
QY
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
DB
XX 61 PKLFGGNSDVTYSPQRAPIAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTKRV 120
QY
XX 121 DVREGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 180
DB
XX 118 ---EGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 174
QY
XX 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKIKYIKRLDSDGFPYITTSRTQFNSLQQLVAYYS 240
DB
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Db      175 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKIKRLDSGGFYITSRTOFNSLQDLVAYYS 234
Qy      241 KHADGLCHRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLAGGCGEGVMWGTWGTTR 300
Db      235 KHADGLCHRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLAGGCGEGVMWGTWGTTR 294
Qy      301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 360
Db      295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 354
Qy      361 GETGKYLRPLQVMAAQIASGMAYVERMNVVHDLAANTLVGENIVCKVADGLARLI 420
Db      355 GETGKYLRPLQVMAAQIASGMAYVERMNVVHDLAANTLVGENIVCKVADGLARLI 414
Qy      421 EDNEYTAROGAKPEIKWTAPBAALYGRFTIKSDVMSFGILLTBLTTKGRVYPGMVNRV 480
Db      415 EDNEYTAROGAKPEIKWTAPBAALYGRFTIKSDVMSFGILLTBLTTKGRVYPGMVNRV 474
Qy      481 LDQVERGYRMPCEPCEPSLHDLQCQWRKEPERPFEYLOAFLEDFYFSTEPQYORGE 540
Db      475 LDQVERGYRMPCEPCEPSLHDLQCQWRKEPERPFEYLOAFLEDFYFSTEPQYORGE 534
Qy      541 NL 542
Db      535 NL 536

```

RESULT 9

ADQ88400 standard; protein; 536 AA.

ADQ88400;

07-OCT-2004 (first entry)

Human wild-type tyrosine kinase protein p60.

Cellular oncogene Src; c-Src; tyrosine kinase protein p60; cancer; infection; inflammation; tumour; gene therapy; human.

Homo sapiens.

US6764833-B1.

20-JUL-2004.

24-NOV-1999; 99US-00444711.

24-NOV-1999; 99US-00444711.

(UYSF-) UNIV SOUTH FLORIDA.

Yeastman TJ, Irbay RB;

WPI; 2004-532511/51.

N-PSDB; ADQ88399.

New isolated c-Src tyrosine kinase polynucleotide, useful for treating diseases associated or caused by mutant Src, cancer, or for preventing infection, inflammation, or tumor formation.

Disclosure; SEQ ID NO 2; 29pp; English.

The invention relates to novel mutant cellular oncogene Src (c-Src) which codes for mutant tyrosine kinase protein p60. c-Src sequences are useful for treating diseases which are associated or caused by mutant Src. They are useful for treating cancer, to delay or prevent infection, inflammation or tumour formation. The invention is also useful in gene therapy. The present sequence is human wild-type tyrosine kinase protein p60.

Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```

Qy      1 MGSNKSXPXASORRSLRLEPAENVHAGAGAFPASQTPSPKASADGRGSPAPAAAE 60
Db      1 MGSNKSXPXASORRSLRLEPAENVHAGAGAFPASQTPSPKASADGRGSPAPAAAE 60
Qy      61 PKLFGFNSSDYTVSPQAPRPLAGVTFVALYDRESRTETDLSFKKGERLQIVNTRKV 120
Db      61 PKLFGFNSSDYTVSPQAPRPLAGVTFVALYDRESRTETDLSFKKGERLQIVNTRKV 117
Qy      121 DVREGDWMLAHSJTGQTYIPSNYVAPSDSIQAEWYFGKITRRESRLLNENPRGT 180
Db      118 ---EGDWMLAHSJTGQTYIPSNYVAPSDSIQAEWYFGKITRRESRLLNENPRGT 174
Qy      181 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKIKRLDSGGFYITSRTOFNSLQDLVAYYS 240
Db      175 FLVRESSTTGAYCLSVSDPDNAKGLNVKHKIKRLDSGGFYITSRTOFNSLQDLVAYYS 234
Qy      241 KHADGLCHRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLAGGCGEGVMWGTWGTTR 300
Db      235 KHADGLCHRLTTCPTSKPQTQGLAKDAMEIPRESLRLEVLAGGCGEGVMWGTWGTTR 294
Qy      301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 360
Db      295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPITYITERNYSGSLDPLK 354
Qy      361 GETGKYLRPLQVMAAQIASGMAYVERMNVVHDLAANTLVGENIVCKVADGLARLI 420
Db      355 GETGKYLRPLQVMAAQIASGMAYVERMNVVHDLAANTLVGENIVCKVADGLARLI 414
Qy      421 EDNEYTAROGAKPEIKWTAPBAALYGRFTIKSDVMSFGILLTBLTTKGRVYPGMVNRV 480
Db      415 EDNEYTAROGAKPEIKWTAPBAALYGRFTIKSDVMSFGILLTBLTTKGRVYPGMVNRV 474
Qy      481 LDQVERGYRMPCEPCEPSLHDLQCQWRKEPERPFEYLOAFLEDFYFSTEPQYORGE 540
Db      475 LDQVERGYRMPCEPCEPSLHDLQCQWRKEPERPFEYLOAFLEDFYFSTEPQYORGE 534
Qy      541 NL 542
Db      535 NL 536

```

RESULT 10

ADQ97772 standard; protein; 536 AA.

ADQ97772;

07-OCT-2004 (first entry)

Human cancer associated sequence HPI0-043, SEQ ID 749.

Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

Homo sapiens.

WO2004060304-A2.

22-JUL-2004.

22-DEC-2003; 2003WO-US041389.

27-DEC-2002; 2002US-00330773.

(SAGR-) SAGRES DISCOVERY INC.

Morris DW, Malandro MS;

WPI; 2004-543781/52.

```

XX OS Unidentified.
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX PH Key Location/Qualifiers
XX Modified-site 216
PT /note= "Tyr phosphorylation site"
PT Modified-site 419
PT /note= "Tyr phosphorylation site"
PT Modified-site 530
PT /note= "Tyr phosphorylation site"
XX PN WC2004092703-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004MO-US010834.
XX PR 11-APR-2003; 2003US-0462083P.
XX PR 11-APR-2003; 2003US-0462472P.
XX PR 25-JUL-2003; 2003US-0490057P.
XX PR 08-MAR-2004; 2004US-0551311P.
XX PR 19-MAR-2004; 2004US-0554701P.
XX PR 08-APR-2004; 2004US-00821231.
XX PA (Purd ) PURDUE RES FOUND.
XX PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
XX WPI; 2004-784629/77.
XX DR
XX PT Obtaining structural characteristic information for separation and
PT detection of e.g. proteins comprises irradiating a region formed by
PT evaporating specimen-containing solvent in a droplet on planar solvo-
PT phobic sample support.
XX PS Example C; Page 25; 91pp; English.
XX CC The present sequence is that of proto-oncogene protein tyrosine kinase
CC Src (p60-src, c-src). The invention relates to the combined use of solid
CC substrates, micro-deposition techniques, spectral imaging methods, and
CC data processing to facilitate the concentration and separate detection of
CC biological molecules including proteins, peptides, polysaccharides,
CC glycans and nucleotides, in a liquid mixture, using spectral analysis
CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
CC assisted laser desorption/ionization (MALDI) time-of-flight mass
CC spectrometry. The methods were demonstrated in examples from the high
CC resolution using peptide fragments of Src. These demonstrated the high
CC level of analyte discrimination that can be achieved and that the method
CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
CC of physiologically important proteins.
XX SQ Sequence 536 AA;
XX Query Match 98.5%; Score 2821; DB 8; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX New isolated cancer associated nucleic acids comprising at least 10
XX contiguous nucleotides, useful for diagnosing, preventing and/or treating
XX cancers such as leukemia and lymphoma.
XX PS Claim 1; SEQ ID NO 749; 199pp; English.
XX CC The present invention relates to cancer associated sequences (ADQ97025-
XX ADQ98004). The sequences are useful for the diagnosis, prevention and/or
XX treatment of cancer, such as leukemia and lymphoma. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 536 AA;
XX
XX Query Match 98.5%; Score 2821; DB 8; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 61 PKLFGFNSSDVTSPQRAGPLAGVTTFYALYDYESRTETDLSFKKGERLQIVNNTTKV 120
XX 61 PKLFGFNSSDVTSPQRAGPLAGVTTFYALYDYESRTETDLSFKKGERLQIVNNTTKV 120
XX 61 PKLFGFNSSDVTSPQRAGPLAGVTTFYALYDYESRTETDLSFKKGERLQIVNNTTKV 120
XX 121 DVREGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 180
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XX 118 ---EGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 174
XX 118 ---EGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 174
XX 181 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 240
XX 181 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 240
XX 175 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 234
XX 175 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 234
XX 241 KHADELCHRLTTCVPTSPKPTQGLAKDAWEIPRESLLEVLKGGCGEYVMGTMTGTR 300
XX 241 KHADELCHRLTTCVPTSPKPTQGLAKDAWEIPRESLLEVLKGGCGEYVMGTMTGTR 300
XX 235 KHADELCHRLTTCVPTSPKPTQGLAKDAWEIPRESLLEVLKGGCGEYVMGTMTGTR 294
XX 235 KHADELCHRLTTCVPTSPKPTQGLAKDAWEIPRESLLEVLKGGCGEYVMGTMTGTR 294
XX 301 VAIKTLKPTGMSPEAFLOEAQVVKQLRHEKLVOLYAVVSEPTIYIVTEYMSKSLDPLK 360
XX 301 VAIKTLKPTGMSPEAFLOEAQVVKQLRHEKLVOLYAVVSEPTIYIVTEYMSKSLDPLK 360
XX 295 VAIKTLKPTGMSPEAFLOEAQVVKQLRHEKLVOLYAVVSEPTIYIVTEYMSKSLDPLK 354
XX 295 VAIKTLKPTGMSPEAFLOEAQVVKQLRHEKLVOLYAVVSEPTIYIVTEYMSKSLDPLK 354
XX 361 GEGKTLRLPOLYDMAQAQISGMAVYERMYVHRDLAANILVGENLVCCVADFGARLI 420
XX 361 GEGKTLRLPOLYDMAQAQISGMAVYERMYVHRDLAANILVGENLVCCVADFGARLI 420
XX 355 GEGKTLRLPOLYDMAQAQISGMAVYERMYVHRDLAANILVGENLVCCVADFGARLI 414
XX 355 GEGKTLRLPOLYDMAQAQISGMAVYERMYVHRDLAANILVGENLVCCVADFGARLI 414
XX 421 EDNEYTAROGAKPPIKWTARPEALYGRFTIKSDVMSFGILLTETLTGRTVPGMVNREV 480
XX 421 EDNEYTAROGAKPPIKWTARPEALYGRFTIKSDVMSFGILLTETLTGRTVPGMVNREV 480
XX 415 EDNEYTAROGAKPPIKWTARPEALYGRFTIKSDVMSFGILLTETLTGRTVPGMVNREV 474
XX 415 EDNEYTAROGAKPPIKWTARPEALYGRFTIKSDVMSFGILLTETLTGRTVPGMVNREV 474
XX 481 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDFYTSPEYQPGE 540
XX 481 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDFYTSPEYQPGE 540
XX 475 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDFYTSPEYQPGE 534
XX 475 LDQVERGYRMPCEPECESLHDLMCQWRKEPERPTFEYLQAFLEDFYTSPEYQPGE 534
XX 541 NL 542
XX 541 NL 542
XX 535 NL 536
XX 535 NL 536
XX
XX RESULT 11
XX ADU04517
XX ID ADU04517 standard; peptide; 536 AA.
XX
XX ADU04517;
XX
XX 13-JUN-2005 (first entry)
XX
XX Protein tyrosine kinase Src.
XX
XX Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;
XX protein structure; enzyme; EC_2.7.1.112.
XX

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XX OS Unidentified.
XX PH Key Location/Qualifiers
XX Modified-site 216
PT /note= "Tyr phosphorylation site"
PT Modified-site 419
PT /note= "Tyr phosphorylation site"
PT Modified-site 530
PT /note= "Tyr phosphorylation site"
XX PN WC2004092703-A2.
XX PD 28-OCT-2004.
XX PF 09-APR-2004; 2004MO-US010834.
XX PR 11-APR-2003; 2003US-0462083P.
XX PR 11-APR-2003; 2003US-0462472P.
XX PR 25-JUL-2003; 2003US-0490057P.
XX PR 08-MAR-2004; 2004US-0551311P.
XX PR 19-MAR-2004; 2004US-0554701P.
XX PR 08-APR-2004; 2004US-00821231.
XX PA (Purd ) PURDUE RES FOUND.
XX PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
XX WPI; 2004-784629/77.
XX DR
XX PT Obtaining structural characteristic information for separation and
PT detection of e.g. proteins comprises irradiating a region formed by
PT evaporating specimen-containing solvent in a droplet on planar solvo-
PT phobic sample support.
XX PS Example C; Page 25; 91pp; English.
XX CC The present sequence is that of proto-oncogene protein tyrosine kinase
CC Src (p60-src, c-src). The invention relates to the combined use of solid
CC substrates, micro-deposition techniques, spectral imaging methods, and
CC data processing to facilitate the concentration and separate detection of
CC biological molecules including proteins, peptides, polysaccharides,
CC glycans and nucleotides, in a liquid mixture, using spectral analysis
CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
CC assisted laser desorption/ionization (MALDI) time-of-flight mass
CC spectrometry. The methods were demonstrated in examples from the high
CC resolution using peptide fragments of Src. These demonstrated the high
CC level of analyte discrimination that can be achieved and that the method
CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
CC of physiologically important proteins.
XX SQ Sequence 536 AA;
XX Query Match 98.5%; Score 2821; DB 8; Length 536;
XX Best Local Similarity 98.9%; Pred. No. 8.2e-242;
XX Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
XX
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 1 MGSNKSXPXASQRRSLRSLPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
XX 61 PKLFGFNSSDVTSPQRAGPLAGVTTFYALYDYESRTETDLSFKKGERLQIVNNTTKV 120
XX 61 PKLFGFNSSDVTSPQRAGPLAGVTTFYALYDYESRTETDLSFKKGERLQIVNNTTKV 120
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XX 121 DVREGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 180
XX 121 DVREGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 180
XX 118 ---EGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 174
XX 118 ---EGDMWMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRSEELLNAENPRGT 174
XX 181 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 240
XX 181 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 240
XX 175 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 234
XX 175 FLVRSSETTGAYCIVSDFDNAKGLNVKIRKLDGSGFYITSRTQFNSIQQLVAYYS 234
XX

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QY 241 KHADELCHRLTTVCPTSKPOTGLAKDAWEIPRESLRLEVLGGCCFGEVMMGTNGTTR 300
DB 235 KHADELCHRLTTVCPTSKPOTGLAKDAWEIPRESLRLEVLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPPGVNREV 480
DB 415 EDNEYTAROGAKFPKIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPPGVNREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLOAFLEDYFTSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLOAFLEDYFTSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536

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RESULT 12
ADY84076 standard; protein; 536 AA.

```

XX AC ADY84076;
XX DT 02-JUN-2005 (first entry)
XX DE Human Src protein isoform 2 SEQ ID NO:2.
XX KM pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX OS Homo sapiens.
XX PN BPI413887-A1.
XX PD 28-APR-2004.
XX PF 22-OCT-2002; 2002EP-00292608.
XX PR 22-OCT-2002; 2002EP-00292608.
XX PA (AVENTIS PHARMA SA.
XX PI Merckken L, Zambirano N, Russo T;
XX DR WPI; 2004-332834/31.
XX PT Identifying therapeutic compound for treating Alzheimer's disease,
XX PT involves providing Src protein and determining inhibitory effect of
XX PS compound on Src activity.
XX PS Claim 4; SEQ ID NO 2; 45pp; English.
XX CC The invention relates to a novel method for identifying (M1) a
XX CC therapeutic compound for the treatment of Alzheimer's disease, involving
XX CC providing a Src protein and determining the inhibitory effect of a
XX CC compound on the Src activity. The method optionally involves providing a
XX CC sequence which regulates Src expression and determining if a compound
XX CC inhibits the expression of Src protein. A compound of the invention has
XX CC neuroprotective and nootropic activity. The compound identified by the
XX CC method of the invention is useful for preparing a pharmaceutical for
XX CC treating Alzheimer's disease. The present sequence represents isoform 2
XX CC of human Src protein.
XX SQ Sequence 536 AA;

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Query Match 98.5%; Score 2821; DB 8; Length 536;
Best Local Similarity 98.9%; Pred. No. 8.2e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```

QY 1 MGSNKSXPKQASQRRSLPEAENVHAGGGAFPASQTPSPKASADGHRGPSAFAAPAAAE 60
DB 1 MGSNKSXPKQASQRRSLPEAENVHAGGGAFPASQTPSPKASADGHRGPSAFAAPAAAE 60
QY 61 PKLFGGNSSPTVTSPQAGPLAGVTTFVALIYTESFTEDLSFKKEERQIVNNTKV 120
DB 61 PKLFGGNSSPTVTSPQAGPLAGVTTFVALIYTESFTEDLSFKKEERQIVNNTKV 117
QY 121 DVREGDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNAENPQGT 180
DB 118 --BQDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNAENPQGT 174
QY 181 FLVRESSTTKGAYCLSYSDPDNAKGLNVKHYIKRLDSGGFYITSRQFNSLQQLVAYYS 240
DB 175 FLVRESSTTKGAYCLSYSDPDNAKGLNVKHYIKRLDSGGFYITSRQFNSLQQLVAYYS 234
QY 241 KHADELCHRLTTVCPTSKPOTGLAKDAWEIPRESLRLEVLGGCCFGEVMMGTNGTTR 300
DB 235 KHADELCHRLTTVCPTSKPOTGLAKDAWEIPRESLRLEVLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIOEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHDLRAANILVGENLVCKVADFGIARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHDLRAANILVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPPGVNREV 480
DB 415 EDNEYTAROGAKFPKIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPPGVNREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLOAFLEDYFTSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEFYLOAFLEDYFTSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536

```

RESULT 13
ADY94834 standard; protein; 536 AA.

```

XX AC ADY94834;
XX DT 10-MAR-2005 (first entry)
XX DE Human wild type c-Src protein.
XX KM cytostatic; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
XX KW breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.
XX OS Homo sapiens.
XX PN US2004261142-A1.
XX PD 23-DEC-2004.
XX PF 09-JUN-2004; 2004US-00887588.
XX PR 24-NOV-1999; 99US-00444711.
XX PA (YEATMAN T J.
XX PA (IRBY/) IRBY R B.
XX PI Yeatman TJ, Irby RB;
XX SQ

```

DR WPI: 2005-038910/04.
 DR N-PSDB; ADV94833.
 XX New truncated c-Src polypeptide, useful for treating and/or preventing
 PT clinical conditions associated with or caused by Src mutation, e.g.
 PT tumors.
 XX
 XX Disclosure; SEQ ID NO 2; 28pp; English.
 XX
 CC The invention relates to a truncated c-Src polypeptide comprising a
 CC sequence of 530 amino acids given in the specification. The polypeptide,
 CC composition and method are useful for treating and/or preventing clinical
 CC conditions associated with or caused by Src mutation e.g. tumors
 CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
 CC the wild type c-Src protein.
 XX
 XX Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 9; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPXOASGRRLSLPEAENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSXPXOASGRRLSLPEAENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY PKLFGFNSSDVTYSQORAGPLAGGTTTVALYDSERTTDLSPFKGGERLQIVNTRKY 120
 DB 61 PKLFGFNSSDVTYSQORAGPLAGGTTTVALYDSERTTDLSPFKGGERLQIVNTRKY 117
 QY 121 DVREGDMWLAHSLSTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
 DB 118 ---EGDMWLAHSLSTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 174
 QY 181 FLVRESEETTKGAYCLSVSPDNNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAYYS 240
 DB 175 FLVRESEETTKGAYCLSVSPDNNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAYYS 234
 QY 241 KHADGICHLTTCYCPSTKPTQGLANDAMEIPRESRLRLEKLGQCGGEGEVMGTNGTTR 300
 DB 235 KHADGICHLTTCYCPSTKPTQGLANDAMEIPRESRLRLEKLGQCGGEGEVMGTNGTTR 294
 QY 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLK 360
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEPIYIVTEYMSKSLDLFLK 354
 QY 361 GETGKYLRLPOLVDMAAQINAGNAVYERMYVHARDLRANILVGENLVCKVADFGIARLI 420
 DB 355 GETGKYLRLPOLVDMAAQINAGNAVYERMYVHARDLRANILVGENLVCKVADFGIARLI 414
 QY 421 EDNEYTAROGAKRPICKTAPBALYGRFTKSDVWSFGILLTELTKGRVPTGGMNREV 480
 DB 415 EDNEYTAROGAKRPICKTAPBALYGRFTKSDVWSFGILLTELTKGRVPTGGMNREV 474
 QY 481 LDQVEGYMPCCPECPESLHDMCCOMRKEPERPFLEYLQAFLEDYFTSTPEYOXPGE 540
 DB 475 LDQVEGYMPCCPECPESLHDMCCOMRKEPERPFLEYLQAFLEDYFTSTPEYOXPGE 534
 QY 541 NL 542
 DB 535 NL 536

RESULT 14
 AEA35914
 ID AEA35914 standard; procein; 536 AA.

AC AEA35914;
 XX
 XX 25-AUG-2005 (first entry)
 DT
 XX Human Src kinase amino acid sequence SEQ ID NO:1.
 DE
 XX

KM Src family kinase; Src kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX
 FT Misc-difference 238
 FT /note= "constant amino acid K in domain SH2"
 FT Misc-difference 341
 FT /note= "constant amino acid T in domain SH2"
 FT Misc-difference 530
 FT /note= "constant amino acid Y in domain SH1"
 FT
 PN EP1541694-A1.
 XX
 PD 15-JUN-2005.
 XX
 XX 12-DEC-2003; 2003EP-00028713.
 XX
 PR 12-DEC-2003; 2003EP-00028713.
 XX
 PA (SIRE-) SIRENADE PHARM AG.
 XX
 PI Obermeier A; Bieger B;
 XX
 DR WPI: 2005-428084/44.
 XX
 PT Identifying compound which modulates Src family kinase (SFK) activity, by
 PT contacting cells expressed with SFK or mutated SFK with test compound,
 PT where change in phenotype of cells indicates that test compound modulates
 PT SFK activity.
 XX
 PS Disclosure; SEQ ID NO 1; 114pp; English.
 XX
 CC The invention relates to a method (M1) for identifying, selecting and/or
 CC characterizing a compound which modulates Src family kinase (SFK)
 CC activity, by expressing nucleic acids encoding SFK or mutated SFK in
 CC cells, contacting cells with test compound and determining whether
 CC phenotype of cells is changed as compared with phenotype of cells not
 CC expressed with above nucleic acids, where difference in phenotype
 CC indicates that test compound modulate SFK activity. Also described: (1) a
 CC compound (I) identified, selected and/or characterized by (M1); and (2) a
 CC pharmaceutical composition (PC1) containing (I), and a carrier, adjuvant
 CC or vehicle. (I) is useful as a medicament, particularly for the treatment
 CC of diseases, which are at least in part caused by a Src family kinase.
 CC (1) and PC1 are useful for producing a medicament for the treatment of
 CC diseases, which are at least in part caused by a Src family kinase,
 CC particularly by a dysfunction of a Src family kinase, in particular
 CC cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis,
 CC symptomatic treatment of bone metastasis, rheumatoid arthritis,
 CC inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
 CC versus host disease, T-cell mediated hypersensitivity disease,
 CC Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
 CC pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
 CC or reperfusion injury, allergic disease, atopic dermatitis, transplant
 CC rejection or allergic rhinitis. The present sequence represents human Src
 CC kinase, which is given in the exemplification of the present invention.
 XX
 XX Sequence 536 AA;

Query Match 98.5%; Score 2821; DB 9; Length 536;
 Best Local Similarity 98.9%; Pred. No. 8.2e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPXOASGRRLSLPEAENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSXPXOASGRRLSLPEAENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY PKLFGFNSSDVTYSQORAGPLAGGTTTVALYDSERTTDLSPFKGGERLQIVNTRKY 120
 DB 61 PKLFGFNSSDVTYSQORAGPLAGGTTTVALYDSERTTDLSPFKGGERLQIVNTRKY 117
 QY 121 DVREGDMWLAHSLSTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
 DB 118 ---EGDMWLAHSLSTQGTGYPNSNYVAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 174

Db 118 ---EGDWMWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 174
 QY 181 FLVRESSTTGAYCLSYSDPDMAGLVNKKYKIKLDSGGYITSRTOFNSLQOLVAYYS 240
 Db 175 FLVRESSTTGAYCLSYSDPDMAGLVNKKYKIKLDSGGYITSRTOFNSLQOLVAYYS 234
 QY 241 KHAAGLCHRLTTVCPSTSPOTQGLAKDAMEIPRESLRLVYLGGCGEVMWGTMNGTTR 300
 Db 235 KHAAGLCHRLTTVCPSTSPOTQGLAKDAMEIPRESLRLVYLGGCGEVMWGTMNGTTR 294
 QY 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDPLK 360
 Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDPLK 354
 QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNTVHRDLAANILVGENLVCKVADFGLARLI 420
 Db 355 GETGKYRLPOLVMAAQIASGMAYVERMNTVHRDLAANILVGENLVCKVADFGLARLI 414
 QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVYPGMVNREV 480
 Db 415 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVYPGMVNREV 474
 QY 481 LDQYERGYRMPCEPCESLHDLQCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYOPGE 540
 Db 475 LDQYERGYRMPCEPCESLHDLQCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYOPGE 534
 QY 541 NL 542
 Db 535 NL 536

RESULT 15

ADY84080
ID ADY84080 standard; protein; 549 AA.

XX ADY84080;

XX 02-JUN-2005 (first entry)

XX Human Src cDNA encoded amino acid #1.

XX pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;

KM Src tyrosine kinase.

XX Homo sapiens.

XX EPI413887-A1.

XX 28-APR-2004.

XX 22-OCT-2002; 2002EP-00292608.

XX 22-OCT-2002; 2002EP-00292608.

XX (AVET) AVENTIS PHARMA SA.

XX Mercken L, Zambirano N, Russo T;

XX WPI; 2004-333834/31.

XX N-PSDB; ADY84078.

XX Identifying therapeutic compound for treating Alzheimer's disease,

XX PT involves providing Src protein and determining inhibitory effect of

XX compound on Src activity.

XX PS Disclosure; SEQ ID NO 4; 45pp; English.

XX The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has

CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence is encoded by the
 CC human Src cDNA. The sequence is represented as part of SEQ ID NO:4 in the
 CC sequence listing of the specification.

XX Sequence 549 AA;

Query Match 98.5%; Score 2821; DB 8; Length 549;
 Best Local Similarity 98.9%; Pred. No. 8.6e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPXASORRSLBPENYHAGGAGFAPSOTPSKXPASADGHRGSPAPAPAAE 60
 Db 14 MGSNKSXPXASORRSLBPENYHAGGAGFAPSOTPSKXPASADGHRGSPAPAPAAE 73
 QY 61 PKLFGFNSSDVTYSPORAGPLAGVTTFVALYDESRTETDLSFKKGERLQIVNNTKRV 120
 Db 74 PKLFGFNSSDVTYSPORAGPLAGVTTFVALYDESRTETDLSFKKGERLQIVNNTKRV 130
 QY 121 DVREGDWMWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 180
 Db 131 ---EGDWMWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 187
 QY 181 FLVRESSTTGAYCLSYSDPDMAGLVNKKYKIKLDSGGYITSRTOFNSLQOLVAYYS 240
 Db 188 FLVRESSTTGAYCLSYSDPDMAGLVNKKYKIKLDSGGYITSRTOFNSLQOLVAYYS 247
 QY 241 KHAAGLCHRLTTVCPSTSPOTQGLAKDAMEIPRESLRLVYLGGCGEVMWGTMNGTTR 300
 Db 248 KHAAGLCHRLTTVCPSTSPOTQGLAKDAMEIPRESLRLVYLGGCGEVMWGTMNGTTR 307
 QY 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDPLK 360
 Db 308 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDPLK 367
 QY 361 GETGKYRLPOLVMAAQIASGMAYVERMNTVHRDLAANILVGENLVCKVADFGLARLI 420
 Db 368 GETGKYRLPOLVMAAQIASGMAYVERMNTVHRDLAANILVGENLVCKVADFGLARLI 427
 QY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVYPGMVNREV 480
 Db 428 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVYPGMVNREV 487
 QY 481 LDQYERGYRMPCEPCESLHDLQCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYOPGE 540
 Db 488 LDQYERGYRMPCEPCESLHDLQCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYOPGE 547
 QY 541 NL 542
 Db 548 NL 549

Search completed: June 5, 2006, 17:07:40
 Job time : 119.845 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.7603 Seconds

(without alignments)

2396.538 Million cell updates/sec

Title: US-10-691-079-1

Sequence: 1 MGSNKSXPKNASQRRSLRP.....AFLEDYPTSTPEYQPGENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2863	100.0	542	1	TVHUSC
2	2820.5	98.5	541	1	A43610
3	2648.5	92.5	533	1	TVCHS
4	2608.5	91.1	587	1	TVFVPR
5	2601.5	90.9	568	1	TVFVSI
6	2586.5	90.3	557	1	TVFVSI
7	2503.5	87.4	526	1	TVFV60
8	2484.5	86.8	526	2	S20808
9	2478.5	86.6	526	1	OKFVVR
10	2471.5	86.3	526	2	S15582
11	2468.5	86.2	526	1	TVFVR
12	2453.5	85.7	526	2	S26420
13	2450	85.6	532	1	B34104
14	2449	85.5	532	1	A34104
15	2440.5	85.2	545	2	S52313
16	2433.5	85.0	546	2	S52314
17	2405	84.0	523	1	TVFVMT
18	2121.5	74.1	537	1	A45501
19	2110.5	73.7	543	1	TVHUS
20	2108.5	73.6	541	1	TVCHS
21	2105.5	73.5	541	2	S15645
22	2052.5	71.2	544	2	S15153
23	2039.5	71.2	528	1	TVFVSI
24	1965	68.6	534	1	A44991
25	1947.5	68.0	537	2	S15152
26	1943	67.9	534	1	S33568
27	1936	67.6	536	2	S33569
28	1919.5	67.0	537	1	TVHUSY
29	1916.5	66.9	542	2	A49114

30	1910	66.7	539	2	B49114	protein-tyrosine k
31	1908.5	66.7	537	1	A43806	protein-tyrosine k
32	1843	64.0	529	1	TVHUR	protein-tyrosine k
33	1832	64.0	517	2	A43807	protein-tyrosine k
34	1800	62.9	517	2	S24547	protein-tyrosine k
35	1594	55.7	663	1	TVFVVR	protein-tyrosine k
36	1587.5	55.4	509	1	TVHAST	protein-tyrosine k
37	1573	54.9	392	2	S04205	protein-tyrosine k
38	1522.5	53.2	505	1	TVHURC	protein-tyrosine k
39	1517.5	52.8	503	1	JQ1321	protein-tyrosine k
40	1512.5	52.0	503	1	TVMSHC	protein-tyrosine k
41	1491	52.1	507	1	A39939	protein-tyrosine k
42	1461	51.0	509	1	OKHULK	protein-tyrosine k
43	1461	51.0	512	1	TVHULX	protein-tyrosine k
44	1453	50.8	512	1	I56160	protein-tyrosine k
45	1452	50.7	509	1	I48845	protein-tyrosine k

ALIGNMENTS

RESULT 1

TVHUSC protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004

C:Accession: A26891; A61083; B61083; A23287; A28832; B34704

R:Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.

A:Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A:Insertions: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 378/3; 430/1; 474/1
C:Function: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; p16
F:1-542/Product: protein-tyrosine kinase src; neuronal #status predicted <MAT>
F:1-117,124-542/Product: protein-tyrosine kinase src; short form #status predicted <MA2>
F:91-146/Domains: SH3 homology <SH3>
F:157-254/Domains: SH2 homology <SH2>
F:274-532/Domains: protein kinase homology <KIN>
F:282-290/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:304/Active site: Lys #status predicted
F:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 2863; DB 1; Length 542;
Best Local Similarity 100.0%; Pred. No. 9,7e-134;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPKASQRRSLRPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLRPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRTEEDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRTEEDLSFKKGERLQIVNTRKY 120
QY 121 DVREGDWMLAHSSTQGTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 180
DB 121 DVREGDWMLAHSSTQGTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 180
QY 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKKYKIRKLDGSGFYITSRTOFNSLQQLVAAYS 240
DB 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKKYKIRKLDGSGFYITSRTOFNSLQQLVAAYS 240
QY 241 KHAADGCHRLTYTCPTSKQTOGLADAMEIPRESLRLEVKGCGCFGEVMGTMNGTTR 300
DB 241 KHAADGCHRLTYTCPTSKQTOGLADAMEIPRESLRLEVKGCGCFGEVMGTMNGTTR 300
QY 301 VALKTLKPGTMSPEALQEAQVMKKLRHEKLVQLVAVSEEPYITVEYMSKSLDPLFK 360
DB 301 VALKTLKPGTMSPEALQEAQVMKKLRHEKLVQLVAVSEEPYITVEYMSKSLDPLFK 360
QY 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
QY 481 LDQVERGYRMPCEPCEBSLHDLMOCKMRKEPERFTPEYLAFLBEDYFTSTPEYQOPGE 540
DB 481 LDQVERGYRMPCEPCEBSLHDLMOCKMRKEPERFTPEYLAFLBEDYFTSTPEYQOPGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
A43610
protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse
N:Alternate names: Rouse sarcoma oncogene
C:Species: Mus musculus (house mouse)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C:Accession: A43610
R:Martinez, R.; Mathey-Prevot, B.; Bernard, A.; Baltimore, D.
Science 237, 411-415, 1987
A:Title: Neuronal p60(c-src) contains a six-amino acid insertion relative to its non-ne
A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610
A:Molecule type: mRNA
A:Residues: 1-541 <MAR>
A:Cross-references: UNIPROT:P05480; UNIPARC:UP100000161D19; GB:U17031; NID:9201056; P1DN;
C:Comment: The neuronal c-src has an 6 residue insertion of RLNVNR within the amino-term
C:Gene: Src
A:Gene: Src
A:Cross-references: MGI:98397
A:Map position: 2.91.0
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; p16
F:156-253/Domains: SH3 homology <SH3>
F:273-531/Domains: SH2 homology <SH2>
F:281-289/Region: protein kinase homology <KIN>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:303/Active site: Lys #status predicted
F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 98.5%; Score 2820.5; DB 1; Length 541;
Best Local Similarity 98.7%; Pred. No. 1.2e-131;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKSXPKASQRRSLRPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLRPAENVHAGGAFPASQTPSKRPASADGHRGSAAPAPAAE 59
QY 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRTEEDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPQAPGLAGVTTFYALYDYSRTEEDLSFKKGERLQIVNTRKY 119
QY 121 DVREGDWMLAHSSTQGTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 180
DB 121 DVREGDWMLAHSSTQGTGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGT 179
QY 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKKYKIRKLDGSGFYITSRTOFNSLQQLVAAYS 240
DB 181 FLVRESEETTKGAYCLSVDPDNAGKLVNKKYKIRKLDGSGFYITSRTOFNSLQQLVAAYS 239
QY 241 KHAADGCHRLTYTCPTSKQTOGLADAMEIPRESLRLEVKGCGCFGEVMGTMNGTTR 300
DB 241 KHAADGCHRLTYTCPTSKQTOGLADAMEIPRESLRLEVKGCGCFGEVMGTMNGTTR 299
QY 301 VALKTLKPGTMSPEALQEAQVMKKLRHEKLVQLVAVSEEPYITVEYMSKSLDPLFK 360
DB 301 VALKTLKPGTMSPEALQEAQVMKKLRHEKLVQLVAVSEEPYITVEYMSKSLDPLFK 359
QY 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 420
DB 361 GETGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGLARLI 419
QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 479
QY 481 LDQVERGYRMPCEPCEBSLHDLMOCKMRKEPERFTPEYLAFLBEDYFTSTPEYQOPGE 540
DB 481 LDQVERGYRMPCEPCEBSLHDLMOCKMRKEPERFTPEYLAFLBEDYFTSTPEYQOPGE 539
QY 541 NL 542
DB 540 NL 541

RESULT 3
TVCHS
protein-tyrosine kinase (BC 2.7.1.112) src - chicken
N:Alternate names: kinase-related transforming protein src
C:Species: Gallus gallus (chicken)
C>Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: A00630; I50217; A41256; C35650; A32432
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983

A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A:Reference number: A00630; MUID:83155664; PMID:6293580
A:Accession: A00630
A:Molecule type: DNA
A:Residues: 1-500; 'R', 502-533 <TAK>
A:Cross-references: UNIPROT:P00523; UNIPROT:Q90993; UNIPARC:UPI000017257F; GB:J00844; NID:15817257
R:Takeya, T.; Hanafusa, H.
Cell 34, 319, 1983
A:Reference number: A90838
A:Contents: annotation; extratum, correct translation of residue 526
R:Takeya, T.; Hanafusa, H.
J. Virol. 44, 12-18, 1982
A>Title: DNA sequence of the viral and cellular src gene of chickens: II comparison of t
A:Reference number: I50217; MUID:83059861; PMID:6292480
A:Accession: I50217
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-7 <TRA2>
A:Cross-references: UNIPARC:UPI0000118887; GB:J00908; NID:g211690; PIDN:AAA48732.1; PID:AAA48732.1; PID:AAA48732.1
A>Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr and
R:Dorai, T.; Levy, J.B.; Kang, L.; Briggge, J.S.; Wang, L.H.
Mol. Cell. Biol. 11, 4165-4176, 1991
A>Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and po
A:Reference number: A41256; MUID:91304409; PMID:1712905
A:Accession: A41256
A:Molecule type: mRNA
A:Residues: 484-533 <DOR1>
A:Cross-references: UNIPARC:UPI0000171468; GB:583579; NID:g1679964; PIDN:AAB19353.1; PID:AAA48732.1; PID:AAA48732.1
A>Note: the authors translated the codon CAG for residue 527 as Glu
R:Dorai, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A>Title: An alternative non-cytosine protein kinase product of the c-src gene in chicken
A:Reference number: A35650; MUID:90318371; PMID:2115117
A:Accession: C35650
A:Molecule type: mRNA
A:Residues: 1-182; 'DPCIP,SGCLC' <DOR2>
A:Cross-references: UNIPARC:UPI000000FFJ3A4; GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:AAA49078.1; PID:AAA49078.1
A>Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle
R:Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.
Cell 57, 763-774, 1989
A>Title: Purified maturation promoting factor phosphorylates p60(c-src) at the sites ph
A:Reference number: A32432; MUID:8524341; PMID:2470512
A:Accession: A32432
A:Molecule type: protein
A:Residues: 2-88 <SHB>
A:Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homolog
C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:17/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:734,46/Binding site: phosphate (Thr) (covalent) #status experimental
F:73/Binding site: phosphate (Ser) (covalent) #status experimental
F:235/Active site: Lys #status predicted
F:416,527/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Db 58 PRLPGGPNISDVTYSPQRAGALAGVITTFVALYDYSRTETDLSFFKGGERLQIVNNT--- 114

Qy 121 DVRGDDMWLAHSLSTGQGTGYIPSNVYAPSDSIOAEWYFSGKITRRBSERLLINANPRGT 180

Db 115 ---EGDWMLAHSLTTGQGTGYIPSNVYAPSDSIOAEWYFSGKITRRBSERLLINANPRGT 171

Qy 181 FLVRSSETTKGAYCYLSVSPFDNAKGLNVGHYKTRKLDGSGEFTYTSRQFNSLOOLVAAYS 240

Db 172 FLVRSSETTKGAYCYLSVSPFDNAKGLNVGHYKTRKLDGSGEFTYTSRQFNSLOOLVAAYS 231

Qy 241 KHADGLCHRLTLYVCPTSPKQTOGLADAMEIPRESRLRLVKGCGCGEYVMGTMGTTR 300

Db 232 KHADGLCHRLTLYVCPTSPKQTOGLADAMEIPRESRLRLVKGCGCGEYVMGTMGTTR 291

Qy 301 VAIKTLKPGTMSPEAFLOEAQVWKKLRHKKLVOLYAVVSEPIYITERNSSKSLDPLK 360

Db 292 VAIKTLKPGTMSPEAFLOEAQVWKKLRHKKLVOLYAVVSEPIYITERNSSKSLDPLK 351

Qy 361 GETGKTYLRPLQYVDMAAQIASGMAYTERNNVYHRRDLRAAIIIVGENLVCKVADGLARLI 420

Db 352 GEMGKTYLRPLQYVDMAAQIASGMAYTERNNVYHRRDLRAAIIIVGENLVCKVADGLARLI 411

Qy 421 EDNETARQAGAFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 480

Db 412 EDNETARQAGAFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVYPGVMNREV 471

Qy 481 LDQVERGYRMPCPPECESLHDLCCQWRKEPERPTFEYLQAFLEADYPTSTEPQYQGE 540

Db 472 LDQVERGYRMPCPPECESLHDLCCQWRKEPERPTFEYLQAFLEADYPTSTEPQYQGE 531

Qy 541 NL 542

Db 532 NL 533

RESULT 4

TVFVPR

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus PR2257

C|Species: avian sarcoma virus PR2257

C|Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004

C|Accession: A30174

R|Geryk, J.; Deesle, P.; Barnier, J.V.; Svoboda, J.; Nelyba, J.; Karakoz, I.; Rynditch, J. Virol. 63, 481-492, 1989

A|Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom.

A|Reference number: A30174; MUID:89094972; PMID:2463376

A|Accession: A30174

A|Molecule type: DNA

A|Residues: 1-587 <GER>

A|Cross-References: UNIPROT:P15054; UNIPARC:UPI0000135F23; GB:M21526; NID:G210264; PIDN::

C|Genetics:

C|Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C|Keywords: ATP, autophosphorylation; blocked amino end; lipidprotein; myristylation; onc

F:148-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 91.1%; Score 2608.5; DB 1; Length 587;

Best Local Similarity 93.1%; Pred. No. 3.3e-121;

Matches 497; Conservative 10; Mismatches 18; Indels 9; Gaps 2;

Qy 1 MGSNKSXPXASQRRSLLEPAENVHAGAGGAPASQTPSPASADGHRGSAAPAPAAE 60

Db 1 MGSNKSXPXDPQRSSLEPPDSTH--HGFPASQTPNKTAAAPDTRRTSPRSRSGFYATE 57

Qy 61 PTLPGGPNISDVTYSPQRAGALAGVITTFVALYDYSRTETDLSFFKGGERLQIVNNTKV 120

Db 58 PTLPGGPNISDVTYSPQRAGALAGVITTFVALYDYSRTETDLSFFKGGERLQIVNNT--- 114

```
QY 121 DVREGMMLAHSLSTGOTGYIPSNVYAPSPDSIOAEEMYPGKTRRSEERLLNAENRGT 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDMWMLAHSLTGTGTIPSNVYAPSDSIQAEEMYPGKTRRSEERLLNAPENRGT 171
QY 181 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 231
QY 241 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 291
QY 301 VALKTLKPGTMSPEALQEAQVMKQLRHEKLVOLYAVVSEEPYIYTERMSKSLDPLK 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VALKTLKPGTMSPEALQEAQVMKQLRHEKLVOLYAVVSEEPYIYTERMSKSLDPLK 351
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GEMGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTBLTTKGRVPYGMVNRREV 480
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTBLTTKGRVPYGMVNRREV 471
QY 481 LDQVERGYRMPCEPCEPSLHDMCOCWRKEPERPFEYLOAFLEDYFTSTEP 534
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCEPCEPSLHDMCOCWRKEPERPFEYLOAFLEDYFTSTEP 525
```

RESULT 5

```
TVPVS1
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
C/Species: avian sarcoma virus S1
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: A25375
R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A/Title: Activation of the cellular src gene by transducing retrovirus.
A/Reference number: A25375; MUID:87064539; PMID:3097513
A/Accession type: DNA
A/Molecule type: DNA
A/Residues: 1-568 <IKA>
A/Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25
C/Genetic:
A/Gene: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
F/88-137/Domain: SH3 homology <SH3>
F/148-245/Domain: SH2 homology <SH2>
F/265-523/Domain: protein kinase homology <KIN>
F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: Lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
```

```
Query Match 90.3%; Score 2601.5; DB 1; Length 568;
Best Local Similarity 92.7%; Pred. No. 7e-121;
Matches 495; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

QY 1 MGSNKSXPDAOSRRSLBPAENVHAGGAPASQTPSKPASADGHRPSAFAAPAAB 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPDAOSRRSLBPAENVHAGGAPASQTPSKPASADGHRPSAFAAPAAB 57
QY 61 PKLFGFNSSDVTYSPQAGAPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKY 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTYSPQAGAPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKY 114
QY 121 DVREGMMLAHSLSTGOTGYIPSNVYAPSPDSIOAEEMYPGKTRRSEERLLNAPENRGT 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDMWMLAHSLTGTGTIPSNVYAPSDSIQAEEMYPGKTRRSEERLLNAPENRGT 171
QY 181 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
```

```
Db 172 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 231
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 291
QY 301 VALKTLKPGTMSPEALQEAQVMKQLRHEKLVOLYAVVSEEPYIYTERMSKSLDPLK 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VALKTLKPGTMSPEALQEAQVMKQLRHEKLVOLYAVVSEEPYIYTERMSKSLDPLK 351
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GEMGKTLRLPOLVDMAQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTBLTTKGRVPYGMVNRREV 480
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTBLTTKGRVPYGMVNRREV 471
QY 481 LDQVERGYRMPCEPCEPSLHDMCOCWRKEPERPFEYLOAFLEDYFTSTEP 534
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCEPCEPSLHDMCOCWRKEPERPFEYLOAFLEDYFTSTEP 525
```

RESULT 6

```
TVPVS2
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
C/Species: avian sarcoma virus S2
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: B25375
R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A/Title: Activation of the cellular src gene by transducing retrovirus.
A/Reference number: A25375; MUID:87064539; PMID:3097513
A/Accession type: DNA
A/Molecule type: DNA
A/Residues: 1-557 <IKA>
A/Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26
C/Genetic:
A/Gene: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F/88-137/Domain: SH3 homology <SH3>
F/148-245/Domain: SH2 homology <SH2>
F/265-523/Domain: protein kinase homology <KIN>
F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: Lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
```

```
Query Match 90.3%; Score 2586.5; DB 1; Length 557;
Best Local Similarity 88.7%; Pred. No. 3.8e-120;
Matches 496; Conservative 14; Mismatches 22; Indels 27; Gaps 3;

QY 1 MGSNKSXPDAOSRRSLBPAENVHAGGAPASQTPSKPASADGHRPSAFAAPAAB 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPDAOSRRSLBPAENVHAGGAPASQTPSKPASADGHRPSAFAAPAAB 57
QY 61 PKLFGFNSSDVTYSPQAGAPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKY 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTYSPQAGAPLAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKY 114
QY 121 DVREGMMLAHSLSTGOTGYIPSNVYAPSPDSIOAEEMYPGKTRRSEERLLNAPENRGT 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDMWMLAHSLTGTGTIPSNVYAPSDSIQAEEMYPGKTRRSEERLLNAPENRGT 171
QY 181 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRESEETTKGAYCLASVDFPDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAAYS 231
QY 241 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KAADGLCHRLTVVCPFSKPTQGLADAMEIPRESLRLEVKLGCGCGEYVMGTWGTTR 291
```

```

Qy 301 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQIYAVVSEPIYIVTEYMSKSLDPLK 360
Db 292 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQIYAVVSEPIYIVTEYMSKSLDPLK 351
Qy 361 GEGTKYRLPOLVMAAQIASGMAYVERMYVHNDLPAANTLVGENLVCKVADGLARLI 420
Db 352 GEMKTYRLPOLVMAAQIASGMAYVERMYVHNDLPAANTLVGENLVCKVADGLARLI 411
Qy 421 EDNEYTRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVYPCGVNREV 480
Db 412 EDNEYTRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVYPCGVNREV 471
Qy 481 LDQVGRGYRMPCEPCESLHDLMCQCRKPEBERPFEYLOAFLEDF----- 529
Db 472 LDQVGRGYRMPCEPCESLHDLMCQCRKPEBERPFEYLOAFLEDFYLGILANTPMDK 531
Qy 530 -----TSTEPQYQGEN 541
Db 532 QEGPRGTASKQKRRPGE 550

```

RESULT 7

TFPV60

procteln-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C:Species: Rous sarcoma virus

C>Date: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004

C:Accession: A38017; A00631; S02726; A38018

R:Cernilovsky, A.P.; Levinson, A.D.; Varmus, H.E.; Blahop, J.M.; Tischer, E.; Goodman, Nature 301, 736-738, 1983

A>Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.

A:Reference number: A38017; MUID:83141780; PMID:6298633

A:Accession: A38017

A:Molecule type: DNA

A:Residues: 1-526 <CZE>

A:Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:J02018; GB:J020

R:Takeya, T.; Hanafusa, H.

A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and Cell 32, 881-890, 1983

A:Reference number: A00630; MUID:83155664; PMID:6299580

A:Accession: A00631

A:Molecule type: DNA

A:Residues: 1-62, 'D', 64-95, 'T', 97-123, 'V', 125-300, 'N', 302-526 <TA>

A:Cross-references: UNIPARC:UPI0000172582

A:Experimental source: strain Schmidt-Ruppin

R:Barnier, J.V.; Dezelee, P.; Marx, M.; Calochy, G.

Nucleic Acids Res. 17, 1252, 1989

A>Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom

A:Reference number: S02726; MUID:89160256; PMID:2531953

A:Accession: S02726

A:Molecule type: DNA

A:Residues: 1-9, 'G', 11-63, 'D', 64-123, 'V', 125-319, 'K', 321-495, 'S', 497-526 <BAR>

A:Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:G61908; PIDN:CAA32012.1; PIT

R:Takeya, T.; Feldman, R.A.; Hanafusa, H.

J. Virol. 44, 1-11, 1982

A>Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucle

A:Reference number: A38018; MUID:83059858; PMID:6292477

A:Accession: A38018

A:Molecule type: DNA

A:Residues: 1-15, 'C', 17-94, 'RT', 97-116, 'D', 118-337, 'T', 339-526 <TA>

A:Cross-references: UNIPARC:UPI0000135F24; GB:K00928; NID:G210187; PIDN:AAA42565.1; PID:

A:Experimental source: strain RASV441

R:Neil, J.C.; Ghyedael, J.; Vogt, P.K.; Smart, J.E.

Nature 291, 675-677, 1981

A>Title: Homologous tyrosine phosphorylation sites in transformation-specific gene prod

A:Reference number: A38019; MUID:81220973; PMID:6263320

A:Contents: annotation; phosphorylation site

C:Comment: The sequence from the Schmidt-Ruppin strain is shown.

C:Genetics:

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; on

F:88-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:295/Active site: Lys #status predicted
 F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 87.4%; Score 2503.5; DB 1; Length 526;
 Best Local Similarity 91.2%; Pred. No. 4.2e-116;
 Matches 479; Conservative 13; Mismatches 24; Indels 9; Gaps 2;

```

Qy 1 MGSKSRKPDASORRSLPEAENVHAGGAFAPASQTPSPASADGRSPAAPAAAE 60
Db 1 MGSSKSRKPDSPQRRSLPEPDSTH--HGQFPASQTPNKTAAPDTHRTSRSFGYATE 57
Qy 61 PKLFGFNSSDPTVTSPPRAGPLAGVTFVALYDRESRTETDLSFKKGERLQIVNTRKV 120
Db 58 PKLFGFNSTDTVTSPPRAGLGGVTFVALYDRESMTETDLSFKKGERLQIVNNT--- 114
Qy 121 DVREGDWMLAHSLSGTGTYIPSNYVAPSDSIQAEENYFGKITRRESERLLANENRGT 180
Db 115 ---EGNMWMLAHSLSGTGTYIPSNYVAPSDSIQAEENYFGKITRRESERLLANENRGT 171
Qy 181 FIVRESRTGAVCLSYSDPDNAKGLVKKYKTRKLDGGGYTSRQFNSLQOLVAYYS 240
Db 172 FLVRESRTGAVCLSYSDPDNAKGLVKKYKTRKLDGGGYTSRQFNSLQOLVAYYS 231
Qy 241 KHADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESRLLEVLAGGCGEVMWGTWGTTR 300
Db 232 KHADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESRLLEVLAGGCGEVMWGTWGTTR 291
Qy 301 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQIYAVVSEPIYIVTEYMSKSLDPLK 360
Db 292 VAIKTLKPGTMSPEAFIQEAVMKLRHEKLVQIYAVVSEPIYIVTEYMSKSLDPLK 351
Qy 361 GEGTKYRLPOLVMAAQIASGMAYVERMYVHNDLPAANTLVGENLVCKVADGLARLI 420
Db 352 GEMKTYRLPOLVMAAQIASGMAYVERMYVHNDLPAANTLVGENLVCKVADGLARLI 411
Qy 421 EDNEYTRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVYPCGVNREV 480
Db 412 EDNEYTRQGAKEPFIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVYPCGVNREV 471
Qy 481 LDQVGRGYRMPCEPCESLHDLMCQCRKPEBERPFEYLOAFLEDF 525
Db 472 LDQVGRGYRMPCEPCESLHDLMCQCRKPEBERPFEYLOAFLEDF 516

```

RESULT 8

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C:Species: Rous sarcoma virus

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C:Accession: S20808; S32774

R:Bozor, J.; Rozkot, F.; Svoboda, J.

submitted to the EMBL Data Library, May 1990

A:Description: Sequence organization of the adjacent chromosomal flanks the LTR.

A:Reference number: S20808

A:Accession: S20808

A:Molecule type: DNA

A:Residues: 1-526 <BD>

A:Cross-references: UNIPROT:Q06057; UNIPARC:UPI00001068B2; EMBL:X52822; NID:G49656; PIDN

A:Experimental source: Mesocricetus auratus (golden hamster) provirus

C:Genetics:

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:295/Active site: Lys #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.8%; Score 2484.5; DB 2; Length 526;

Best Local Similarity 90.7%; Pred. No. 3,6e-115;

Matches 476; Conservative 11; Mismatches 29; Indels 9; Gaps 2;

```

QY 1 MGSNKKPNDASORRRSLPEAENVHAGGGAFPASQTPSPKASADHGRGSAAPAPAAE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKKPNDASORRRSLPEPDSTH--HGGFPASQTPDDETAAPDAHRNPSRGVATE 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PKLFGFNSSDVTSPQAGPLAGGVTTFVALYDYESRTETDLSFFKGERLQIVNTRKY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTSPQAGALAGGVTTFVALYDYESMTETDLSFFKGERLQIVNNT--- 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DVREGMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENPRGT 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENPRGT 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRKSETAKGACLSVSDPDNAGKGVNKHVKICLYSGGFYITSTRQFNSLQOLVAAYS 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEAKLGQCGFGEVWMTNGTTR 291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VAIKTLKPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVSEEPYIYIEYWSKGSLLDFLK 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VAIKTLKPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVSEEPYIYIEYWSKGSLLDFLK 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 GETGKTLRLPOLVDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GETGKTLRLPOLVDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 411
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 EDNEYTAROGAKEPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGVPYPGMVNREV 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKEPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGVPYPGMVNREV 471
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 LDQVERGYRMPCCPECPESLHDLCCQMKRKEPERPTEYLOAF 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCCPECPESLHDLCCQMKRKEPERPTEYLOAF 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 9

OKREVR

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)

N:Alternate names: kinase-related transforming protein src

C:Species: Rous sarcoma virus

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C:Accession: S09609

A:Reference number: S09609; PMID:90067864; PMID:2587228

A:Accession: S09609

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-526 <SD>

A:Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; MID:561706; PIDN

C:Genetics:

A:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.8%; Score 2478.5; DB 1; Length 526;

Best Local Similarity 90.5%; Pred. No. 7.1e-115;

Matches 475; Conservative 11; Mismatches 30; Indels 9; Gaps 2;

```

QY 1 MGSNKKPNDASORRRSLPEAENVHAGGGAFPASQTPSPKASADHGRGSAAPAPAAE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKKPNDASORRRSLPEPDSTH--HGGFPASQTPDDETAAPDAHRNPSRGVATE 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PKLFGFNSSDVTSPQAGPLAGGVTTFVALYDYESRTETDLSFFKGERLQIVNTRKY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 PKLFGFNSSDVTSPQAGALAGGVTTFVALYDYESMTETDLSFFKGERLQIVNNT--- 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DVREGMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENPRGT 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 ---EGDMWLAHSITGQTGYIPSNVYAPSDSIOAEEMYPGKTRRSERLLNAENPRGT 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 FLVRKSETAKGACLSVSDPDNAGKGVNKHVKICLYSGGFYITSTRQFNSLQOLVAAYS 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTR 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 KHAADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEAKLGQCGFGEVWMTNGTTR 291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VAIKTLKPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVSEEPYIYIEYWSKGSLLDFLK 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VAIKTLKPGTMSPEAFLOEAQVWKRLRHEKLVOLYAVSEEPYIYIEYWSKGSLLDFLK 351
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 GETGKTLRLPOLVDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 GETGKTLRLPOLVDMAQAISGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 411
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 EDNEYTAROGAKEPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGVPYPGMVNREV 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 412 EDNEYTAROGAKEPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGVPYPGMVNREV 471
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 LDQVERGYRMPCCPECPESLHDLCCQMKRKEPERPTEYLOAF 525
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 472 LDQVERGYRMPCCPECPESLHDLCCQMKRKEPERPTEYLOAF 516
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 10

S15582

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)

C:Species: Rous sarcoma virus

A:Variety: strain Prague A

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004

C:Accession: S15582; S09665

A:Accession: S15582; S09665

R:Lin, Z.; Hackelt, P.B.

Nucleic Acids Res. 17, 3986, 1989

A:Title: Sequence variation of the Rous sarcoma virus PTA src gene.

A:Reference number: S15582; PMID:89282411; PMID:2543959

A:Accession: S15582

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-526 <LIN>

A:Cross-references: UNIPROT:Q64994; UNIPROT:Q92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP

A:Experimental source: strain Prague A

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

A>Note: only a list of differences from sequence S09665 is given; however, the list is in

R:Fincham, V.J.; Wyke, J.A.

J. Virol. 58, 694-699, 1986

A:Title: Localization of temperature-sensitive transformation mutations and back mutator

A:Reference number: S09665; PMID:86200422; PMID:3009882

A:Accession: S09665

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 231-241, 'TH', '244-287', 'G', '289-463', 'P', '465-501', 'N', '503-526' <FIN>

A:Cross-references: UNIPARC:UPI00001755F1

C:Genetics:

A:Gene: src

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc

F:88-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F/265-523/Domain: protein kinase homology <KIN>
 F/273-281/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/255/Active site: lys #status predicted
 F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.3%; Score 2471.5; DB 2; Length 526;
 Best Local Similarity 90.3%; Pred. No. 1.6e-114;
 Matches 474; Conservative 11; Mismatches 31; Indels 9; Gaps 2;

```

QY 1 MGSNKSXPKASQRRRLLEPAENVHAGGAFSPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSSKSRKDPSPQRRRLLEPPDSTH--HGGFPAQTPDETAADAHNPFERSFGTVAATE 57
QY 61 PKLFGFNSSDVTYSPQACPLAGGYTTFFVALDYESTETDLSFKKGERLQIVNTRKV 120
DB 58 PKLFGFNSTDTYVSPQACPLAGGYTTFFVALDYESTETDLSFKKGERLQIVNNT--- 114
QY 121 DVREGDWMHLASLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESERLILNENPRGT 180
DB 115 ---EGDWMHLASLTTGQGYIPSNYVAPSDSIQAEVYFGKITRRESERLILNENPRGT 171
QY 181 FLVRESETTGAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
DB 172 FLVRSSTTGAYCLSYSDPDNAKGPVKKHYKIKLXSGGFYITSRTQFNSLQQLVAYYS 231
QY 241 KHAADGLCHRLITTVCPPTKPTQGLAKDAWEIPRESLLEVLGCGCCGGEVWMTWNGTTR 300
DB 232 KHAADGLCHRLANVCPTKPTQGLAKDAWEIPRESLLEVLGCGCCGGEVWMTWNTTTR 291
QY 301 VAIKTLKPTGMSPEAFQEAQVWKLRHEKLVQYAVVSEBPITYIVETYSKSGSLDPLK 360
DB 292 VAIKTLKPTGMSPEAFQEAQVWKLRHEKLVQYAVVSEBPITYIVETYSKSGSLDPLK 351
QY 361 GETGKYLRLPOLVDMQAQISGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 420
DB 352 GEMGKYLRPLQVDMQAQISGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 411
QY 421 EDNEYTRAQAKPPIKMTAPBAALYGRFTTKSDVWSGILLTETTTGKRVYPGMVNRREV 480
DB 412 EDNEYTRAQAKPPIKMTAPBAALYGRFTTKSDVWSGILLTETTTGKRVYPGMVNRREV 471
QY 481 LDVERGYRMPCEPCEPSLHDLMCQCRKEPEREPFEYLOAF 525
DB 472 LDVERGYRMPCEPCEPSLHDLMCQCRKDPBERPFTKYLQQL 516

```

RESULT 11

TVFVR protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)

C/Species: Rous sarcoma virus
 C/Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
 C/Accession: A00632

R/Schwartz, D.; Tizard, R.; Gilbert, W.
 submitted to the Nucleic Acid Sequence Database, September 1982

A/Reference number: A00632

A/Accession: A00632

A/Molecule type: genomic RNA

A/Residues: 1-526 <SCH>

A/Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63

A/Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and R/Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.

A/Title: Homologous tyrosine phosphorylation sites in transformation-specific gene product Nature 291, 675-677, 1981

A/Reference number: A38019; MUID:81220979; PMID:6264320

A/Contents: annotation; phosphorylation site

C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
 F/48-245/Domain: SH2 homology <SH2>
 F/265-523/Domain: protein kinase homology <KIN>

F/273-281/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/255/Active site: lys #status predicted
 F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.2%; Score 2468.5; DB 1; Length 526;
 Best Local Similarity 90.1%; Pred. No. 2.2e-114;
 Matches 473; Conservative 11; Mismatches 32; Indels 9; Gaps 2;

```

QY 1 MGSNKSXPKASQRRRLLEPAENVHAGGAFSPASQTPSPKASADGHRGSAAPAPAAE 60
DB 1 MGSSKSRKDPSPQRRRLLEPPDSTH--HGGFPAQTPDETAADAHNPFERSFGTVAATE 57
QY 61 PKLFGFNSSDVTYSPQACPLAGGYTTFFVALDYESTETDLSFKKGERLQIVNTRKV 120
DB 58 PKLFGFNSTDTYVSPQACPLAGGYTTFFVALDYESTETDLSFKKGERLQIVNNT--- 114
QY 121 DVREGDWMHLASLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESERLILNENPRGT 180
DB 115 ---EGDWMHLASLTTGQGYIPSNYVAPSDSIQAEVYFGKITRRESERLILNENPRGT 171
QY 181 FLVRESETTGAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 240
DB 172 FLVRSSTTGAYCLSYSDPDNAKGPVKKHYKIKLXSGGFYITSRTQFNSLQQLVAYYS 231
QY 241 KHAADGLCHRLITTVCPPTKPTQGLAKDAWEIPRESLLEVLGCGCCGGEVWMTWNGTTR 300
DB 232 KHAADGLCHRLANVCPTKPTQGLAKDAWEIPRESLLEVLGCGCCGGEVWMTWNTTTR 291
QY 301 VAIKTLKPTGMSPEAFQEAQVWKLRHEKLVQYAVVSEBPITYIVETYSKSGSLDPLK 360
DB 292 VAIKTLKPTGMSPEAFQEAQVWKLRHEKLVQYAVVSEBPITYIVETYSKSGSLDPLK 351
QY 361 GETGKYLRLPOLVDMQAQISGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 420
DB 352 GEMGKYLRPLQVDMQAQISGMAVYERMYVHRDLPAANILVGENLVCKVADFGRLRI 411
QY 421 EDNEYTRAQAKPPIKMTAPBAALYGRFTTKSDVWSGILLTETTTGKRVYPGMVNRREV 480
DB 412 EDNEYTRAQAKPPIKMTAPBAALYGRFTTKSDVWSGILLTETTTGKRVYPGMVNRREV 471
QY 481 LDVERGYRMPCEPCEPSLHDLMCQCRKEPEREPFEYLOAF 525
DB 472 LDVERGYRMPCEPCEPSLHDLMCQCRKDPBERPFTKYLQQL 516

```

RESULT 12

S26420 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C/Species: Rous sarcoma virus
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
 C/Accession: S26420; S20676

R/Kashuba, V.I.; Rynditch, A.V.; Dostajova, V.; Hlozaneck, I.; Zubak, S.V.; Kavanan, V.M.
 submitted to the EMBL Data Library, September 1992

A/Description: Molecular cloning and DNA sequence analysis of duck-adapted variant of Rous sarcoma virus

A/Reference number: S26417

A/Accession: S26420

A/Molecule type: preliminary

A/Residues: 1-526 <KAS>

A/Cross-references: UNIPROT:Q07461; UNIPARC:UPI000010512B; EMBL:X68524; NID:961903; PIDN
 submitted to the EMBL Data Library, March 1990

A/Reference number: S20676

A/Accession: S20676

A/Molecule type: DNA

A/Residues: 1-526 <KAS>
 A/Cross-references: UNIPARC:UPI000010512B; EMBL:X51861; NID:961896; PIDN:CAA36154.1; PID
 C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosph

F:88-137/Domain: SH2 homology <SH2>
F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>

F:773-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted

F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.7%; Score 2453.5; DB 2; Length 526;
Best Local Similarity 89.5%; Pred. No. 1,2e-113;

Matches 470; Conservative 13; Mismatches 33; Indels 9; Gaps 2;

```

QY 1 MGSNKSXPDAQRRLSPLEPAENVHAGGAPAPASQTPSPKPSADGHRPSAFAFAAAE 60
DB 1 MGSNKSXPDAQRRLSPLEPAENVHAGGAPAPASQTPSPKPSADGHRPSAFAFAAAE 57
QY 61 PKLFGFNSSDVTITSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
DB 58 PKLFGFNSSDVTITSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 114
QY 121 DVREGDWMLAHSSTGQTGYTPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 180
DB 115 ---EGYMWLAHSJLTGQTGYTPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 171
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 240
DB 172 FLVRKSETAKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 231
QY 241 KPADGLCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNQTR 300
DB 232 KPADGLCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNQTR 291
QY 301 VAIKTKLPKGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYIETEMSGSLDPLK 360
DB 292 VAIKTKLPKGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYIETEMSGSLDPLK 351
QY 361 GETGKYLRLPOLVDMAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 352 GETGKYLRLPOLVDMAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 480
DB 412 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 471
QY 481 LDQVEGGRMPCPPECPESLHLMCCQCKREBERPTEFYLOAPL 525
DB 472 LDQVEGGRMPCPPECPESLHLMCCQCKREBERPTEFYLOAPL 516

```

RESULT 13

B34104 protein-tyrosine kinase (BC 2.7.1.112) src 2 [similarity] - African clawed frog

N/Alternate names: kinase-related transforming protein (src); kinase-related transforming

C/Species: Xenopus laevis (African clawed frog)

C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004

C/Accession: B34104; 151563

R/Steale, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.

J. Biol. Chem. 264, 10649-10653, 1989

A/Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional

A/Reference number: A34104; PMID:89278134; PMID:2499582

A/Accession: B34104

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-532 <STE>

A/Cross-references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g21

R/Steale, R.E.

Nucleic Acids Res. 13, 1747-1761, 1985

A/Title: Two divergent cellular src genes are expressed in Xenopus laevis.

A/Reference number: 151563

A/Accession: 151563

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 439-492 <ST2>

A/Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; P1DN:AAA51644.1; P1D:5

C/Genes: src

A/Accession: 464/1

C/Species: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;

F:2/Modified site: myristylated amino end; lipoprotein; myristylation; phos

F:417-244/Domain: SH2 homology <SH2>

F:264-522/Domain: protein kinase homology <KIN>

F:272-280/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:294/Active site: Lys #status predicted

F:415/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 85.6%; Score 2450; DB 1; Length 532;
Best Local Similarity 86.9%; Pred. No. 1.8e-113;

Matches 471; Conservative 24; Mismatches 37; Indels 10; Gaps 4;

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QY 1 MGSNKSXPDAQRRLSPLEPAENVHAGGAPAPASQTPSPKPSADGHRPSAFAFAAAE 60
DB 1 MGSNKSXPDAQRRLSPLEPAENVHAGGAPAPASQTPSPKPSADGHRPSAFAFAAAE 56
QY 61 PKLFGFNSSDVTITSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
DB 57 PKLFGFNSSDVTITSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 113
QY 121 DVREGDWMLAHSSTGQTGYTPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 180
DB 114 ---EGDWMILARSLSSGQTGYTPSNVYAPSDSIQAEWYFGKTRRESERLLNAENPRGT 170
QY 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 240
DB 171 FLVRESEETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 230
QY 241 KPADGLCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNQTR 300
DB 231 KPADGLCHRLTVTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVWMTGNQTR 290
QY 301 VAIKTKLPKGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYIETEMSGSLDPLK 360
DB 291 VAIKTKLPKGTMSPEAFLOEAQVWKKLRHEKLVQLYAVVSEEPYIYIETEMSGSLDPLK 350
QY 361 GETGKYLRLPOLVDMAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 351 GETGKYLRLPOLVDMAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 410
QY 421 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 480
DB 411 EDNEYTARQAGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 470
QY 481 LDQVEGGRMPCPPECPESLHLMCCQCKREBERPTEFYLOAPLEDYFTSRPOQGE 540
DB 471 LDQVEGGRMPCPPECPESLHLMCCQCKREBERPTEFYLOAPLEDYFTSRPOQGE 530
QY 541 NL 542
DB 531 NL 532

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RESULT 14

A34104 protein-tyrosine kinase (BC 2.7.1.112) src 1 [similarity] - African clawed frog

N/Alternate names: kinase-related transforming protein (src); kinase-related transforming

C/Species: Xenopus laevis (African clawed frog)

C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 31-Dec-2004

C/Accession: A34104; 151564

R/Steale, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.

J. Biol. Chem. 264, 10649-10653, 1989

A/Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional

A/Reference number: A34104; PMID:89278134; PMID:2499582

A/Accession: A34104

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-532 <STE>
A/Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g21
R/Seelie, R.E.; Choer, R.; Ral, B.B.A.; Winkur, S.T.; Unger, T.F.
Oncogene 7, 2345-2350, 1992
A/Title: Structural organization of a src gene from xenopus laevis.
A/Reference number: 151564; MUID:93064714; PMID:1437158
A/Accession: 151564
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-113 <ST2>
A/Cross-references: UNIPARC:UPI00000PD97A; GB:M33646; NID:g214808; PIDN:AAA49963.1; PID:
C/Genetics:
A/Intons: 80/1
C/Superfamily: protein kinase homology; SH2 homology; SH3 homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F/87-136/Domain: SH3 homology <SH3>
F/147-244/Domain: SH2 homology <SH2>
F/264-522/Domain: protein kinase homology <KIN>
F/272-280/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/294/Active site: lys #status predicted
F/415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 85.5%; Score 2449; DB 1; Length 532;
Best Local Similarity 86.5%; Pred. No. 2e-113;
Matches 469; Conservative 25; Mismatches 38; Indels 10; Gaps 4;

QY 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAFAPASQTPSKAPADGHRGSPAPAAAE 60
DB 1 MGATKSPKRPGRSRSLDIVEGSH-QPFTSLASQTPNK--SLDSHRPAPGPG-GNCD 56
QY 61 PKLPGFNSSDVTYSPAPPLAGVTTFVALDYESTRTEDLSFKKGERLQIVNTRKY 120
DB 57 LTFPGGINFSDITTSPORTPLAGVTTFVALDYESTRTEDLSFKKGERLQIVNNT--- 113
QY 121 DVREGDWMLAHSSTGQGYIPSNYVAPSPDSIOAEWYFGKITRRESERLLNAENRGT 180
DB 114 ---EGDWMLAHSSTGQGYIPSNYVAPSPDSIOAEWYFGKITRRESERLLNAENRGT 170
QY 181 FLVRESSTTGAYCLSVSDPDNAKGLVVKHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 171 FLVRESSTTGAYCLSVSDPDNAKGLVVKHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 230
QY 241 KAADGLCHRLTTVCPTISKPTQGLAKDAWEIPRESLFLVYKLGCCGCGEVMGTWNGTTR 300
DB 231 KAADGLCHRLTTVCPTISKPTQGLAKDAWEIPRESLFLVYKLGCCGCGEVMGTWNGTTR 290
QY 301 VAIKTLKPGTMSPEAFLOEAOVMKRLRHEKLVOLYAVVSEEPYIVTEVMSKSLDLPLK 360
DB 291 VAIKTLKPGTMSPEAFLOEAOVMKRLRHEKLVOLYAVVSEEPYIVTEVMSKSLDLPLK 350
QY 361 GETGKYLRPLQVDMAAQIASGMAYVERMYVHRDLPAANILVGENIVCKVADGLARLI 420
DB 351 GEMGRYLRPLQVDMAAQIASGMAYVERMYVHRDLPAANILVGENIVCKVADGLARLI 410
QY 421 EDNEYTARQAKPEIKMTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 480
DB 411 EDNEYTARQAKPEIKMTAPBAALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 470
QY 481 LDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEYLOAFLEFYSTEEQYQGE 540
DB 471 LDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEYLOAFLEFYSTEEQYQGE 530
QY 541 NL 542
DB 531 NL 532

RESULT 15
S52313
protein-tyrosine kinase (BC 2.7.1.112) src - Rous sarcoma virus
C/Species: Rous sarcoma virus
C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004

C/Accession: S52313
R/Tsao, A.; Yatsula, B.; Shuter, M.; Molnova, E.; Kaverina, I.; Musackina, E.; Lee
submitted to the EMBL Data Library, January 1995
A/Description: Two new isoforms of v-src oncogene isolated from low and high metastatic i
A/Reference number: S52313
A/Accession: S52313
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-545 <TAT>
A/Cross-references: UNIPROT:Q96362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:G663083; PID
C/Superfamily: Tyrosine-protein kinase, proto-oncogene src type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F/108-157/Domain: SH3 homology <SH3>
F/168-265/Domain: SH2 homology <SH2>
F/285-543/Domain: protein kinase homology <KIN>
F/293-301/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/315/Active site: lys #status predicted
F/436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.2%; Score 2440.5; DB 2; Length 545;
Best Local Similarity 87.0%; Pred. No. 5.4e-113;
Matches 474; Conservative 13; Mismatches 29; Indels 29; Gaps 4;

QY 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAFAPASQTPSK-----PAS--- 43
DB 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAFAPASQTPSK-----PAS--- 43
QY 44 ---ADGHRGSAAPAPAAEPKLFPGFNSSDVTYSPAPPLAGVTTFVALDYESTRT 100
DB 58 AAPDTHRTSRSGVTANPKLFGDFTNSDVTYSPAPPLAGVTTFVALDYESTRT 117
QY 101 TDSFKKGERLQIVNTRKYDVREGDWMLAHSSTGQGYIPSNYVAPSPDSIOAEWYFG 160
DB 118 TDSFKKGERLQIVNNT-----EGNWMLAHSSTGQGYIPSNYVAPSPDSIOAEWYFG 171
QY 161 KITRRESERLLNAENRGTFLVRESSTTGAYCLSVSDPDNAKGLVVKHYKIRKLDGSG 220
DB 172 KITRRESERLLNAENRGTFLVRESSTTGAYCLSVSDPDNAKGLVVKHYKIRKLDGSG 231
QY 221 FYITSRTQFNSLQOLVAYYSKHAADGLCHRLTTVCPTISKPTQGLAKDAWEIPRESLFLV 280
DB 232 FYITSRTQFNSLQOLVAYYSKHAADGLCHRLTTVCPTISKPTQGLAKDAWEIPRESLFLV 291
QY 281 KLGGCGEVMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLRHEKLVOLYAVVSE 340
DB 292 KLGGCGEVMGTWNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLRHEKLVOLYAVVSE 351
QY 341 EPIYIVTEVMSKSLDLKGEKGYLRPLQVDMAAQIASGMAYVERMYVHRDLPAAN 400
DB 352 EPIYIVTEVMSKSLDLKGEKGYLRPLQVDMAAQIASGMAYVERMYVHRDLPAAN 411
QY 401 ILVGENIVCKVADGLARLIEDNEYTARQAKPEIKMTAPBAALYGRFTIKSDVMSFGIL 460
DB 412 ILVGENIVCKVADGLARLIEDNEYTARQAKPEIKMTAPBAALYGRFTIKSDVMSFGIL 471
QY 461 LTLETTKGRVYPGMVNRVLDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEY 520
DB 472 LTLETTKGRVYPGMVNRVLDQVERGYRMPCEPCESLHDLCCQWRKEPERPFEY 531
QY 521 LQAF 525
DB 532 LQAF 536

Search completed: June 5, 2006, 17:16:40
Job time : 22.7603 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 155.335 Seconds
(without alignments)
3227.587 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MSGNKSXPKNASQRRSLRP.....AFLEDYFTSTPEYQPENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2863	100.0	542	2	Q76P87 HUMAN
2	2828.5	98.8	541	2	Q2M414 MOUSE
3	2823	98.6	542	2	Q9J10 RAT
4	2816	98.4	535	1	SRC HUMAN
5	2815.5	98.3	540	1	SRC MOUSE
6	2786.5	97.3	535	2	Q80XU2 MOUSE
7	2759.5	96.7	535	2	Q3UKD6 MOUSE
8	2758	96.3	535	1	SRC RAT
9	2693	94.1	523	1	Q45QJ2 RAT
10	2648.5	92.5	532	1	SRC CHICK
11	2603.5	90.9	567	1	SRC AVIS2
12	2596.5	90.7	567	1	SRC AVIS
13	2595.5	90.7	587	2	Q64817 GRETR
14	2581.5	90.2	556	1	SRC AVIS1
15	2515.5	87.9	525	1	SRC AVISR
16	2515.5	87.9	525	1	SRC RSVSA
17	2484.5	86.8	526	2	Q60567 GRETR
18	2475.5	86.5	537	2	Q7ZX73 XENLA
19	2473.5	86.4	525	1	SRC RSVAH
20	2473	86.4	532	2	Q5MAS9 XENR
21	2472.5	86.4	526	2	Q64994 GRETR
22	2470.5	86.3	526	2	Q33080 GRETR
23	2469	86.2	523	2	Q85477 GRETR
24	2469	86.2	535	2	Q92957 RSVSB
25	2468.5	86.2	526	2	Q92806 GRETR
26	2467.5	86.2	525	1	SRC RSVSR
27	2463.5	86.0	525	1	SRC RSVP
28	2457.5	85.8	526	2	Q64993 RSVSR
29	2453.5	85.7	526	2	Q07461 GRETR
30	2450	85.6	532	2	Q2TARI XENLA
31	2445	85.4	531	1	SRC2_XENLA

32	2441	85.3	531	1	SRC1 XENLA	P13115 xenopus lae
33	2440.5	85.2	545	2	Q86362 GRETR	Q86362 rous sarcom
34	2433.5	85.0	546	2	Q86363 GRETR	Q86363 rous sarcom
35	2400	83.8	522	1	SRC RSVPA	P31693 rous sarcom
36	2305	80.5	534	2	Q6EWH0 BRARE	Q6EWH0 brachydanio
37	2180.5	76.2	527	2	Q91952 XIPXI	Q91952 xiphophorus
38	2124.5	74.2	537	2	Q64089 XENR	Q64089 xenopus tro
39	2123.5	74.2	537	2	Q6PF70 XENLA	Q6PF70 xenopus lae
40	2116.5	73.9	537	2	Q498G3 XENLA	Q498G3 xenopus lae
41	2114.5	73.9	541	2	Q99PW1 RAT	Q99PW1 rattus norv
42	2112.5	73.8	536	1	YES XENLA	P10936 xenopus lae
43	2110.5	73.7	541	2	Q8C762 MOUSE	Q8C762 mus musculu
44	2109	73.7	542	1	YES HUMAN	P07947 homo sapien
45	2105.5	73.5	540	1	YES_MOUSE	Q04736 mus musculu

ALIGNMENTS

RESULT 1
ID Q76P87 HUMAN PRELIMINARY; PRT; 542 AA.
AC Q76P87;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE OTTHUMP0000030931.
GN Name=SRC; ORFNames=RP5-823N20.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC
EMBL: AL133293; CAC10573.1; -; Genomic DNA.
DR HSSP; P12931; 1A09.
DR SMR; Q76P87; 87-542.
DR Ensembl; ENSG00000197122; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_Chr_Kinase.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR008266; Tyr_Kinase_AS.
DR Pfam; PF07714; Kinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH3DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SMO0252; SH2; 1.
DR SMART; SMO0326; SH3; 1.
DR SMART; SMO0219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR SEQUENCE 542 AA; 60589 MW; C12D30FBBCDSFFEB CRC64;

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Best Local Similarity 100.0%; Pred. No. 5,4e-181;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPKDASORRRSLRPAENVHAGAGGAFPASOTPSKPSADHGRGSAAPAPAAE 60
DB 1 MGSNKKPKDASORRRSLRPAENVHAGAGGAFPASOTPSKPSADHGRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKY 120
QY 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
DB 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGGFYITSRTOFNSLQOLVAAYYS 240
DB 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGGFYITSRTOFNSLQOLVAAYYS 240
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DB 241 KHAADGLCHRLTTCPTSPKPTOTGGLADAMEIPRESLRLEVYKLGQGCFCGEVWMTNGTTR 300
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DB 301 VALKTLLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPIYITVEMSKGSLDPLK 360
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERVMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
DB 361 GETGKYLRLPOLVDMAQIASGMAVYERVMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
QY 421 EDNEYTARQAKPPIKWTABEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVNREV 480
DB 421 EDNEYTARQAKPPIKWTABEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVNREV 480
QY 481 LDQVEGYRMPCCPPECBSLHDMCCMRKEPERPTFYLQAFLEDFYFSTEPYOYQGE 540
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QY 541 NL 542
DB 541 NL 542

RESULT 2
Q2M414_MOUSE PRELIMINARY; PRT; 541 AA.
AC Q2M414_MOUSE
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DE 21-FEB-2006, entry version 1.
DE Src.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=CAS/BLU; TISSUE=Brain;
RA Farber C.R., Corva P.M., Medrano J.F.;
RT "Characterization of quantitative trait loci influencing growth and
RT adiposity using congenic mouse strains."
RT Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC EMBL; AY902331; AAX90616.1; -; Genomic DNA.
DR SEQUENCE 541 AA; 60645 MW; 0534AF027783BCFC CRC64;
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Query Match      98.8%; Score 2828.5; DB 2; Length 541;
Best Local Similarity 98.9%; Pred. No. 1e-178;
Matches 536; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGSNKKPKDASORRRSLRPAENVHAGAGGAFPASOTPSKPSADHGRGSAAPAPAAE 60
DB 1 MGSNKKPKDASORRRSLRPAENVHAGAGGAFPASOTPSKPSADHGRGSAAPAPAAE 59
QY 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKY 120
DB 61 PKLFGFNSSDVTYSPOKAPPLAGVTTVALYDYSRTETDLSFKKGERLQIVNTRKY 119
QY 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 180
DB 121 DVREGMWMALHSLSTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRRESERLLNAENPRGT 179
QY 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGGFYITSRTOFNSLQOLVAAYYS 240
DB 181 FLVRESEETTKGAYCLSVSPDNAGKLVNKHVKIRKLDGSGGFYITSRTOFNSLQOLVAAYYS 239
QY 241 KHAADGLCHRLTTCPTSPKPTOTGGLADAMEIPRESLRLEVYKLGQGCFCGEVWMTNGTTR 300
DB 241 KHAADGLCHRLTTCPTSPKPTOTGGLADAMEIPRESLRLEVYKLGQGCFCGEVWMTNGTTR 299
QY 301 VALKTLLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPIYITVEMSKGSLDPLK 360
DB 301 VALKTLLKPGTMSPEALQEAQVWKLRHEKLVOLYAVVSEBPIYITVEMSKGSLDPLK 359
QY 361 GETGKYLRLPOLVDMAQIASGMAVYERVMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
DB 361 GETGKYLRLPOLVDMAQIASGMAVYERVMYVHRDLRAANIIVGENLVCKVADFGIARLI 419
QY 421 EDNEYTARQAKPPIKWTABEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVNREV 480
DB 421 EDNEYTARQAKPPIKWTABEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVNREV 479
QY 481 LDQVEGYRMPCCPPECBSLHDMCCMRKEPERPTFYLQAFLEDFYFSTEPYOYQGE 540
DB 481 LDQVEGYRMPCCPPECBSLHDMCCMRKEPERPTFYLQAFLEDFYFSTEPYOYQGE 539
QY 541 NL 542
DB 540 NL 541

RESULT 3
Q9JUI0_RAT PRELIMINARY; PRT; 542 AA.
AC Q9JUI0_RAT
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DE 07-FEB-2006, entry version 21.
DE Neuronal C-SRC tyrosine-specific protein kinase.
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=21148003; PubMed=11249956; DOI=10.1016/S0028-3908(00)00185-4;
RX Linden A., Storch M., Lakso M., Haapasalo A., Lee D., Wickin J.M.,
RA Sei Y., Caestre E., Wong G.;
RT "Increased expression of neuronal Src and tyrosine phosphorylation of
RT NMDA receptors in rat brain after systemic treatment with MK-801."
RT Neuropharmacology 40:469-481(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP Linden A.-M., Storch M., Lakso M., Wong G., Caestre E.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -----
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CC EMBL AF157016; AAF80335.1; -; mRNA.
 CC HSSP; P12931; 1043.
 DR SMK; Q9J710; 87-542.
 DR Ensembl; ENSRNOG0000009495; Rattus norvegicus.
 DR RGD; 620795; Src.
 DR GO; GO:0016301; F-kinase activity; TAS.
 DR GO; GO:0004713; F-protein-tyrosine kinase activity; IDA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PSS0107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PSS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PSS5001; SH2; 1.
 DR PROSITE; PSS5002; SH3; 1.
 KM Kinase.
 SO 'SEQUENCE 542 AA; 60727 MW; 6AC21D6DD6B0B39 CRC64;

Query Match 98.6%; Score 2823; DB 2; Length 542;
 Best Local Similarity 98.9%; Pred. No. 2,4e-178;
 Matches 537; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

QY 1 MGSNKSAPKQASQRRSLSEPLENVHAGGAGFAPASQTPSPKPSADGHRGSAFAA-PAAA 59
 DB 1 MGSNKSAPKQASQRRSLSEPLENVHAGGAGFAPASQTPSPKPSADGHRGSAFAA-PAAA 59
 QY 60 EPLKFGGFSNDDYVTSQRAAGPLAGVYTFVALYDYSRTETDLSFKKGERLQIVNNTRK 119
 DB 60 EPLKFGGFSNDDYVTSQRAAGPLAGVYTFVALYDYSRTETDLSFKKGERLQIVNNTRK 119
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 DB 120 VDVREGGWMVLAHSLSTGQTGYTPSNYVAFSDSIQAEWYFKKTRRSEERLLNAENPRG 179
 QY 180 TFLVRESETTKGAVCSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQOLVAYY 239
 DB 180 TFLVRESETTKGAVCSVSDPDNAKGLNVKHYKIRKLDGSGFYTSRQFNSLQOLVAYY 239
 QY 240 SKHADGICHRLLTVTCPTSKPTQGLADAMEIPRESRLREYKLGQGGFGEVWMTWNGTT 299
 DB 240 SKHADGICHRLLTVTCPTSKPTQGLADAMEIPRESRLREYKLGQGGFGEVWMTWNGTT 299
 QY 300 RVALIKTLKPGTMSPEALFOEAQVWKKLRHEKLVOLYAVVSEEPYIYTEYVNNKSSLDLDFL 359
 DB 300 RVALIKTLKPGTMSPEALFOEAQVWKKLRHEKLVOLYAVVSEEPYIYTEYVNNKSSLDLDFL 359
 QY 360 KGETGKTLRLPOLVDMAAOIASGMAVYERMMYVHRDI,RAANII,LYGENM,VCVADPGLARL 419
 DB 360 KGETGKTLRLPOLVDMAAOIASGMAVYERMMYVHRDI,RAANII,LYGENM,VCVADPGLARL 419
 QY 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVWFGILLTLETLTKGRVYPGVMVRE 479
 DB 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVWFGILLTLETLTKGRVYPGVMVRE 479
 QY 480 VLDOVERGYRMPCCPBCPESLHDLIMCCGMRKEPERPTEYLQAFLEDYFTSTEPYQOPG 539

DB 480 VLDOVERGYRMPCCPBCPESLHDLIMCCGMRKEPERPTEYLQAFLEDYFTSTEPYQOPG 539
 QY 540 ENL 542
 DB 540 ENL 542

RESULT 4
 SRC_HUMAN STANDARD; PRT; 535 AA.
 ID P12531; O86V89; O9H5A8;
 AC 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-MAR-2006, entry version 79.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-Src) (pp60c-src).
 GN Name=SRC; Synonyms=SRC1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,
 RA Levanon D., Levanon M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McKussey A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prattalingam S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hateln F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempelen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshibayashi S., Cantucci P., Prange C.,
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Kizywiniski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RX MEDLINE=97257903; PubMed=3299057;
 RA Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.;
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes.";
 RL Mol. Cell. Biol. 7:1978-1983(1987).
 RN [4]
 RN NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RX MEDLINE=85213483; PubMed=2582238;
 RA Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.;
 RT "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT pp60c-src.";
 RL Mol. Cell. Biol. 5:1122-1129(1985).
 RN [5]
 RN NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RX MEDLINE=9040822; PubMed=2681803;
 RA Pyper J.M., Bolen J.B.;
 RT "Neuron-specific splicing of C-SRC RNA in human brain.";
 RL J. Neurosci. Res. 24:89-96(1989).
 RN [6]
 RN NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RX MEDLINE=85187981; PubMed=2581127;
 RA Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.;
 RT "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20.";
 RL Mol. Cell. Biol. 5:831-838(1985).
 RN [7]
 RN ALTERNATIVE SPLICING.
 RX PubMed=1691439;
 RA Pyper J.M., Bolen J.B.;
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain.";
 RL Mol. Cell. Biol. 10:2035-2040(1990).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535.
 RX MEDLINE=97177105; PubMed=9026557; DOI=10.1038/385595a0;
 RA Xu W., Harrison S.C., Eck M.J.;
 RT "Three-dimensional structure of the tyrosine kinase c-Src.";
 RL Nature 385:595-602(1997).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RX MEDLINE=97317069; PubMed=9174343; DOI=10.1021/bi970019n;
 RA Charifson P.S., Shewchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pacotibay G.J., Peel M.R., Rodriguez M., Sternbach D.D.,
 RA Consler T.G.;
 RT "Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
 RT structural study.";
 RL Biochemistry 36:6283-6293(1997).
 RN [10]
 RN STRUCTURE BY NMR OF 203-248.
 RX MEDLINE=95161382; PubMed=7532003;
 RA Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.;
 RT "Solution structure of the human pp60c-src SH2 domain complexed with a
 RT phosphorylated tyrosine pentapeptide.";
 RL Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC 06NF1, csrcd3 (xeno); NDBExp=3; InPact=EBI-621482, EBI-621463;
 CC 09YK9, KKBG; NDBExp=1; InPact=EBI-621482, EBI-81279;
 CC 060749; NdbDbl (xeno); NDBExp=1; InPact=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoform=2;
 CC Name=1;

CC IsoId=P12931-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P12931-2; Sequence=VSP_012134;
 CC -1- PTM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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 DR EMBL: AL133293; CAC34523.1; -; Genomic_DNA.
 DR EMBL: BC011566; AAH11566.1; -; mRNA.
 DR EMBL: BC051270; AAH51270.2; -; mRNA.
 DR EMBL: K03218; AAA60584.1; -; Genomic_DNA.
 DR EMBL: M16237; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16243; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16244; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: M16245; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03212; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03213; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03214; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03215; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03216; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: K03217; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL: X02647; CAA26485.1; -; Genomic_DNA.
 DR EMBL: X03995; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: X03996; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: X03997; CAA26485.1; JOINED; Genomic_DNA.
 DR EMBL: X03998; CAA26485.1; JOINED; Genomic_DNA.
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 DR EMBL: X04000; CAA26485.1; JOINED; Genomic_DNA.
 DR PIR: A26891; TVHUSC.
 DR PDB: 1A07; X-ray; A/B=143-248.
 DR PDB: 1A08; X-ray; A/B=143-248.
 DR PDB: 1A09; X-ray; A/B=143-248.
 DR PDB: 1A1A; X-ray; A/B=143-248.
 DR PDB: 1A1B; X-ray; A/B=143-248.
 DR PDB: 1A1C; X-ray; A/B=143-248.
 DR PDB: 1A1E; X-ray; A/B=143-248.
 DR PDB: 1FMK; X-ray; @=85-535.
 DR PDB: 1HCS; NMR; B=143-248.
 DR PDB: 1HCT; NMR; B=143-248.
 DR PDB: 1KSW; X-ray; A=85-535.
 DR PDB: 1O41; X-ray; A=144-251.
 DR PDB: 1O42; X-ray; A=144-251.
 DR PDB: 1O43; X-ray; A=144-251.
 DR PDB: 1O44; X-ray; A=144-251.
 DR PDB: 1O45; X-ray; A=144-251.
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 DR PDB: 1O4G; X-ray; A=144-251.
 DR PDB: 1O4H; X-ray; A=144-251.
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 Best Local Similarity 98.9%; Pred. No. 6, 9e-178;
 Matches 535; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
 QY 2 GSNKSRPKDASQRRRLBPAENVHGAAGGAFPASQTPSPKASADGHRGSSAFAFAAAB 61
 DB 1 GSNKSRPKDASQRRRLBPAENVHGAAGGAFPASQTPSPKASADGHRGSSAFAFAAAB 60

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QY 62 KLRGFGNSDPTVTSPOBAGPLAGGVTTFVALLYDESESTETDLSFKGKERLQIVNNTRKVD 121
DB 61 KLRGFGNSDPTVTSPOBAGPLAGGVTTFVALLYDESESTETDLSFKGKERLQIVNNTRKVD 116
QY 122 VREGDMMWLAHSLSTGQGYIPSNVYAPSDSIQAEWFGKTRRESRLLLNAENPRGTF 181
DB 117 --BGDMMWLAHSLSTGQGYIPSNVYAPSDSIQAEWFGKTRRESRLLLNAENPRGTF 174
QY 182 LVRESEFTTKGAYCISVSDPDNAKGLNVKHYKIRLDSGGFYITSRTPNSIQQULVAYYSK 241
DB 175 LVRESEFTTKGAYCISVSDPDNAKGLNVKHYKIRLDSGGFYITSRTPNSIQQULVAYYSK 234
QY 242 HADGLCHRLTTCGTSKPOQGLAKDAMEIPRESLRLEVLKGGCCPGEVMMGTNGTTRV 301
DB 235 HADGLCHRLTTCGTSKPOQGLAKDAMEIPRESLRLEVLKGGCCPGEVMMGTNGTTRV 294
QY 302 AITKLKFGTMSPEAFLOEAQVMKLRHEKLVQLYAAVSEBPIYIVTEYMSKSLDPLK 361
DB 295 AITKLKFGTMSPEAFLOEAQVMKLRHEKLVQLYAAVSEBPIYIVTEYMSKSLDPLK 354
QY 362 ETGKYRLPOLVDMAQIASGMAYVERMNVYHDLRAANILVGENLYCKVADFGIARLIE 421
DB 355 ETGKYRLPOLVDMAQIASGMAYVERMNVYHDLRAANILVGENLYCKVADFGIARLIE 414
QY 422 DNEVTAQGAKEPRTKWAPEALYGRFTIKSDVMSFGILLTELTKGRVPRGKVVNREVL 481
DB 415 DNEVTAQGAKEPRTKWAPEALYGRFTIKSDVMSFGILLTELTKGRVPRGKVVNREVL 474
QY 482 DOVERGRMPCPECPESLHDLMOQCWRKEPERPTEYLOAFLEDYFTSTPEPOYGEN 541
DB 475 DOVERGRMPCPECPESLHDLMOQCWRKEPERPTEYLOAFLEDYFTSTPEPOYGEN 534
QY 542 L 542
DB 535 L 535

RESULT 5
SRC_MOUSE STANDARD; PRT; 540 AA.
ID SRC_MOUSE
AC P05480;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DE 07-MAR-2006, entry version 65.
DE Neuronal proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112)
DE (p60-Src) (c-Src) (pp60c-src).
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIB=BAJB/c;
RX MEDLINE=87263406; PubMed=2440106;
RA Martinez R., Machey-Prevot B., Bernards A., Baltimore D.;
RT "Neuronal pp60c-src contains a six-amino acid insertion relative to
its non-neuronal counterpart.";
RL Science 237:411-415(1987).
RN [2]
RP INTERACTION WITH DDEF1/ASAP1.
RX MEDLINE=99038209; PubMed=9819391;
RA Brown M.T., Andrade J., Radhakrishna H., Donaldson J.G., Cooper J.A.,
RA Randazzo P.A.;
RT "ASAP1, a phospholipid-dependent arf GTPase-activating protein that
associates with and is phosphorylated by Src.";
RL Mol. Cell. Biol. 18:7038-7051(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine kinase = ADP + a protein
tyrosine phosphate.
CC -1- SUBUNIT: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC -1- INTERACTION:
P07141:Cell; NDBxp=2; IntAct=EBI-298680, EBI-777188;
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CC -1- P.TM: Phosphorylated on Tyr-534 by c-Src kinase (CSK). The
CC phosphorylated form is termed pp60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC
EMBL: M17031; AAA40135.1; -, mRNA.
DR PIR; A43610; A43610.
DR HSSP; P12931; 1A09.
DR SMK; P05480; 85-540.
DR Intact; P05480; -.
DR Ensembl; ENSMUSG00000027646; Mus musculus.
DR MGI; MGI:98397; Src.
DR GO; GO:0005515; F:Protein binding; IPI.
DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IMP.
DR GO; GO:0006468; P:Protein amino acid phosphorylation; IDA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT INT_MET 0
FT CHAIN 1 540
FT
FT DOMAIN 82 149
FT FT 155 252
FT FT 274 527
FT DOMAIN 274 527
FT NP_BIND 280 288
FT ACT_SITE 393 393
FT BINDING 302 302
FT MOD_RES 423 423
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SQ SEQUENCE 540 AA; 60487 MW; 424BA0EBE5D752AA CRC64;

Query Match 98.3%; Score 2815.5; DB 1; Length 540;
Best Local Similarity 98.7%; Pred. No 7.6e-178;
Matches 534; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
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QY 2 GSNKSKPKDASQRRRLSEPAENVHAGAGGAPPAAGTPEKPSADGHRGSAAPAPAAAP 61
DB 1 GSNKSKPKDASQRRRLSEPAENVHAGAGGAPPAAGTPEKPSADGHRGSAAPAPAAAP 59
QY 62 KLRGFGNSDPTVTSPOBAGPLAGGVTTFVALLYDESESTETDLSFKGKERLQIVNNTRKVD 121
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Db 60 KLFGRFNSSTVTYSPPQAGALAGVTTFFVALYDYESTETDLSFKKGERLQIYNNTRKV 119
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Db 120 VREGDWMLAHSLSGTGCTGYTPSNVVAAPSDSIQAEWYFGKITRRESRLLLNANPRGTF 179
Qy 182 LVRESSETTGAYCLSVSDPDNAKGLNVKHYKIRKLDSCGGFYITSRQFNSLQQLVAVYSK 241
Db 180 LVRESSETTGAYCLSVSDPDNAKGLNVKHYKIRKLDSCGGFYITSRQFNSLQQLVAVYSK 239
Qy 242 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLEVLKGGCGCFGEVMMGTWNGTTRV 301
Db 240 HADGLCHRLTTVCPTSPKQTOGLAKDAWEIPRESLRLEVLKGGCGCFGEVMMGTWNGTTRV 299
Qy 302 AITKLKPGTMSPPAFLQEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMGSLDLDFLK 361
Db 300 AITKLKPGTMSPPAFLQEAQVMKKLRHEKLVOLYAVVSEEPYIYVTEYMGSLDLDFLK 359
Qy 362 ETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANLVGENLVCKVADFGIARLIE 421
Db 360 ETGKYRLPOLVMAAQIASGMAYVERMNVVHDLRAANLVGENLVCKVADFGIARLIE 419
Qy 422 DNEYTARQGAKEPFIKWTAPPAALYGRFTIKSDVMSFGILLETITTKGRVPEYGMVAREVL 481
Db 420 DNEYTARQGAKEPFIKWTAPPAALYGRFTIKSDVMSFGILLETITTKGRVPEYGMVAREVL 479
Qy 482 DQVERGYRMPCEPCEPSLHDLMCQCKRKEPPEPFIYQAFLEDFYFSTEPQYQGEN 541
Db 480 DQVERGYRMPCEPCEPSLHDLMCQCKRKEPPEPFIYQAFLEDFYFSTEPQYQGEN 539
Qy 542 L 542
Db 540 L 540

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RESULT 6
Q8OXU2_MOUSE PRELIMINARY; PRT; 535 AA.
ID Q8OXU2;
AC Q8OXU2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Rous sarcoma oncogene, isoform 2.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
R1 NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=salivary gland;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ueda T.B., Tohliyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=salivary gland;
RG NIH MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
Db EMBL: BC039953; AAH39953.1; -; mRNA.
Db HSSP: P12931; 1043.
Db SMR: Q8OXU2; 86-535.
Db Ensemble: ENSMUSG00000027646; Mus musculus.
Db MGI: MGI:98397; Src.
Db GO: GO:000515; P:protein binding; IPT.
Db GO: GO:0004674; P:protein serine/threonine kinase activity; RCA.
Db GO: GO:0004713; P:protein-tyrosine kinase activity; IMP.
Db GO: GO:0006468; P:protein amino acid phosphorylation; IDA.
Db InterPro: IPR000719; Prot kinase.
Db InterPro: IPR002280; Ser_Thr_kinase.
Db InterPro: IPR000980; SH2.
Db InterPro: IPR001452; SH3.
Db InterPro: IPR001245; Tyr_kinase.
Db InterPro: IPR008266; Tyr_kinase_AS.
Db Pfam: PF07714; Pkinase_Tyr; 1.
Db Pfam: PF00017; SH2; 1.
Db Pfam: PF00018; SH3; 1; 1.
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Db PRINTS: PR00109; TYRKINASE.
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Db ProDom: PD000066; SH3; 1.
Db SMART: SM00252; SH2; 1.
Db SMART: SM00326; SH3; 1.
Db SMART: SM00219; TYRK; 1.
Db PROSITE: PS00107; PROTEIN KINASE ATP; 1.
Db PROSITE: PS00013; PROTEIN KINASE DOM; 1.
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SQ SEQUENCE 535 AA; 59891 MW; 22CB5C6B7A061C0 CRC64;

Query Match 97.3%; Score 2786.5; DB 2; Length 535;
Best Local Similarity 97.8%; Pred. No. 6.2e-176;
Matches 530; Conservative 3; Mismatches 2; Indels 7; Gaps 2;

Qy 1 MGSNKSPPDASQRRSLPEAPENVHAGAGGAPASQTPSKPASADGHRQPSAFAFAAE 60
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Qy 121 DVREGDWMLAHSLSGTGCTGYTPSNVVAAPSDSIQAEWYFGKITRRESRLLLNANPRGT 180
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 DB 414 EDNEYTARQGAKEPPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGRVPPQGVNREV 473
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 DB 474 LDQVGGYRMPCCPECCESLHDLMOCCWKEPERPFYFLQALBENYFTSTEQVQGE 533
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 DB 534 NL 535

RESULT 7
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 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
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 DT 07-FEB-2006, entry version 5.
 DE 12 days pregnant adult female placenta cDNA, RIKEN full-length
 DE enriched library, clone:1530027F01 product:Rous sarcoma oncogene, full
 DE insert sequence.
 GN Name=Src;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
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 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilmink L.G., Aldins V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banerji M., Baxter L., Belsel K.W., Bersano T., Bono H., Chaik A.M.,
 RA Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
 RA Guncionich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelich L., Iacono M., Ikeo K., Ikawa A., Ishikawa T.,
 RA Jaki D., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kikuchi H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuura S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Moteugui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Seesla L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yagi K.,
 RA Yamashita H., Zharovskiy E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,

RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Ikida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tegan M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense transcription in the mammalian transcriptome.",
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishio T., Osada N., Saito R., Suzuki H., Yamashita K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corzani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guncionich S., Hirokawa N., Jackson J.D., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido K., Oxley M., Perlee G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Vetrato R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmink L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kikuchi T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shimada K.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nishio T., Pesole G., Quackenbush J.,
 RA Schirini L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Bokfelld D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guncionich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.",

RL Nature 409:685-690(2001).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=2053093; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kikunishi T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
 Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
 Muramatsu M., Hayashizaki Y.;
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL, AK146056; BAE26865.1; -; mRNA.
 CC
 DR MGI; MGI:98397; Src.
 DR GO; GO:000515; F:protein binding; IPT.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IMP.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002280; Src_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; Tyr_kinase.
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 DR Pfam; PF00017; SH2; 1.
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 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
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 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
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 SO SEQUENCE 535 AA; 59995 MW; 0E56EA36892D9715 CRC64;

Query Match 96.7%; Score 2769.5; DB 2; Length 535;
 Best Local Similarity 97.2%; Pred. No. 8.3e-175;
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QY 1 MGSNKKPKDASQRRSLRPAENVHAGGAFPAQSOTPSKPSADGHRGSAAPAAAE 60
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 QY 181 FLVRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDSCGFYITSTRQFNSLOOLVAAYS 240
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 DB 534 NL 535

RESULT 8
 SRC_RAT STANDARD; PRT; 535 AA.
 AC 96ND9;
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
 DT 07-MAR-2006, entry version 46.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DS (c-Src) (pp60c-src).
 GN Name=Src;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RA Stockand J.D., Al-Khalili O., Spier B.J., Eaton D.C.;
 RT "Rattus norvegicus proto-oncogene encoding tyrosine-protein kinase
 RT pp60-c-src.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity
 CC (by similarity).
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.

Db	23	KHADG,CHRLTTCPTS,KPQTG,LANDA,MEI,PRESL,RLEVLA,GQCGFGEVMMGT,NGTTR	233
Qy	301	VAIKTLKPGTMSPEAFLQDAQVWKGLRHKVLVOLYAVVSEPIITYIYTEMYSKGLDLDFLK	360C
Db	294	VAIKTLKPGTMSPEAFLQDAQVWKGLRHKVLVOLYAVVSEPIITYIYTEMYSKGLDLDFLK	353S
Qy	361	GETGKTLRLPOLVDMAAQASGMAVYERNYVHRDLRAANLIVGENLVCKRADGGLARLI	420C
Db	354	GETGKTLRLPOLVDMSAQJASGMAVYDRNMYVHRDLRAANLIVGENLVCKRADGGLARLI	413S
Qy	421	EDNEYTARQAKFPKIMTAPALYGRFTISDVNSFGILLTELTGKRVYPGMVNRV	480C
Db	414	EDNEYTARQAKFPKIMTAPALYGRFTISDVNSFGILLTELTGKRVYPGMVNRV	473S
Qy	481	LDOVERGYTMCPPCEPESLHDLMQCKRKKEPERPTEYIQAFLDYFTSTEQYOPGE	540C
Db	474	LDOVERGYTMCPPCEPESLHDLMQCKRKKEPERPTEYIQAFLDYFTSTEQYOPGE	533S
Qy	541	NL 542	
Db	534	NL 535	
RESULT 9			
ID	Q45QJ2_RAT	PRELIMINARY; PRT; 523 AA.	
AC	Q45QJ2		
DT	13-SEP-2005, integrated into UniProtKB/TrEMBL.		
DT	13-SEP-2005, sequence version 1.		
DE	07-FEB-2006, entry version 7.		
DE	Tyrosine protein kinase c-src (Fragment).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=SHR, and WKY;		
RA	Jackson B.K., Zhu C.;		
RT	"Genetic Similarity Between Spontaneously Hypertensive Rats and		
RT	Wistar-Kyoto Rats in the Coding Regions of Signal Transduction		
RL	Proteins.";		
CC	Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.		
CC	-I CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein		
CC	tyrosine phosphate.		
CC	-I SIMILARITY: Contains 1 SH3 domain.		
CC	-----		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	-----		
DR	EMBL; DOI20510; AA223849.1; -; mRNA.		
DR	EMBL; DOI20509; AA223848.1; -; mRNA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0000166; F:nucleotide binding; IEA.		
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.		
DR	GO; GO:0006688; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR000980; SH2.		
DR	InterPro; IPR001452; SH3.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR008266; Tyr_kinase_AS.		
DR	Pfam; PF07714; PKinase_Tyr; 1.		
DR	Pfam; PF00017; SH2; 1.		
DR	Pfam; PF00018; SH3; 1.		
DR	PRINTS; PRO0401; SH2DOMAIN.		
DR	PRINTS; PRO0453; SH3DOMAIN.		
DR	PRINTS; PRO0109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	ProDom; PD000093; SH2; 1.		

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DR Prodom; PD000066; SH3; 1.
DR SMART; SM00252; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 1.
DR ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT NON TER 1
FT NON TER 523
SQ SEQUENCE 523 AA; 58672 MW; 8D5D6C2644FD2FC CRC64;

Query Match 94.1%; Score 2693; DB 2; Length 523;
Best Local Similarity 97.2%; Pred. No. 9,4e-170;
Matches 515; Conservative 4; Mismatches 3; Indels 8; Gaps 3;

QY 7 KPRDASORRSLEPANNVHAGAGGAPASQTPSKPASADHRGPPSAFA-PAAAPPLRG 65
DB 1 KPRDASORRSLEPANNVHAGAGGAPASQTPSKPASADHRGPPSAFA-PAAAPPLRG 59
QY 66 GFNSDPTVTSPPQAPGLAGGVTFVALYDYSRTETDLSFKGGERLQIVNTRKVDVREG 125
DB 60 GFNSDPTVTSPPQAPGLAGGVTFVALYDYSRTETDLSFKGGERLQIVNTRKVDVREG 113
QY 126 DWMLAHSLSTGQTGYIPSNVAPDSIQAEEMYPGKTRRESERLLINAEPRGTFLVRE 185
DB 114 DWMLAHSLSTGQTGYIPSNVAPDSIQAEEMYPGKTRRESERLLINAEPRGTFLVRE 173
QY 186 SETTKAYCLSVSDPNNAGLANKYKIRKLDGSGFRTSRQENSLQOULVAYYSKADG 245
DB 174 SETTKAYCLSVSDPNNAGLANKYKIRKLDGSGFRTSRQENSLQOULVAYYSKADG 233
QY 246 LCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLKGOCFGEVMMGTNGTTRVALIKT 305
DB 234 LCHRLTTVCPSTKPTQGLAKDAMEIPRESLRLEVLKGOCFGEVMMGTNGTTRVALIKT 293
QY 306 LKPGTMSPEAFLOEAOVMKKLRHEKLVQLYAVVSEEPITYVTEYMSKSLDPLKGETGK 365
DB 294 LKPGTMSPEAFLOEAOVMKKLRHEKLVQLYAVVSEEPITYVTEYMSKSLDPLKGETGK 353
QY 366 YRLPOLVMAAAGIAGMAVVERMYVHRDLRAANILVGNILVCKVADPELALIDNEY 425
DB 354 YRLPOLVMAAAGIAGMAVVERMYVHRDLRAANILVGNILVCKVADPELALIDNEY 413
QY 426 TARQAKFPPIKMTAPAPALYGRFTIKSDVMSFGILITELTKGRVVPYPGVNNREVLDOYE 485
DB 414 TARQAKFPPIKMTAPAPALYGRFTIKSDVMSFGILITELTKGRVVPYPGVNNREVLDOYE 473
QY 486 RGYRMPCEPCEPSLHDMCMQCKRKEPERPTEFYLAFLIEDYFTSTEQ 535
DB 474 RGYRMPCEPCEPSLHDMCMQCKRKEPERPTEFYLAFLIEDYFTSTEQ 523

RESULT 10
SRC_CHICK STANDARD; PRT; 532 AA.
AC P00523; Q90992; Q91343; Q91345; Q92013; Q98915;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1999, sequence version 3.
DT 07-MAR-2006, entry version 78.
DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
DE (c-src) (pp60c-src).
DE Name=SRC;
GN Name=SRC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN (1)
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RX MEDLINE=83155664; PubMed=6299580; DOI=10.1016/0092-8674(83)90073-9;
RA Takeya T., Hanafusa H.;
RT "Structure and sequence of the cellular gene homologous to the Rev arc
RT gene and the mechanism for generating the transforming virus.";
RL Cell 32:881-890(1983).
RN (2)
RP ERRATUM, AND SEQUENCE REVISION TO 525.
RA Takeya T., Hanafusa H.;
RL Cell 34:319-319(1983).
RN (3)
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=pectoralis muscle;
RX MEDLINE=90318371; PubMed=21151117;
RA Dorai T., Wang L.-H.;
RT "An alternative non-tyrosine protein kinase product of the c-src gene
RT in chicken skeletal muscle.";
RL Mol. Cell. Biol. 10:4068-4079(1990).
RN (4)
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
RP TYR-435.
RX MEDLINE=97008971; PubMed=8856081;
RA Weijand A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
RA Superti-Furga G.;
RT "The purification and characterization of the catalytic domain of Src
RT expressed in Schistosoma chromocyes pombe. Comparison of unphosphorylated
RT and tyrosine phosphorylated species.";
RL Eur. J. Biochem. 240:756-764(1996).
RN (5)
RP NUCLEOTIDE SEQUENCE OF 1-6.
RX MEDLINE=83059861; PubMed=6292480;
RA Takeya T., Hanafusa H.;
RT "DNA sequence of the viral and cellular src gene of chickens. II.
RT Comparison of the src genes of two strains of Avian sarcoma virus and
RT of the cellular homolog.";
RL J. Virol. 44:12-18(1982).
RN (6)
RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
RX MEDLINE=91304409; PubMed=1712905;
RA Dorai T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
RT exon and possible mechanism for the genesis of the 3' end of v-src.";
RL Mol. Cell. Biol. 11:4165-4176(1991).
RN (7)
RP ATP-BINDING SITE.
RX MEDLINE=84270751; PubMed=6431300;
RA Kampe K.P., Taylor S.S., Sefton B.M.;
RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
RT dependent protein kinase have homologous ATP-binding sites.";
RL Nature 310:589-592(1984).
RN (8)
RP PHOSPHORYLATION.
RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
RA Gould K.L., Woodgett J.R., Cooper J.A., Buse J.E., Shalloway D.,
RA Hunter T.;
RT "Protein kinase C phosphorylates pp60src at a novel site.";
RL Cell 42:849-857(1985).
RN (9)
RP PHOSPHORYLATION SITE TYR-415.
RX MEDLINE=82082387; PubMed=6273838;
RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F.,
RA Erickson R.L., Bishop J.M.;
RT "Characterization of sites for tyrosine phosphorylation in the
RT transforming protein of Rous sarcoma virus (pp60v-src) and its normal
RT cellular homologue (pp60c-src).";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
RN (10)
RP PHOSPHORYLATION SITE TYR-526.
RX MEDLINE=86151652; PubMed=2420005;
RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT "Ty527 is phosphorylated in pp60c-src: implications for regulation.";
RL Science 231:1431-1434(1986).
RN (11)
RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.

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RX MEDLINE:989243341; PubMed:2470512; DOI=10.1016/0092-8674(89)90791-5;
 RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Maller J.L.,
 RA Shailoway D.;
 RT "Purified maturation promoting factor phosphorylates pp60c-src at the
 RT sites phosphorylated during fibroblast mitosis.";
 RL Cell 57:763-774(1989).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
 RX MEDLINE:98070614; PubMed:9405157; DOI=10.1006/jmbi.1997.1426;
 RA Williams J.C., Weiland A., Gonfloni S., Thompson A.,
 RA Courtenidge S.A., Superti-Furga G., Wierenga R.K.;
 RT "The 2.35 A crystal structure of the inactivated form of chicken Src:
 RT a dynamic molecule with multiple regulatory interactions.";
 RL J. Mol. Biol. 274:757-775(1997).
 RN [13]
 RP STRUCTURE BY NMR OF 80-139.
 RX MEDLINE:92279385; PubMed:8504863; DOI=10.1016/0014-5793(93)81538-B;
 RA Yu H., Rosen M.K., Schreiber S.L.;
 RT "H1 and 15N assignments and secondary structure of the Src SH3
 RT domain.";
 RL FEBS Lett. 324:87-92(1993).
 CC -1- FUNCTION: Unknown.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
 CC phosphorylation site is not phosphorylated. It can also be
 CC activated by point mutations as well as by truncations at the C-
 CC terminal end or by other mutations.
 CC -1- SUBUNIT: pp60c-src forms a complex with polyoma virus middle T
 CC antigen.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P00523-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
 CC Note=Membrane-bound;
 CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
 CC degree of kinase activity, in certain fully differentiated cells
 CC such as neurons, platelets and macrophages. Isoform 1 is widely
 CC expressed. Isoform 2 is expressed only in the muscle.
 CC -1- PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL: V00402; CAA23596.1; -; Genomic DNA.
 DR EMBL: J00908; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL: M57290; AAA49078.1; -; mRNA.
 DR EMBL: S43604; AAD13831.1; -; mRNA.
 DR EMBL: S43616; AAD13835.1; -; mRNA.
 DR EMBL: S43587; AAD13830.1; -; mRNA.
 DR EMBL: S43609; AAD13832.1; -; mRNA.
 DR EMBL: S43614; AAD13834.1; -; mRNA.
 DR EMBL: S43579; AAB19353.2; -; mRNA.
 DR PIR: A00630; TVCHS.
 DR PDB: 1PTW; X-ray; A=144-246.
 DR PDB: 1FZF; X-ray; A=144-246.
 DR PDB: 1NLO; NMR; C=80-139.
 DR PDB: 1PLP; NMR; C=80-139.
 DR PDB: 1PL3; X-ray; A/B=144-245.
 DR PDB: 1PRM; NMR; C=76-139.
 DR PDB: 1RLP; NMR; C=76-139.
 DR PDB: 1RLQ; NMR; C=76-139.
 DR PDB: 1SRL; NMR; @=76-139.

DR	PDB: 1SRM; NMR; @=76-139.
DR	PDB: 2PTK; X-ray; @=-.
DR	Ensembl; ENSGALG0000003855; Gallus gallus.
DR	LinkHub; P00523; -.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR001452; SH3.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	InterPro; IPR008266; Tyr_pkinase_AS.
DR	Pfam; PF07714; Kinase_Tyr; 1.
DR	Pfam; PF00017; SH2; 1.
DR	Pfam; PF00018; SH3_1; 1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	Prodomb; PD000001; Prot_kinase; 1.
DR	Prodomb; PD000093; SH2; 1.
DR	Prodomb; PD000066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00219; Tyrc; 1.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50001; SH2; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW	Mylristate; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW	SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT	INTT_MET 0 0 By similarity
FT	CHAIN 1 532 Proto-oncogene tyrosine-protein kinase
FT	/FTId=PRO_0000088144.
FT	SIC.
FT	DOMAIN 80 141 SH3.
FT	DOMAIN 147 244 SH2.
FT	NP_BIND 266 519 Protein kinase.
FT	ACT_SITE 272 280 ATP (By similarity).
FT	ACT_SITE 385 385 Proton acceptor (By similarity).
Query Match:	92.5%; Score 2648.5; DB 1; Length 532;
Best Local Similarity	93.2%; Pred. No. 8.5e-167;
Matches 504; Conservative	10; Mismatches 18; Indels 9; Gaps 2
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Db	1 GSSSKRPDPQRKRSLPPDSTH---HGFPASQTPKNAAPDHRRPSSFCVATPE 57
DQ	62 KLFGFENSSDTVTSPORAPLAGGVTFVALVDSERTETDLSPFKGGRLOIVNTRKYD 121
Db	58 KLFGGFNTSDTVTSPOKAGALAGGVTFVALVDYSERTETDLSPFKGGRLOIVNNT --- 113
DQ	122 VREGDMWLASHLSLTCGCYITSNVABEDSIQAEEWYGKLTTRRESEILLNAEPRGT 181
Db	114 --EGDMWLASHLLTGQCYIISNVABDSIQAEWMYGKLTTRRESEILLNPNPRGT 171
DQ	182 LVRSSETTKGYCYSVPDFDNAKGLNVGHYIKRLKLDSCGFYTSTRQFNLSLOQLVAAYYSK 241
Db	172 LVRSSETTKGYCYSVPDFDNAGLVNHYYIKRLKLDSCGFYTSTRQFNLSLOQLVAAYYSK 231
DQ	242 HADGICHRLITVCPTSPKQTOGLAKDAWEIPRESLRILEVKLGQCFCGEVMNGTNQITRV 301
Db	232 HADGICHRLITVNCPTSPKQTOGLAKDAWEIPRESLRILEVKLGQCFCGEVMNGTNQITRV 291
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Db	292 AIKTLKPETSPEAFLOEAQIMKTLRHKKVLQVLAAYVEEPPIYLYTEYMSKSLLDFLKG 351
DQ	362 ETGKYLRLPOLVDMAAQIASGMAYVERNNVYHRDLRAANILVGENLYCKVADFGLARLIE 421
Db	352 EMGKITRLPOLVDMAAQIASGMAYVERNNVYHRDLRAANILVGENLYCKVADFGLARLIE 411
DQ	422 DNEYTAARGAFPRIKMTAPEALAYGRFTIKSDVMSFGILLTELTTKGAVPYPGMVNRREV 481

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Db 412 DNEYTAROGAKFPILKMTAPEALALYGRFTISDVWVSFFILLTELTKGRVYPGVMVREVL 471
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Db 472 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPTFEYLQAFLEDFYFSTEPYQGEN 531
Qy 542 L 542
Db 532 L 532

RESULT 11
SRC AVIS2 STANDARD; PRT; 586 AA.
AC P15054;
DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 64.
DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain PR2257). Retroviridae; Orthoretrovirinae;
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxId=11879;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=89094972; PubMed=2463376;
RA Geryk J., Dezelee P., Barnier J.V., Svoboda J., Nehyba J., Karakoz I.,
RA Rynditch A.V., Yatsula B.A., Calothy G.;
RT "Transduction of the cellular src gene and 3' adjacent sequences in
RT avian sarcoma virus PR2257."
RL J. Virol. 63:481-492 (1989).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calothy G.,
RA Dezelee P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- PTM: The phosphorylated form is termed pp60v-src.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
Cc EMBL; M21526; AAA42583.1; -; Genomic RNA.
Cc EMBL; X51863; CA436156.1; -; Genomic RNA.
Cc PIR; A30174; TVFVPR..
Cc HSSP; P00523; 2PTK.
Cc SMR; P15054; 83-524.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2_1; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot Kinase; 1.
DR ProDom; PD000093; SH2_1.

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DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT INIT MET 0
FT CHAIN 1 586
FT DOMAIN 80 141
FT DOMAIN 147 244
FT DOMAIN 266 519
FT NP_BIND 272 280
FT ACT_SITE 385 385
FT BINDING 294 294
FT MOD_RES 415 415
FT LIPID 1 1
FT SEQUENCE 586 AA; 65670 MW; 76520EF485B5CD02 CRC64;
SQ
Query Match 90.9%; Score 2603.5; DB 1; Length 586;
Best Local Similarity 93.1%; Pred. No. 9,3e-164;
Matches 496; Conservative 10; Mismatches 18; Indels 9; Gaps 2;
Qy 2 GSNKSKPKDASGRRSLRPEENVHGGAGFAFSPQSPASADGHRGSPAPAAAP 61
Db 1 GSSKSKPKDPSQRRSLRLEPDSTH--HGSPASQTPNKTAAPDTRTPRSRGVATEP 57
Qy 62 KLEFGFNSSDPTVSPAPAGLGGVTFVALYDSERTETDLSFKKGERLQIVNTRKYD 121
Db 58 KLEFGFNSTDTVSPAPAGLGGVTFVALYDSERTETDLSFKKGERLQIVNNT---- 113
Qy 122 VREGDWLHSLSTGQGYIPSNVYVAPSDSIQAEVYFGKITRSEERLLINENPRGTF 181
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Qy 182 LVRESSETGAYCLVSDFDNAGLNVKHYKIRKLDGSGFYTSRQFNSLOOLVAVYSK 241
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Qy 242 HADGLCHRLTTCPTSKPQTQGLAKDAWEI PRESRLREVLGSGCGEVMGTWNGTTRV 301
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Qy 482 DQYRGYRMPCEPCESLHDLMOCCWRKPEERPTFEYLQAFLEDFYFSTEP 534
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RESULT 12
SRC AVIS2 STANDARD; PRT; 567 AA.
AC P14084;

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DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-ANG-2005, sequence version 2.
 DT 07-MAY-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
 DE Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain 51).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=1181;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagiino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT Activation of the cellular src gene by transducing retrovirus. "
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation
 CC and the maintenance of neoplastic transformation, is a protein
 CC kinase that catalyzes the phosphorylation of tyrosine residues in
 CC vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pp60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC PIR; A25375; TVPVS1.
 DR HSP; P00523; 2PTK.
 DR SMR; P14084; 83-524.
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 DR InterPro: IPR002290; Ser_Thr_kinase.
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 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
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 DR PRINTS; PR00109; TYRKINASE.
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 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PSS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PSS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PSS0109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PSS0002; SH2; 1.
 DR PROSITE; PSS0001; SH3; 1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KM Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KM Tyrosine-protein kinase.
 FT INIT_MET 0
 FT CHAIN 1 567
 FT DOMAIN 80 141
 FT DOMAIN 147 244
 FT DOMAIN 266 519
 FT NP_BIND 272 280
 FT ACT_SITE 385 385
 FT BINDING 294 294
 FT MOD_RES 415 415
 FT LIPID 1 1
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SEQ SEQUENCE 567 AA; 63501 MW; EA4FC3B195A098D CRC64;
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 DB 58 KLRGFNTSDVTYSPQAGLAGGVTFVALYDESRTERTDLSFKGSRLOIVNTRKVD 113
 QY 122 VREGDWLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGKTRRESERLLINAEPRGTF 181
 DB 114 --EGDWLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGKTRRESERLLINAEPRGTF 171
 QY 182 LVRESSETTKAYCLSVSDPDNAGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYSK 241
 DB 172 LVRESSETTKAYCLSVSDPDNAGLNVKHYKIRKLDGSGFYTSRTQFNSIQQLVAYYSK 231
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 DB 232 HADGLCHRLTNVCPTSPKPTQGLAKDAMEIPRESLRLEVKLGQCFSGVMNGTTRV 291
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 DB 412 DNEYTARQAKFPFKMTAPAPAAAYGRFTIKSDVMSFGILLTELTKKRVPPGAVNREVL 471
 QY 482 DVERGYRMCPEPCPESLDHLMQCCKRKEPERPTEYIQAFLDYFTSTEP 534
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 AC Q64817;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 28.
 DE Protein-tyrosine kinase.
 GN Name=src;
 OS Avian sarcoma virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=1181;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=PR2257/16;
 RX MEDLINE=95016532; PubMed=7931166;
 RA Yatsuda B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
 RT "Evolution and origin of virus PR2257, a recent c-src transducing
 RT virus.";
 RL J. Gen. Virol. 75:2777-2781(1994).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL; L21974; AAC37877.1; -; Genomic_DNA.
 DR HSP; P00523; 2PTK.
 DR SMR; Q64817; 84-525.
 DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
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 DR InterPro; IPR001452; SH3.
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 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR Kinase; Tyrosine-protein kinase.
 KW SEQUENCE 587 AA; 65779 MW; BAAC3FSA44234F02 CRC64;

Query Match 90.7%; Score 2595.5; DB 2; Length 587;
 Best Local Similarity 92.7%; Pred. No. 3.2e-163;
 Matches 465; Conservative 10; Mismatches 20; Indels 9; Gaps 2;

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 QY 121 DVREGDMWLASHSTGQGYIPSNVYAPSDSIQAEEMVFGKIRRSERLLLAENPRGT 180
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RESULT 14
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AC P14085; Integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1990, sequence version 2.
 DT 30-AUG-2005, entry version 60.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 OS Name=V-SRC;
 GN Avian sarcoma virus (strain S2).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=11882;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87064539; PubMed=3097513;
 RA Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT "Activation of the cellular src gene by transducing retrovirus";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation and the maintenance of neoplastic transformation, is a protein kinase that catalyzes the phosphorylation of tyrosine residues in vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pp60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC Copyrighited by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 DR HSSP; P00523; 2PTR.
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 FT Proton acceptor (By similarity).
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 FT Phosphotyrosine (by autocatalysis) (By similarity).


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Query Match 87.9%; Score 2515.5; DB 1; Length 525;

Best Local Similarity 91.8%; Pred. No. 5,4e-158;

Matches 481; Conservative 12; Mismatches 22; Indels 9; Gaps 2;

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DB 58 KLFGGFNTSDTVTSPOGAGLAGVTFVALYDYESRTEFDLSFKGERLQIVNNT---- 113
QY 122 VREGDWLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESERLLINAEPRGTF 181
DB 114 --EGDWMLANSLTTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESERLLINAEPRGTF 171
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Job time : 156.335 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 31.134 Seconds
(without alignments)
1523.786 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/H COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/PC COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/biofile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2821	98.5	536	1	US-07-820-011A-4	Sequence 4, Appli
2	2821	98.5	536	2	US-08-426-509A-13	Sequence 13, Appli
3	2821	98.5	536	2	US-08-232-545-13	Sequence 13, Appli
4	2821	98.5	536	2	US-09-444-711A-2	Sequence 2, Appli
5	2821	98.5	536	2	US-09-929-266-10	Sequence 10, Appli
6	2821	98.5	536	2	US-09-977-261-13	Sequence 13, Appli
7	2821	98.5	536	5	PCT-US93-00445-4	Sequence 13, Appli
8	2821	98.5	536	5	PCT-US95-05008-13	Sequence 13, Appli
9	2821	98.5	537	2	US-09-949-016-10282	Sequence 10282, A
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11	2650.5	92.6	533	2	US-09-470-881-3	Sequence 3, Appli
12	2647.5	92.5	533	1	US-07-820-011A-2	Sequence 2, Appli
13	2647.5	92.5	533	5	PCT-US93-00445-2	Sequence 2, Appli
14	2110.5	73.7	543	2	US-08-426-509A-14	Sequence 14, Appli
15	2110.5	73.7	543	2	US-08-232-545-14	Sequence 14, Appli
16	2110.5	73.7	543	2	US-09-470-881-8	Sequence 8, Appli
17	2110.5	73.7	543	2	US-09-538-092-870	Sequence 870, App
18	2110.5	73.7	543	2	US-09-977-261-14	Sequence 14, Appli
19	2110.5	73.7	543	5	PCT-US95-05008-14	Sequence 14, Appli
20	2108.5	73.6	541	2	US-09-864-281-20	Sequence 20, Appli
21	1936	67.6	536	2	US-08-426-509A-12	Sequence 12, Appli
22	1936	67.6	536	2	US-08-232-545-12	Sequence 12, Appli
23	1936	67.6	536	2	US-09-977-261-12	Sequence 12, Appli
24	1936	67.6	536	5	PCT-US95-05008-12	Sequence 12, Appli
25	1931	67.4	532	1	US-08-594-447-1	Sequence 1, Appli
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27	1919.5	67.0	537	2	US-08-426-509A-11	Sequence 11, Appli
28	1919.5	67.0	537	2	US-08-232-545-11	Sequence 11, Appli
29	1919.5	67.0	537	2	US-09-977-261-11	Sequence 11, Appli
30	1919.5	67.0	537	5	PCT-US95-05008-11	Sequence 11, Appli
31	1919.5	67.0	536	2	US-09-538-092-859	Sequence 859, App
32	1911.5	66.8	537	2	US-09-771-161A-212	Sequence 212, App
33	1911.5	66.8	537	2	US-09-771-161A-213	Sequence 213, App
34	1843	64.4	529	2	US-08-426-509A-15	Sequence 15, Appli
35	1843	64.4	529	2	US-08-232-545-15	Sequence 15, Appli
36	1843	64.4	529	2	US-09-538-092-885	Sequence 885, App
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39	1735.5	60.6	485	2	US-10-094-749-2726	Sequence 2726, Ap
40	1529	53.4	573	2	US-09-949-016-10415	Sequence 10415, A
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42	1525.5	53.3	505	2	US-08-232-545-17	Sequence 17, Appli
43	1525.5	53.3	505	2	US-09-977-261-17	Sequence 17, Appli
44	1525.5	53.3	505	5	PCT-US95-05008-17	Sequence 17, Appli
45	1461	51.0	508	2	US-09-862-154-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-820-011A-4
Sequence 4, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasmidogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.

AUTHORS: Glibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: pp60c-src
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Glibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

Query Match 98.5%; Score 2821; DB 1; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

1 MGSNKKPKDASGRRSLSPAENVHAGGAGAPASQTPSKPASADGHRPSAFAFAAAE 60
1 MGSNKKPKDASGRRSLSPAENVHAGGAGAPASQTPSKPASADGHRPSAFAFAAAE 60
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
121 DVREGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRT 180
118 --EGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRT 174
181 FLVRESEETTKGAYCLSVSPDNAGKLVNKGKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 240
175 FLVRESEETTKGAYCLSVSPDNAGKLVNKGKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 234
241 KHAADGLCHRLTTCPTSKPTQTOGLADAMEIPRESLRLEVKLGQGCFGVWMTWNGTTR 300
235 KHAADGLCHRLTTCPTSKPTQTOGLADAMEIPRESLRLEVKLGQGCFGVWMTWNGTTR 294
301 VAIKTKLKPFGMSPEARLQEAQWVKLRHEKLVQLYAVNSEEPYIYITEVWSKSLDPLK 360
295 VAIKTKLKPFGMSPEARLQEAQWVKLRHEKLVQLYAVNSEEPYIYITEVWSKSLDPLK 354
361 GETGKYLRLPOLVDMAQAISGNAVYERMYVARDLRAANILVGENLVCKVADFLARLI 420
355 GETGKYLRLPOLVDMAQAISGNAVYERMYVARDLRAANILVGENLVCKVADFLARLI 414
421 EDNEYTARQAKPEPKMTAEBALYGRFTTKSDVMSFGILLTELTKGRVPYEGMVNREV 480
415 EDNEYTARQAKPEPKMTAEBALYGRFTTKSDVMSFGILLTELTKGRVPYEGMVNREV 474
481 LDQVGVGYMPCPECPESLHDMCCWKRKEPERPTFEYLQAFLEDYFTSTPQYQPG 540
475 LDQVGVGYMPCPECPESLHDMCCWKRKEPERPTFEYLQAFLEDYFTSTPQYQPG 534

Qy 541 NL 542
Db 535 NL 536

RESULT 2
US-08-426-509A-13
Sequence 13, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Gishizky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-426-509A-13

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

1 MGSNKKPKDASGRRSLSPAENVHAGGAGAPASQTPSKPASADGHRPSAFAFAAAE 60
1 MGSNKKPKDASGRRSLSPAENVHAGGAGAPASQTPSKPASADGHRPSAFAFAAAE 60
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 120
61 PKLFGFNSSDVTYSPQRAGPLAGVTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 117
121 DVREGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRT 180
118 --EGDWMLAHSLSTQGTGYIPSNVYAPSDSIQAEWYFGKTRRSEERLLNAENPRT 174
181 FLVRESEETTKGAYCLSVSPDNAGKLVNKGKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 240
175 FLVRESEETTKGAYCLSVSPDNAGKLVNKGKIRKLDGSGFYITSTRTOFNSLQQLVAYYS 234
241 KHAADGLCHRLTTCPTSKPTQTOGLADAMEIPRESLRLEVKLGQGCFGVWMTWNGTTR 300

Db 235 KHAADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLBLEVYLGCGCGEYVMGTWNGTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 354
Qy 361 GETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLPAANILVGENLVCKVADGRLRI 420
Db 355 GETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLPAANILVGENLVCKVADGRLRI 414
Qy 421 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSFGILLTTLTKGRVPYPGMVNREV 480
Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSFGILLTTLTKGRVPYPGMVNREV 474
Qy 481 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPFTEYLQAFLEDFYFSTEPQYQGE 540
Db 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPFTEYLQAFLEDFYFSTEPQYQGE 534
Qy 541 NL 542
Db 535 NL 536

RESULT 3
US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ulirich, Axel
; APPLICANT: Giehlitzky, Mikhail
; APPLICANT: Sures, Iman G. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: No. 6506578e1
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-232-545-13

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
Qy 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAPAAE 60

Db 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 PKLPGFNSSDYTSPQAPAGVTFVALYDYESRTETDLSFKKGERLQIVNTRKV 120
Db 61 PKLPGFNSSDYTSPQAPAGVTFVALYDYESRTETDLSFKKGERLQIVNTRKV 117
Qy 121 DVREBGMWLAHSLSTGQTYIPSNYVAPSPDSIQAEENVYFGKITRESEBRLLNENRGT 180
Db 118 ---EGDWMLAHSLSLTGQTYIPSNYVAPSPDSIQAEENVYFGKITRESEBRLLNENRGT 174
Qy 181 FLVRESSTGAYCLSTSDPDNAKGLVVKHYKIRKLDSSGFYTSRTOFNSLQOLVAYYS 240
Db 175 FLVRESSTGAYCLSTSDPDNAKGLVVKHYKIRKLDSSGFYTSRTOFNSLQOLVAYYS 234
Qy 241 KHAADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLBLEVYLGCGCGEYVMGTWNGTTR 300
Db 235 KHAADGLCHRLTTCPTSKPOTQGLAKDAMEIPRESLBLEVYLGCGCGEYVMGTWNGTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 354
Qy 361 GETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLPAANILVGENLVCKVADGRLRI 420
Db 355 GETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLPAANILVGENLVCKVADGRLRI 414
Qy 421 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSFGILLTTLTKGRVPYPGMVNREV 480
Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSFGILLTTLTKGRVPYPGMVNREV 474
Qy 481 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPFTEYLQAFLEDFYFSTEPQYQGE 540
Db 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPFTEYLQAFLEDFYFSTEPQYQGE 534
Qy 541 NL 542
Db 535 NL 536

RESULT 4
US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764833
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Iddy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-7136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-src coding region
US-09-444-711A-2

Query Match 98.5%; Score 2821; DB 2; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
Qy 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPDASQRRRLSEPAENVHAGGAGFAPSQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 PKLPGFNSSDYTSPQAPAGVTFVALYDYESRTETDLSFKKGERLQIVNTRKV 120

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Db 61 PKLFGFNSSDVTYTSQBARAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNT --- 117
Qy 121 DVREGDWMHLAHSISTGQTGYIPSNYYVAPSDSIQAEEMYPFGKTRRESERLLNAENPRGT 180
Db 118 ---EGDWMHLAHSISTGQTGYIPSNYYVAPSDSIQAEEMYPFGKTRRESERLLNAENPRGT 174
Qy 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFPYITSRTOFNSLQOLVAYYS 240
Db 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFPYITSRTOFNSLQOLVAYYS 234
Qy 241 KHADGCHRLTYTCPTSPKPTQGLADKAMEIPRESRLRVLKGGCGFGEVMGTNGTTR 300
Db 235 KHADGCHRLTYTCPTSPKPTQGLADKAMEIPRESRLRVLKGGCGFGEVMGTNGTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYMSKGSLLDFLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYMSKGSLLDFLK 354
Qy 361 GETGKTLRLPOLVDMAAQIASGMAYYERMMYVHRDLRAANILVGENLVCKVADPGLARLI 420
Db 355 GETGKTLRLPOLVDMAAQIASGMAYYERMMYVHRDLRAANILVGENLVCKVADPGLARLI 414
Qy 421 EDNEYTAROGAKFPICKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 480
Db 415 EDNEYTAROGAKFPICKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 474
Qy 481 LDQVERGYMPCPECPESLHDLMCQWKEPEBERPTFEYLQAFLEDYFTSTEPYOQPG 540
Db 475 LDQVERGYMPCPECPESLHDLMCQWKEPEBERPTFEYLQAFLEDYFTSTEPYOQPG 534
Qy 541 NL 542
Db 535 NL 536
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RESULT 5

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US-09-929-266-10
/ Sequence 10, Application US/09929266
/ Patent No. 6824981
/ GENERAL INFORMATION:
/ APPLICANT: Brian T. Chait
/ APPLICANT: Darin R. Lattimer
/ APPLICANT: Paul M. Lizardi
/ APPLICANT: Eric R. Kershner
/ APPLICANT: Jon S. Morrow
/ APPLICANT: Matthew E. Roth
/ APPLICANT: Martin J. McConnell
/ APPLICANT: Kevin J. McConnell
/ TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
/ FILE REFERENCE: 01173.000302
/ CURRENT APPLICATION NUMBER: US/09/929,266
/ PRIOR FILING DATE: 2001-08-13
/ PRIOR APPLICATION NUMBER: 60/224,939
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/283,498
/ PRIOR FILING DATE: 2000-04-12
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FaalSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 98.5%; Score 2821; DB 2; Length 536;

Best Local Similarity 98.9%; Pred. No. 6,4e-214;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Qy 1 MGSNKKPKDASQRRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
Db 1 MGSNKKPKDASQRRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
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Qy 61 PKLFGFNSSDVTYTSQBARAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNT RYK 120
Db 61 PKLFGFNSSDVTYTSQBARAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNT --- 117
Qy 121 DVREGDWMHLAHSISTGQTGYIPSNYYVAPSDSIQAEEMYPFGKTRRESERLLNAENPRGT 180
Db 118 ---EGDWMHLAHSISTGQTGYIPSNYYVAPSDSIQAEEMYPFGKTRRESERLLNAENPRGT 174
Qy 181 FLVRESEETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFPYITSRTOFNSLQOLVAYYS 240
Db 175 FLVRESEETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFPYITSRTOFNSLQOLVAYYS 234
Qy 241 KHADGCHRLTYTCPTSPKPTQGLADKAMEIPRESRLRVLKGGCGFGEVMGTNGTTR 300
Db 235 KHADGCHRLTYTCPTSPKPTQGLADKAMEIPRESRLRVLKGGCGFGEVMGTNGTTR 294
Qy 301 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYMSKGSLLDFLK 360
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIYTEYMSKGSLLDFLK 354
Qy 361 GETGKTLRLPOLVDMAAQIASGMAYYERMMYVHRDLRAANILVGENLVCKVADPGLARLI 420
Db 355 GETGKTLRLPOLVDMAAQIASGMAYYERMMYVHRDLRAANILVGENLVCKVADPGLARLI 414
Qy 421 EDNEYTAROGAKFPICKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 480
Db 415 EDNEYTAROGAKFPICKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREV 474
Qy 481 LDQVERGYMPCPECPESLHDLMCQWKEPEBERPTFEYLQAFLEDYFTSTEPYOQPG 540
Db 475 LDQVERGYMPCPECPESLHDLMCQWKEPEBERPTFEYLQAFLEDYFTSTEPYOQPG 534
Qy 541 NL 542
Db 535 NL 536
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RESULT 6

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US-09-977-261-13
/ Sequence 13, Application US/09977261
/ Patent No. 6908984
/ GENERAL INFORMATION:
/ APPLICANT: ULRICH, AXEL
/ APPLICANT: GISHIZKY, MIKHAIL
/ APPLICANT: SURES, IRMINGARD
/ TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
/ FILE REFERENCE: 038602/1259
/ CURRENT APPLICATION NUMBER: US/09/977,261
/ PRIOR FILING DATE: 2001-10-16
/ PRIOR APPLICATION NUMBER: 08/232,545
/ PRIOR FILING DATE: 1994-04-22
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 536
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 98.5%; Score 2821; DB 2; Length 536;

Best Local Similarity 98.9%; Pred. No. 6,4e-214;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Qy 1 MGSNKKPKDASQRRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
Db 1 MGSNKKPKDASQRRRSLPEAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAAE 60
Qy 61 PKLFGFNSSDVTYTSQBARAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNT RYK 120
Db 61 PKLFGFNSSDVTYTSQBARAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNT --- 117
Qy 121 DVREGDWMHLAHSISTGQTGYIPSNYYVAPSDSIQAEEMYPFGKTRRESERLLNAENPRGT 180
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Db 118 ---BGDMWLAHSLSTGOTGYIPSNVAPSDSIOAEWYFGKITRRESRLILNENPCT 174
QY 181 FLVRESETTKAYCCLSVSDPNNAGLNVKHKIRKLDGSGFYITSRTQFNSIQOLVAYYS 240
Db 175 FLVRESETTKAYCCLSVSDPNNAGLNVKHKIRKLDGSGFYITSRTQFNSIQOLVAYYS 234
QY 241 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVMMGTWNGTTR 300
Db 235 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVMMGTWNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAOVMKCLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFIOEAOVMKCLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADFGLARLI 420
Db 355 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADFGLARLI 414
QY 421 EDNEYTAROGAKFPKMTAPAPALYGRFTIKSDVMSFGILLTELTTKGRVYPCGMVNRV 480
Db 415 EDNEYTAROGAKFPKMTAPAPALYGRFTIKSDVMSFGILLTELTTKGRVYPCGMVNRV 474
QY 481 LDQVERGYRMPCEPCEPSLHDLMOQCRKEPSEBPIYIOAFLEDYFTSTEPQOPGE 540
Db 475 LDQVERGYRMPCEPCEPSLHDLMOQCRKEPSEBPIYIOAFLEDYFTSTEPQOPGE 534
QY 541 NL 542
Db 535 NL 536

RESULT 7
PCT-US93-00445-4
; Sequence 4, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madril, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820,011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear

MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Tanaka, Akio
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: Human Cellular src Gene:
; TITLE: Nucleotide Sequence and Derived Amino
; TITLE: Acid Sequence of the Region Coding for
; TITLE: the Carboxy-Terminal Two-Thirds of
; TITLE: p60c-src
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; ISSUE: 5
; PAGES: 1122-1129
; DATE: May, 1985
; PUBLICATION INFORMATION:
; AUTHORS: Tanaka, Akio
; AUTHORS: Gibbs, Carol P.
; AUTHORS: Arthur, Richard R.
; AUTHORS: Anderson, Stephen K.
; AUTHORS: Kung, Hsing-Jien
; AUTHORS: Fujita, Donald J.
; TITLE: DNA Sequence Encoding the
; TITLE: Amino-Terminal Region of the Human c-src
; TITLE: Protein: Implications of Sequence
; TITLE: Divergence among src-Type Kinase
; TITLE: Oncogenes
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 7
; ISSUE: 5
; PAGES: 1978-1983
; DATE: May, 1987
; PCT-US93-00445-4
Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 6.4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAFPPASQTPSKPASADGHRGPSAFAAPAAB 60
Db 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAFPPASQTPSKPASADGHRGPSAFAAPAAB 60
QY 61 PKLFGGRSSPTVTSPQAGPLAGGYTFVALYDESETEITDLSFKKGBRLQIVNNTKV 120
Db 61 PKLFGGRSSPTVTSPQAGPLAGGYTFVALYDESETEITDLSFKKGBRLQIVNNTKV 117
QY 121 DVREGDMWLAHSLSTGOTGYIPSNVAPSDSIOAEWYFGKITRRESRLILNENPCT 180
Db 118 ---BGDMWLAHSLSTGOTGYIPSNVAPSDSIOAEWYFGKITRRESRLILNENPCT 174
QY 181 FLVRESETTKAYCCLSVSDPNNAGLNVKHKIRKLDGSGFYITSRTQFNSIQOLVAYYS 240
Db 175 FLVRESETTKAYCCLSVSDPNNAGLNVKHKIRKLDGSGFYITSRTQFNSIQOLVAYYS 234
QY 241 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVMMGTWNGTTR 300
Db 235 KHAAGLCHRLTTVCPPTSKEPOTQGLAKDAMEIPRESLRLEVLDGCGCFGEVMMGTWNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIOEAOVMKCLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEAFIOEAOVMKCLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADFGLARLI 420
Db 355 GETGKYLRPLQVDMAAQIASGMAVERMNVYHRDLRAANILVGENLVCKVADFGLARLI 414
QY 421 EDNEYTAROGAKFPKMTAPAPALYGRFTIKSDVMSFGILLTELTTKGRVYPCGMVNRV 480

Db 415 EDNEYTARQAKFPKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPYPMVNRREV 474
Qy 481 LDQVGRGYMPCPEPCESLHDMCCQWKREPERPTFEYLOAFLEDTSTEPQYQPG 540
Db 475 LDQVGRGYMPCPEPCESLHDMCCQWKREPERPTFEYLOAFLEDTSTEPQYQPG 534
Qy 541 NL 542
Db 535 NL 536

RESULT 8
PCT-US95-05008-13
Sequence 13, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wiscenchaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Db 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Qy 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 120

Db 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNT--- 117
Qy 121 DVREGWMLAHSISTQGTGYIPSNYAPBDSIOAEMVYGKTRRSERLLNAENPRGT 180
Db 118 --EGDWMLAHSISTQGTGYIPSNYAPBDSIOAEMVYGKTRRSERLLNAENPRGT 174
Qy 181 FLVRESETTKGAICYLSPDFDNAGKLNHGYKLRKLDGSGGFYITSTRTOFNSLOQLVAAYS 240
Db 175 FLVRESETTKGAICYLSPDFDNAGKLNHGYKLRKLDGSGGFYITSTRTOFNSLOQLVAAYS 234
Qy 241 KHAADGLCHRLTYCPTSKPQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNNGTTR 300
Db 235 KHAADGLCHRLTYCPTSKPQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNNGTTR 294
Qy 301 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEEPYITETMSKSLDPLK 360
Db 295 VAIKTLKPGTMSPEALQEAQVMKKLRHEKLVOLYAVVSEEPYITETMSKSLDPLK 354
Qy 361 GETGKTLRLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLI 420
Db 355 GETGKTLRLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLI 414
Qy 421 EDNEYTARQAKFPKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPYPMVNRREV 480
Db 415 EDNEYTARQAKFPKMTAPEALYGRFTIKSDVMSGILLTELTTKGRVPYPMVNRREV 474
Qy 481 LDQVGRGYMPCPEPCESLHDMCCQWKREPERPTFEYLOAFLEDTSTEPQYQPG 540
Db 475 LDQVGRGYMPCPEPCESLHDMCCQWKREPERPTFEYLOAFLEDTSTEPQYQPG 534
Qy 541 NL 542
Db 535 NL 536

RESULT 9
US-09-949-016-10282
Sequence 10282, Application US/09949016
Patent No. 6812338
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match 98.5%; Score 2821; DB 2; Length 537;
Best Local Similarity 98.9%; Pred. No. 6,4e-214;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 60
Db 2 MGSNKSXPDAQORRRSLPEAENVHAGAGGAFPASQTPSKPASAADGHRGSAFAFAAAE 61
Qy 61 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 120
Db 62 PKLFGGFNSSDVTSPQAGPLAGVTTFFVALYDYESRTEITDLSFKKGERLQIVNNT--- 118

QY 301 VAIKTLKPGTMSBEAFLOEAQVWKKLRHEKLVOLYAVVSEBPIYITEVMSKSLDPLK 360
DB 292 VAIKTLKPGTMSBEAFLOEAQVWKKLRHEKLVOLYAVVSEBPIYITEVMSKSLDPLK 351
QY 361 GETGKYLRLPOLVDMAAOIASGNAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 352 GEMGKTLRLPOLVDMAAOIASGNAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 480
DB 412 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 471
QY 481 LDQVERGYRMPCCPECSLHDLCCQWKPERPFEYLOAFLEBDFSTPEYOPGE 540
DB 472 LDQVERGYRMPCCPECSLHDLCCQWKPERPFEYLOAFLEBDFSTPEYOPGE 531
QY 541 NL 542
DB 532 NL 533

RESULT 12
US-07-820-011A-2
Sequence 2, Application US/07820011A
Patent No. 533615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the

TITLE: Cellular Gene Homologous to the RSV arc
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Value
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
US-07-820-011A-2

Query Match 92.5%; Score 2647.5; DB 1; Length 533;
Best Local Similarity 92.8%; Pred. No. 3e-200;
Matches 503; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

QY 1 MGSNKSXPDOASORRSLSLPAENVHAGAGGAFPASQTPKPSADGHRGSAFAFAAAE 60
DB 1 MGSNKSXPDOASORRSLSLPAENVHAGAGGAFPASQTPKPSADGHRGSAFAFAAAE 57
QY 61 PKLFGGNSSDVTSPQAGAPLAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 120
DB 58 PKLFGGNSSDVTSPQAGAPLAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 114
QY 121 DVREGDWMILASHSTGCTGYIPSNVYAPSDSIOAEWYFGKTRRESERLLNAENPRGT 180
DB 115 ---EGDWMILASHSTGCTGYIPSNVYAPSDSIOAEWYFGKTRRESERLLNAENPRGT 171
QY 181 FLVRESBTTKGAAYCLSDPFDNAKGLNMGHYKIRKLDGSGFYTSRTQFNSLQQLVAAYS 240
DB 172 FLVRESBTTKGAAYCLSDPFDNAKGLNMGHYKIRKLDGSGFYTSRTQFNSLQQLVAAYS 231
QY 241 KHADGCHRLTVTCPTSPKQTOGLADAEIPRESLRLEVKLGQCGFGEVWGTNNGTTR 300
DB 232 KHADGCHRLTVTCPTSPKQTOGLADAEIPRESLRLEVKLGQCGFGEVWGTNNGTTR 291
QY 301 VAIKTLKPGTMSBEAFLOEAQVWKKLRHEKLVOLYAVVSEBPIYITEVMSKSLDPLK 360
DB 292 VAIKTLKPGTMSBEAFLOEAQVWKKLRHEKLVOLYAVVSEBPIYITEVMSKSLDPLK 351
QY 361 GETGKYLRLPOLVDMAAOIASGNAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 420
DB 352 GEMGKTLRLPOLVDMAAOIASGNAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 411
QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 480
DB 412 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYGMVNRREV 471
QY 481 LDQVERGYRMPCCPECSLHDLCCQWKPERPFEYLOAFLEBDFSTPEYOPGE 540
DB 472 LDQVERGYRMPCCPECSLHDLCCQWKPERPFEYLOAFLEBDFSTPEYOPGE 531
QY 541 NL 542
DB 532 NL 533

RESULT 13
PCT-US93-00445-2
Sequence 2, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: AIX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHEICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the RSV src
TITLE: Cellular Gene Homologous to the
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-2

Query Match 92.5%; Score 2647.5; DB 5; Length 533;
Best Local Similarity 92.8%; Pred. No. 3e-200;
Matches 503; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

1 MGSNKRPKDASQRRSLPEAENVHAGAGAFPASQTPSKPASADGHRGSAAPAAAE 60
1 MGSKSRPKDPSQRRSLPEPDSH--HGFPAHQTPNKTAADTHRTSPRSFGVATE 57
61 PKLFGFNSSDVTSPORAGPLAGVTTFVALYDSESTETDLSFKKGERLQIVNTRKV 120
58 PKLFGFNSTSDVTSPORAGALAGVTTFVALYDESRTETDLSFKKGERLQIVNNT-- 114
121 DVREGDWMHLAHSLSGTQGTGYPSPNYVAPSDSIQAEWYFGKITTRRESERLLNENPRGT 180
115 ---EGDWMHLAHSLSGTQGTGYPSPNYVAPSDSIQAEWYFGKITTRRESERLLNENPRGT 171
181 FLVSESETTGAYCCLSYSDPNAKGLNVKHYKIRKLDGCGGYTSRTPFNSLQOLVAYYS 240
172 FLVSESETTGAYCCLSYSDPNAKGLNVKHYKIRKLDGCGGYTSRTPFNSLQOLVAYYS 231
241 KHADGLCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVLKAGOCFGEVWVGWNGTTR 300
232 KHADGLCHRLTTCVPTSPKPTQGLAKDAWEIPRESLRLEVLKAGOCFGEVWVGWNGTTR 291
301 VAITLKPRTMSPEAFLOEAQVMKLRREKLVOLYAVVSEPIYITVTFYMKSGSLDPLK 360
292 VAITLKPRTMSPEAFLOEAQVMKLRREKLVOLYAVVSEPIYITVTFYMKSGSLDPLK 351
361 GETGKYRLPOLYMAAQIASGMAVVERMYVHDLRAANILVGENLVCYVADFGLARLI 420
352 GEMKTYRLPOLYMAAQIASGMAVVERMYVHDLRAANILVGENLVCYVADFGLARLI 411

421 EDNEYTAQGAKEPIKWTAPALYGRFTIKSDVMSFGILLTETLTGKRVYPGVNREV 480
412 EDNEYTAQGAKEPIKWTAPALYGRFTIKSDVMSFGILLTETLTGKRVYPGVNREV 471
481 LDQVGRGYMPCPECESEIHDIMCQWRKPEPERPTEFYLOAFLEDFYFSTPEQYQGE 540
472 LDQVGRGYMPCPECESEIHDIMCQWRKPEPERPTEFYLOAFLEDFYFSTPEQYQGE 531
541 NL 542
532 NL 533

RESULT 14
US-08-426-509A-14
Sequence 14, Application US/08426509A
Patent No. 6326469
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizaky, Mikhail
APPLICANT: Sures, Iman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-399
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: No. 6326469e
US-08-426-509A-14

Query Match 73.7%; Score 2110.5; DB 2; Length 543;
Best Local Similarity 73.7%; Pred. No. 6.6e-158;
Matches 407; Conservative 51; Mismatches 75; Indels 19; Gaps 5;

1 MGSNKRPKDASQRRSLPEAENVHAGAG--GAFPASQTPSKPASADGHRGSAAPAAFA 57
1 MGCTKSXENKSPAKIKYPPENTPEVSTSVSHYGAEPTTVSCPSSA---KGTAVNBSL 57
58 AABP-----KLFGFNSSDVTSPORAGPLAGVTTFVALYDSESTETDLSFKKGER 110
58 SMTPFGSSGVTTPFGASSSFSVPSYPAGLTGVTILFVALYDSEARTETDLSFKKGER 117
111 LQIVNTRKVDVREGDWMHLAHSLSGTQGTGYPSPNYVAPSDSIQAEWYFGKITTRRESERL 170

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Db      118  FQIINNT-----EGDWMEARSITATGKNGYIPSNYYVAPADSIQAEWYFGMKGRKDAERL 171
Qy      171  LLAENPRGFLVRESSTTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTQFN 230
Db      172  LNPGRNGRGFLVRESSTTGAYSLSRDWDGIRGDNVKKYKIRKLDNGGYITTRAQFD 231
Qy      231  SLQOLVAAYYSKHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESRLLEVYLGQGCFCGEV 290
Db      232  TLQOLVAHYTHHADGLCHKLTVCPTVKPOTQGLAKDAMEIPRESRLLEVYLGQGCFCGEV 291
Qy      291  WMGTNNGTTVAIKTLKPGTMSPEAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYIYTEM 350
Db      292  WMGTNNGTTVAIKTLKPGTMSPEAPLOEAQIMKKLRHDKLVLYAVVSEEPITYIYTEM 351
Qy      351  SKGSLDLFLKGGTGYKRLPOLVDMAAQIASGAAVYERNNYVRDLRAANILVGENLVCK 410
Db      352  SKGSLDLFLKGGTGYKRLPOLVDMAAQIADGMAVIERNNYIHRDLRAANILVGENLVCK 411
Qy      411  VADFGLARLIEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILITELTTKGRV 470
Db      412  IADFGLARLIEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILITELVTYGRV 471
Qy      471  PYGMYNREVLDOVERGYRMPCEPCEPSIHDLMCCMRKEPERPTEFYLOAFLEDYFT 530
Db      472  PYGMYNREVLDOVERGYRMPCEPCEPSIHELMNLCKMKDPDBRPTEFYIQSFLDYFT 531
Qy      531  STEPQYQPGENTL 542
Db      532  ATEPQYQPGENTL 543

```

RESULT 15

```

US-08-232-545-14
; Sequence 14, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Axel
; APPLICANT: Glabizky, Mikhail
; APPLICANT: Sures, Iman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-Apr-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

```

MOLECULE TYPE: protein
US-08-232-545-14

Query Match 73.7%; Score 2110.5; DB 2; Length 543;
Best Local Similarity 73.7%; Pred. No. 6,6e-158;
Matches 407; Conservative 51; Mismatches 75; Indels 19; Gaps 5;

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Qy      1  MGSNKSMP--KDAQRBRSLERPAENVAGAG--GAPPASQPSKAPASGDHGRGSAAPAPA 57
Db      1  MGCISKENKSPAIKTRPEPTPEVSTSVSHYAEPTVSPCCSSA--KGTAVNFSL 57
Qy      58  AAEF-----KLFGFNSSDVTYSPORAGPLAGVTFPAALDYDSRRTDLSFKKGR 110
Db      58  SMPFGSSGVTFPGGASSSFVSYPAGLGGVTIFPALVDYARTTEDLSFKKGR 117
Qy      111  LQIVNTRKVDVREGDWMLAHSLSTQGTGYPNNYVAPSDSIOAEWYFGKTRRESERL 170
Db      118  FQIINNT-----EGDWMEARSITATGKNGYIPSNYYVAPADSIQAEWYFGMKGRKDAERL 171
Qy      171  LLAENPRGFLVRESSTTGAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSRTQFN 230
Db      172  LNPGRNGRGFLVRESSTTGAYSLSRDWDGIRGDNVKKYKIRKLDNGGYITTRAQFD 231
Qy      231  SLQOLVAAYYSKHADGLCHRLTTVCPTSKPOTQGLAKDAMEIPRESRLLEVYLGQGCFCGEV 290
Db      232  TLQOLVAHYTHHADGLCHKLTVCPTVKPOTQGLAKDAMEIPRESRLLEVYLGQGCFCGEV 291
Qy      291  WMGTNNGTTVAIKTLKPGTMSPEAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYIYTEM 350
Db      292  WMGTNNGTTVAIKTLKPGTMSPEAPLOEAQIMKKLRHDKLVLYAVVSEEPITYIYTEM 351
Qy      351  SKGSLDLFLKGGTGYKRLPOLVDMAAQIASGAAVYERNNYVRDLRAANILVGENLVCK 410
Db      352  SKGSLDLFLKGGTGYKRLPOLVDMAAQIADGMAVIERNNYIHRDLRAANILVGENLVCK 411
Qy      411  VADFGLARLIEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILITELTTKGRV 470
Db      412  IADFGLARLIEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILITELVTYGRV 471
Qy      471  PYGMYNREVLDOVERGYRMPCEPCEPSIHDLMCCMRKEPERPTEFYLOAFLEDYFT 530
Db      472  PYGMYNREVLDOVERGYRMPCEPCEPSIHELMNLCKMKDPDBRPTEFYIQSFLDYFT 531
Qy      531  STEPQYQPGENTL 542
Db      532  ATEPQYQPGENTL 543

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Search completed: June 5, 2006, 17:18:19
Job time : 33.134 secs

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OM protein - protein search, using SW model

Run on: June 5, 2006, 17:37:14 ; Search time 108.467 Seconds
(without alignments)
2314.645 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXPKQASQRRSLRP.....AFLEDYRTSTPEYQPGENL 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_sids3/prodata/2/pubppa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_sids3/prodata/2/pubppa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_sids3/prodata/2/pubppa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_sids3/prodata/2/pubppa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_sids3/prodata/2/pubppa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_sids3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2863	100.0	542	US-10-691-079-1	Sequence 1, Appl1
2	2823	98.6	542	US-10-732-923-13447	Sequence 13447, A
3	2821	98.5	536	US-09-977-260-13	Sequence 13, Appl1
4	2821	98.5	536	US-09-928-266-10	Sequence 10, Appl1
5	2821	98.5	536	US-09-977-261-13	Sequence 13, Appl1
6	2821	98.5	536	US-10-691-079-2	Sequence 2, Appl1
7	2821	98.5	536	US-10-887-588-2	Sequence 2, Appl1
8	2821	98.5	536	US-10-497-641-2	Sequence 2, Appl1
9	2821	98.5	536	US-10-825-568-10	Sequence 10, Appl1
10	2821	98.5	536	US-10-821-231-C-1	Sequence 10, Appl1
11	2821	98.5	536	US-10-469-469-273	Sequence 273, App
12	2821	98.5	536	US-11-233-510-24	Sequence 24, Appl1
13	2821	98.5	541	US-10-691-079-3	Sequence 3, Appl1
14	2816	98.4	535	US-10-394-322A-56	Sequence 56, Appl1
15	2816	98.4	535	US-10-814-109-4	Sequence 4, Appl1
16	2788	97.4	530	US-10-887-588-4	Sequence 4, Appl1
17	2754	96.2	530	US-10-330-773-749	Sequence 749, App
18	2653.5	92.7	533	US-10-276-633-1	Sequence 1, Appl1
19	2653.5	92.7	533	US-10-732-923-13652	Sequence 13652, A
20	2650.5	92.6	533	US-10-732-923-13654	Sequence 13654, A
21	2650.5	92.6	533	US-11-230-995-3	Sequence 3, Appl1
22	2648.5	92.5	533	US-10-732-923-13650	Sequence 13650, A
23	2628.5	91.8	533	US-10-276-633-2	Sequence 2, Appl1
24	2608.5	91.1	587	US-10-732-923-13472	Sequence 13472, A
25	2601.5	90.9	568	US-10-732-923-13474	Sequence 13474, A
26	2595.5	90.7	587	US-10-732-923-13469	Sequence 13469, A
27	2586.5	90.3	557	US-10-732-923-13475	Sequence 13475, A

28	2520.5	88.0	526	5	US-10-732-923-13499	Sequence 13499, A
29	2503.5	87.4	526	5	US-10-732-923-13484	Sequence 13484, A
30	2503.5	87.4	772	5	US-10-732-923-13485	Sequence 13485, A
31	2484.5	86.8	526	5	US-10-732-923-13483	Sequence 13483, A
32	2478.5	86.6	526	5	US-10-732-923-13497	Sequence 13497, A
33	2475.5	86.5	537	5	US-10-732-923-13636	Sequence 13636, A
34	2472.5	86.4	526	5	US-10-732-923-13493	Sequence 13493, A
35	2472.5	86.4	526	5	US-10-732-923-13498	Sequence 13498, A
36	2471.5	86.3	526	5	US-10-732-923-13489	Sequence 13489, A
37	2470.5	86.3	526	5	US-10-732-923-13486	Sequence 13486, A
38	2469	86.2	523	5	US-10-732-923-13488	Sequence 13488, A
39	2469	86.2	535	5	US-10-732-923-13495	Sequence 13495, A
40	2468.5	86.2	526	5	US-10-732-923-13491	Sequence 13491, A
41	2457.5	85.8	526	5	US-10-732-923-13487	Sequence 13487, A
42	2453.5	85.7	526	5	US-10-732-923-13487	Sequence 13487, A
43	2450	85.6	532	5	US-10-732-923-13633	Sequence 13633, A
44	2449	85.5	532	5	US-10-732-923-13635	Sequence 13635, A
45	2446	85.4	532	5	US-10-732-923-13637	Sequence 13637, A

ALIGNMENTS

RESULT 1

US-10-691-079-1

Sequence 1, Application US/10691079

Publication No. US20040176313A1

GENERAL INFORMATION:

APPLICANT: AVENTIS PHARMA S.A.

TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease

FILE REFERENCE: PRAV002/00030

CURRENT APPLICATION NUMBER: US/10/691,079

CURRENT FILING DATE: 2003-10-22

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 542

TYPE: PRT

ORGANISM: Homo sapiens

US-10-691-079-1

Query Match 100.0%; Score 2863; DB 4; Length 542;

Best Local Similarity 100.0%; Pred. No. 7.6e-179;

Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	12	DVREGDMMHLS	STSGQGYIPSNYVA	PSDSIOAEEMVFGKITRRESRLLNENP	PGT	180
Db	121	DVREGDMMHLS	STSGQGYIPSNYVA	PSDSIOAEEMVFGKITRRESRLLNENP	PGT	180
QY	181	FLVRESSTKGAAYCL	SYSDPDNAKGLVVKYIK	IKRLDSGGFYITSRTQFNSIQQLV	AYYS	240
Db	181	FLVRESSTKGAAYCL	SYSDPDNAKGLVVKYIK	IKRLDSGGFYITSRTQFNSIQQLV	AYYS	240
QY	241	KHADGLCHRLTTC	PTSPKPTQGLAKDAWEI	IPRESLLEVLGGCGCTGEBVMG	TGNGTTR	300
Db	241	KHADGLCHRLTTC	PTSPKPTQGLAKDAWEI	IPRESLLEVLGGCGCTGEBVMG	TGNGTTR	300
QY	301	VAITLKPQTMSPAF	IOEAOVMKCLRHKK	LVOLYAVVSEBPITYIVTEVMS	KGSLDPLK	360
Db	301	VAITLKPQTMSPAF	IOEAOVMKCLRHKK	LVOLYAVVSEBPITYIVTEVMS	KGSLDPLK	360
QY	361	GETGKYRLPOLV	MAAQIASGMAVVERMYV	HRDLRPAANTLVGENTVCKVADE	GLARLI	420
Db	361	GETGKYRLPOLV	MAAQIASGMAVVERMYV	HRDLRPAANTLVGENTVCKVADE	GLARLI	420

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QY 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 480
DB 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 480
QY 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 540
DB 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 540
QY 541 NL 542
DB 541 NL 542

RESULT 2
US-10-732-923-13447
; Sequence 13447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13447
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13447
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Query Match 98.6%; Score 2823; DB 5; Length 542;
Best Local Similarity 98.9%; Pred. No. 3,1e-176;
Matches 537; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

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QY 1 MGSNKSXPQDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAFAFAFAA 59
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QY 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 119
DB 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 119
QY 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 119
DB 60 EPLKFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 119
QY 120 VDVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 179
DB 120 VDVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 179
QY 120 VDVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 179
DB 120 VDVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 179
QY 180 TPLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 239
DB 180 TPLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 239
QY 180 TPLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 239
DB 180 TPLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 239
QY 240 SKHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 299
DB 240 SKHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 299
QY 240 SKHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 299
DB 240 SKHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 299
QY 300 RVALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 359
DB 300 RVALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 359
QY 300 RVALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 359
DB 300 RVALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 359
QY 360 KSGTGYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 419
DB 360 KSGTGYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 419
QY 360 KSGTGYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 419
DB 360 KSGTGYLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 419
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DB 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRE 479
QY 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRE 479
DB 420 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRE 479
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DB 480 VLDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPG 539
QY 540 ENL 542
DB 540 ENL 542
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DB 540 ENL 542

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RESULT 3
US-09-977-260-13
; Sequence 13, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: ULIRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-260-13
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Query Match 98.5%; Score 2821; DB 3; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 61 PKLFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 120
DB 61 PKLFGFNSSDVTYSPQRAGPLAGVTTFFVALVDYESTRTETDLSFKKGERLQIVNNTRK 120
QY 121 DVVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 180
DB 121 DVVBEGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 180
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DB 118 --EGDWMVLAHSLSTQGTGYIPSNVYAPSDSIOAEEMWFGKTRRESERLLNAENPRG 174
QY 181 FLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 240
DB 181 FLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 240
QY 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 234
DB 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTOFNSLQQLVAYY 234
QY 241 KHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 300
DB 241 KHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 300
QY 235 KHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 294
DB 235 KHADGLCHRLTTCPTSKPQTQGLADAMEIPRESIRLEVKLGQCGFGEVMMGTNNGTTR 294
QY 301 VALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 360
DB 301 VALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 360
QY 295 VALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 354
DB 295 VALIKTLKPGTMSPEAFLOEAQVMKLRHKLQVLVAVSEBPIYIYTEVMSKSLDPLK 354
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 420
DB 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 420
QY 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 414
DB 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNVYHRDLRAANILVGENLVCKVADFGLARL 414
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DB 421 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 480
QY 415 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 474
DB 415 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNREV 474
QY 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 540
DB 481 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 540
QY 475 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 534
DB 475 LDQVERGYRMPCCPECPESLHDLMOCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYOPGE 534
QY 541 NL 542
DB 541 NL 542
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RESULT 4
US-09-929-266-10

Sequence 10, Application US/09929266
Publication No. US20030045694A1
GENERAL INFORMATION:
APPLICANT: Brian T. Chait
APPLICANT: Darin R. Latimer
APPLICANT: Paul M. Lizardi
APPLICANT: Eric R. Kershner
APPLICANT: Jon S. Morrow
APPLICANT: Matthew E. Roth
APPLICANT: Martin J. Matlesseich
APPLICANT: Kevin J. McConnell
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.000302
CURRENT APPLICATION NUMBER: US/09/929,266
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/224,939
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/283,498
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: RabsSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-929-266-10

Query Match 98.5%; Score 2821; DB 3; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSFKPKDASQRRRLSLPAAENVHAGGAGFPASQTPSKPASADGHRGSPAAPAAAE 60
DB 1 MGSNKSFKPKDASQRRRLSLPAAENVHAGGAGFPASQTPSKPASADGHRGSPAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRT 180
DB 118 ---BGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRT 174
QY 181 FLVRESEITTKAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
DB 175 FLVRESEITTKAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 241 KHADELCHRLTTVCPTSKPOTQGLAKDAMEI PRESLELVKLGCGCGEVMGTWNGTTR 300
DB 235 KHADELCHRLTTVCPTSKPOTQGLAKDAMEI PRESLELVKLGCGCGEVMGTWNGTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLNHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKCLNHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 420
DB 355 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 414
QY 421 EDNEYTRAGAKKPIIKMTAPEALYGRFTIKSDVWSGILLTETLTGKRVYPGMVREV 480
DB 415 EDNEYTRAGAKKPIIKMTAPEALYGRFTIKSDVWSGILLTETLTGKRVYPGMVREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMOCKRKEPERPTFEYLQAFLEDFYFTSTEBQYQGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMOCKRKEPERPTFEYLQAFLEDFYFTSTEBQYQGE 534
QY 541 NL 542
DB 535 NL 536

RESULT 5

US-09-977-261-13
Sequence 13, Application US/09977261
Publication No. US20030054527A1
GENERAL INFORMATION:
APPLICANT: ULRICH, AXEL
APPLICANT: GISHIZKY, MICHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1259
CURRENT APPLICATION NUMBER: US/09/977,261
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-261-13

Query Match 98.5%; Score 2821; DB 3; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;

Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSFKPKDASQRRRLSLPAAENVHAGGAGFPASQTPSKPASADGHRGSPAAPAAAE 60
DB 1 MGSNKSFKPKDASQRRRLSLPAAENVHAGGAGFPASQTPSKPASADGHRGSPAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRT 180
DB 118 ---BGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESERLLNENPRT 174
QY 181 FLVRESEITTKAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 240
DB 175 FLVRESEITTKAYCLSYSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 241 KHADELCHRLTTVCPTSKPOTQGLAKDAMEI PRESLELVKLGCGCGEVMGTWNGTTR 300
DB 235 KHADELCHRLTTVCPTSKPOTQGLAKDAMEI PRESLELVKLGCGCGEVMGTWNGTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVMKCLNHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVMKCLNHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLK 354
QY 361 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 420
DB 355 GETGKYRLPOLVDMAAQIASGMAVYERMYVHRDLPAANILVGENIVCKYADGLARLI 414
QY 421 EDNEYTRAGAKKPIIKMTAPEALYGRFTIKSDVWSGILLTETLTGKRVYPGMVREV 480
DB 415 EDNEYTRAGAKKPIIKMTAPEALYGRFTIKSDVWSGILLTETLTGKRVYPGMVREV 474
QY 481 LDQVERGYRMPCEPCEBSLHDLMOCKRKEPERPTFEYLQAFLEDFYFTSTEBQYQGE 540
DB 475 LDQVERGYRMPCEPCEBSLHDLMOCKRKEPERPTFEYLQAFLEDFYFTSTEBQYQGE 534
QY 541 NL 542
DB 535 NL 536

RESULT 6
US-10-691-079-2

Sequence 2, Application US/10691079
Publication No. US2004017631A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease

FILE REFERENCE: FRAV2002/0030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-691-079-2

Query Match 98.5%; Score 2821; DB 4; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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DB 1 MGSNKKPXDASQRRSLPEAEVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPQAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 120
DB 61 PKLFGFNSSDVTSPQAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 117
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 180
DB 118 ---EGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAICYLSVDFDNAGKLVNHYKIRKLDSCGFYITSTRQFNSLQQLVAYYS 240
DB 175 FLVRESETTKGAICYLSVDFDNAGKLVNHYKIRKLDSCGFYITSTRQFNSLQQLVAYYS 234
QY 241 KPADGLCHRLTTCPTSPKQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVWMTGNTTR 300
DB 235 KPADGLCHRLTTCPTSPKQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVWMTGNTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 354
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGIARLI 420
DB 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 415 EDNEYTAROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 474
QY 481 LQOVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDYFTSTEPYOQGE 540
DB 475 LQOVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDYFTSTEPYOQGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 7
US-10-887-588-2
Sequence 2, Application US/10887588
Publication No. US20040261142A1
GENERAL INFORMATION:
APPLICANT: Irbay, Rosalyn B.
TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
FILE REFERENCE: USF-T136
CURRENT APPLICATION NUMBER: US/10/887,588
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/444,711
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)-(536)
OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
US-10-887-588-2

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4,2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```
QY 1 MGSNKKPXDASQRRSLPEAEVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKKPXDASQRRSLPEAEVNHGAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPQAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 120
DB 61 PKLFGFNSSDVTSPQAGPLAGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRY 117
QY 121 DVREGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 180
DB 118 ---EGDMWLAHSLSTGQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRGT 174
QY 181 FLVRESETTKGAICYLSVDFDNAGKLVNHYKIRKLDSCGFYITSTRQFNSLQQLVAYYS 240
DB 175 FLVRESETTKGAICYLSVDFDNAGKLVNHYKIRKLDSCGFYITSTRQFNSLQQLVAYYS 234
QY 241 KPADGLCHRLTTCPTSPKQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVWMTGNTTR 300
DB 235 KPADGLCHRLTTCPTSPKQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVWMTGNTTR 294
QY 301 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLK 354
QY 361 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGIARLI 420
DB 355 GETGKTLRLPOLVDMAAOIASGMAVYERNNYHRDLRAANIIVGENLVCKVADFGIARLI 414
QY 421 EDNEYTAROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
DB 415 EDNEYTAROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 474
QY 481 LQOVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDYFTSTEPYOQGE 540
DB 475 LQOVERGYMPCPPECBSLHDMCCMKRKEBERPTFEYLQAFLEDYFTSTEPYOQGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 8
US-10-497-641-2
Sequence 2, Application US/10497641
Publication No. US20050037446A1
GENERAL INFORMATION:
APPLICANT: Schmitt and Stork
TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
FILE REFERENCE: 65064-02
CURRENT APPLICATION NUMBER: US/10/497,641
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: PCT/US02/41564
PRIOR FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: 60/345,888
PRIOR FILING DATE: 2001-12-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRT

ORGANISM: Homo sapiens
US-10-497-641-2

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```
QY 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAGFPASQTPSKRPSADGHRGSPAAFPAAAE 60
DB 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAGFPASQTPSKRPSADGHRGSPAAFPAAAE 60
QY 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFVALYYESRTEITDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFVALYYESRTEITDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 180
DB 118 --EGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
QY 181 FLVRESSETTKGAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 175 FLVRESSETTKGAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIQEAOVMKKLRHEKLVOLYAVVSEBPITYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIQEAOVMKKLRHEKLVOLYAVVSEBPITYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHRDLPAANILVGENLVCKVADFGARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHRDLPAANILVGENLVCKVADFGARLI 414
QY 421 EDNEYTARQAGKFPKKTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 480
DB 415 EDNEYTARQAGKFPKKTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCRKSPBERPFEYLQAFLEDYFSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKSPBERPFEYLQAFLEDYFSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 9
US-10-825-568-10
; Sequence 10, Application US/10825568
; Publication No. US20050069916A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Keremnar
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matthesich
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.0003U2
; CURRENT FILING DATE: US/10/825,568
; PRIOR APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-825-568-10

Query Match 98.5%; Score 2821; DB 5; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

```
QY 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAGFPASQTPSKRPSADGHRGSPAAFPAAAE 60
DB 1 MGSNKSXPKDASQRRRLSEPAENVHAGGAGFPASQTPSKRPSADGHRGSPAAFPAAAE 60
QY 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFVALYYESRTEITDLSFKKGERLQIVNTRKV 120
DB 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFVALYYESRTEITDLSFKKGERLQIVNTRKV 117
QY 121 DVREGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 180
DB 118 --EGDWMLAHSLSGTGTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
QY 181 FLVRESSETTKGAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 240
DB 175 FLVRESSETTKGAYCLSVDFPNAGLANVGHYKIRKLDGSGFYITSRTQFNSLQOLVAYYS 234
QY 241 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 300
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVTLGGCCFGEVMMGTNGTTR 294
QY 301 VAIKTLKPGTMSPEAFIQEAOVMKKLRHEKLVOLYAVVSEBPITYIVTEYMSKSLDPLK 360
DB 295 VAIKTLKPGTMSPEAFIQEAOVMKKLRHEKLVOLYAVVSEBPITYIVTEYMSKSLDPLK 354
QY 361 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHRDLPAANILVGENLVCKVADFGARLI 420
DB 355 GETGKYLRPLPOLVMAAQAISGMAVERMNVYHRDLPAANILVGENLVCKVADFGARLI 414
QY 421 EDNEYTARQAGKFPKKTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 480
DB 415 EDNEYTARQAGKFPKKTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVVPYPGVNRREV 474
QY 481 LDQVERGYRMPCEPCESLHDLMCQCRKSPBERPFEYLQAFLEDYFSTEPQYORGE 540
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKSPBERPFEYLQAFLEDYFSTEPQYORGE 534
QY 541 NL 542
DB 535 NL 536
```

RESULT 10
US-10-821-231C-1
; Sequence 1, Application US/10821231C
; Publication No. US20050275837A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongmano
; APPLICANT: Ben-Amotz, Dor
; APPLICANT: Xie, Yong
; APPLICANT: Davison, Vincent J.
; APPLICANT: Mrozek, Melissa
; APPLICANT: Ortiz, Coraai
; TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
; FILE REFERENCE: 12264/17
; CURRENT FILING DATE: US/10/821,231C
; PRIOR APPLICATION NUMBER: US 60/462,083
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/462,472
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/490,057
; PRIOR FILING DATE: 2003-07-25

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-11-233-510-24

Query Match 98.5%; Score 2821; DB 6; Length 536;
Best Local Similarity 98.9%; Pred. No. 4.2e-176;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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OY 1 MGSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 60
DB 1 MGSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 60
OY 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFFVALDYESTETDLSFKKGERLQIVNNTKRV 120
DB 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFFVALDYESTETDLSFKKGERLQIVNNTKRV 117
OY 121 DVREGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 180
DB 118 ---BGDWMLAHSLSGTQGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 174
OY 181 FLVRESSTKGAAYCLSYSDPNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAAYS 240
DB 175 FLVRESSTKGAAYCLSYSDPNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAAYS 234
OY 241 KHADGLCHRLTTVCPPTSKPOTQGLAKDAMEIPRESLRLEVKGQCGFGEVMMGTWGTTR 300
DB 235 KHADGLCHRLTTVCPPTSKPOTQGLAKDAMEIPRESLRLEVKGQCGFGEVMMGTWGTTR 294
OY 301 VAITLKPGTMSPEAFIQEAVMKKLHREKLVOLYAVVSEPIYIVTEYMSKGSILDFLK 360
DB 295 VAITLKPGTMSPEAFIQEAVMKKLHREKLVOLYAVVSEPIYIVTEYMSKGSILDFLK 354
OY 361 GETGKYRLPOLYVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKYADGGLARLI 420
DB 355 GETGKYRLPOLYVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKYADGGLARLI 414
OY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
DB 415 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 474
OY 481 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTEFYIQAFLQEDYFTSTEPQYQGE 540
DB 475 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTEFYIQAFLQEDYFTSTEPQYQGE 534
OY 541 NL 542
DB 535 NL 536
```

RESULT 13

US-10-691-079-3
Sequence 3, Application US/10691079
Publication No. US2004017631A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: PRAV2002/0030
CURRENT APPLICATION NUMBER: US/10/691.079
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 541
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-691-079-3

Query Match 98.5%; Score 2820.5; DB 4; Length 541;
Best Local Similarity 98.7%; Pred. No. 4.6e-176;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

```
OY 1 MGSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 60
DB 1 MGSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 59
OY 61 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFFVALDYESTETDLSFKKGERLQIVNNTKRV 120
DB 60 PKLFGFNSSDPTVTSPOBAGPLAGGVTTFFVALDYESTETDLSFKKGERLQIVNNTKRV 119
OY 121 DVREGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 180
DB 120 DVREGDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRESERLLLNENPRGT 179
OY 181 FLVRESSTKGAAYCLSYSDPNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAAYS 240
DB 180 FLVRESSTKGAAYCLSYSDPNAKGLNVKHKIRKLDGSGFYITSRQFNSLQOLVAAYS 239
OY 241 KHADGLCHRLTTVCPPTSKPOTQGLAKDAMEIPRESLRLEVKGQCGFGEVMMGTWGTTR 300
DB 240 KHADGLCHRLTTVCPPTSKPOTQGLAKDAMEIPRESLRLEVKGQCGFGEVMMGTWGTTR 299
OY 301 VAITLKPGTMSPEAFIQEAVMKKLHREKLVOLYAVVSEPIYIVTEYMSKGSILDFLK 360
DB 300 VAITLKPGTMSPEAFIQEAVMKKLHREKLVOLYAVVSEPIYIVTEYMSKGSILDFLK 359
OY 361 GETGKYRLPOLYVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKYADGGLARLI 420
DB 360 GETGKYRLPOLYVMAAQIASGMAYVERMNVVHDLRAANILVGENLVCKYADGGLARLI 419
OY 421 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 480
DB 420 EDNEYTAROGAKFPDKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPCGVNREV 479
OY 481 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTEFYIQAFLQEDYFTSTEPQYQGE 540
DB 480 LDQVERGRMPCPECEBSLHDLMCQCKRKEPERPTEFYIQAFLQEDYFTSTEPQYQGE 539
OY 541 NL 542
DB 540 NL 541
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RESULT 14

US-10-394-322A-56
Sequence 56, Application US/10394322A
Publication No. US20030232391A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394.322A
CURRENT FILING DATE: 2003-03-20
PRIORITY APPLICATION NUMBER: US 60/366,892
PRIORITY FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 535
TYPE: PRT
ORGANISM: Homo sapiens
US-10-394-322A-56

Query Match 98.4%; Score 2816; DB 4; Length 535;
Best Local Similarity 98.9%; Pred. No. 8.9e-176;
Matches 535; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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OY 2 GSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 61
DB 1 GSNKSFKPKDASQRRRSLEPAENVHAGCGGAFPPASQTPSKPASADGHRGSPAAFAAPAAAE 60
OY 62 KLFSGFNSSDPTVTSPOBAGPLAGGVTTFFVALDYESTETDLSFKKGERLQIVNNTKRV 121
```

```
Db      61 KLFGEFNSDPTVTSPOAGPLAGGVTTFVALYDYESRTEETDLSFKKGERLQIVNNT---- 116
Qy      122 VREGDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPGTF 181
Db      117 --BQDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPGTF 174
Qy      182 LVRESSETTKGAYCLSVSDFDNAGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 241
Db      175 LVRESSETTKGAYCLSVSDFDNAGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 234
Qy      242 HADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNGTTRV 301
Db      235 HADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNGTTRV 294
Qy      302 AITTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPITYIVTEYMSKSLDPLKG 361
Db      295 AITTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPITYIVTEYMSKSLDPLKG 354
Qy      362 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGRLARLIE 421
Db      355 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGRLARLIE 414
Qy      422 DNEYTAROGAKFPFKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGKVNREVL 481
Db      415 DNEYTAROGAKFPFKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGKVNREVL 474
Qy      482 DVERGYRMPCEPCEPSLHDLMCQCWKKEPBERPFEYLOAFLEDFYFTSTEPQYOGEN 541
Db      475 DVERGYRMPCEPCEPSLHDLMCQCWKKEPBERPFEYLOAFLEDFYFTSTEPQYOGEN 534
Qy      542 L 542
Db      535 L 535
```

```
RESULT 15
US-10-814-109-4
; Sequence 4, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; APPLICANT: Ganglich, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of S
; FILE REFERENCE: 2560.004
; CURRENT APPLICATION NUMBER: US/10/814,109
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 535
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-814-109-4
```

```
Query Match      98.4%; Score 2816; DB 5; Length 535;
Best Local Similarity 98.9%; Pred. No. 8,9e-176;
Matches 535; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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```
Qy      2 GSNKSKPKDASQRRRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSAFAFAAFAAEP 61
Db      1 GSNKSKPKDASQRRRSLEPAENVHAGGAFPAASQTPSKPASADGHRGSAFAFAAFAAEP 60
Qy      62 KLFGEFNSDPTVTSPOAGPLAGGVTTFVALYDYESRTEETDLSFKKGERLQIVNNTRKVD 121
Db      61 KLFGEFNSDPTVTSPOAGPLAGGVTTFVALYDYESRTEETDLSFKKGERLQIVNNT---- 116
Qy      122 VREGDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPGTF 181
Db      117 --BQDWMLAHSLSGTGGYI PSNYVAPSDSIQAEEMVFGKITRRESRLILNENPGTF 174
Qy      182 LVRESSETTKGAYCLSVSDFDNAGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 241
Db      175 LVRESSETTKGAYCLSVSDFDNAGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSK 234
```

```
Qy      242 HADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNGTTRV 301
Db      235 HADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNGTTRV 294
Qy      302 AITTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPITYIVTEYMSKSLDPLKG 361
Db      295 AITTLKPGTMSPEAFLOEAOVMKKLRHEKLVOLYAVVSEEPITYIVTEYMSKSLDPLKG 354
Qy      362 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGRLARLIE 421
Db      355 ETGKYLRLPOLVMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGRLARLIE 414
Qy      422 DNEYTAROGAKFPFKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGKVNREVL 481
Db      415 DNEYTAROGAKFPFKWTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYPGKVNREVL 474
Qy      482 DVERGYRMPCEPCEPSLHDLMCQCWKKEPBERPFEYLOAFLEDFYFTSTEPQYOGEN 541
Db      475 DVERGYRMPCEPCEPSLHDLMCQCWKKEPBERPFEYLOAFLEDFYFTSTEPQYOGEN 534
Qy      542 L 542
Db      535 L 535
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Job time : 110.467 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 7.03027 Seconds
(without alignments)
891.618 Million cell updates/sec

Title: US-10-691-079-1

Perfect score: 2863
Sequence: 1 MGSNKSXPKXASQRRSLRP.....AFLEDYFTSTPQYQENL 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /EMC_Celerra_SIDS3/prodata/1/pubppa/US09_NEW_PUB.pbp:*
 - 2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB.pbp:*
 - 3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB.pbp:*
 - 4: /EMC_Celerra_SIDS3/prodata/1/pubppa/US08_NEW_PUB.pbp:*
 - 5: /EMC_Celerra_SIDS3/prodata/1/pubppa/US09_NEW_PUB.pbp:*
 - 6: /EMC_Celerra_SIDS3/prodata/1/pubppa/US10_NEW_PUB.pbp:*
 - 7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB.pbp:*
 - 8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB.pbp:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1525.5	53.3	505	US-10-511-937-2991	Sequence 2991, App
2	1461	51.0	512	US-10-505-928-353	Sequence 353, App
3	1461	51.0	512	US-10-511-937-2492	Sequence 2492, App
4	1458	50.9	519	US-10-511-937-2467	Sequence 2467, App
5	834	29.1	659	US-10-511-937-2593	Sequence 2593, App
6	829.5	29.0	631	US-11-312-958-60	Sequence 60, App
7	787.5	27.5	620	US-10-511-937-2959	Sequence 2959, App
8	589	20.6	983	US-11-302-678-2	Sequence 2, App
9	571	19.9	994	US-11-303-935-12	Sequence 12, App
10	569.5	19.9	993	US-11-303-935-11	Sequence 11, App
11	569	19.9	998	US-11-303-935-2	Sequence 2, App
12	556.5	19.4	1130	US-11-312-958-52	Sequence 52, App
13	489	17.1	894	US-11-251-465-21	Sequence 21, App
14	482.5	16.9	885	US-10-505-928-432	Sequence 432, App
15	482.5	16.9	885	US-11-251-465-20	Sequence 20, App
16	482.5	16.8	806	US-11-251-465-22	Sequence 22, App
17	481	16.8	806	US-11-251-465-22	Sequence 22, App
18	477.5	16.7	346	US-11-251-465-67	Sequence 67, App
19	477.5	16.7	346	US-11-251-465-67	Sequence 67, App
20	476.5	16.6	422	US-11-251-465-70	Sequence 70, App
21	476.5	16.6	422	US-11-251-465-70	Sequence 70, App
22	469	16.0	972	US-11-248-122-2	Sequence 2, App
23	459	15.6	999	US-10-196-749-434	Sequence 434, App
24	448	15.4	391	US-11-223-945-38	Sequence 38, App
25	442	15.4	391	US-11-223-945-38	Sequence 38, App

26	442	15.4	1259	US-11-223-945-40	Sequence 40, App
27	441	15.4	550	US-10-538-066-757	Sequence 757, App
28	441	15.4	1255	US-10-538-066-364	Sequence 364, App
29	441	15.4	1255	US-11-223-945-43	Sequence 43, App
30	439	15.3	993	US-10-511-937-2463	Sequence 2463, App
31	432	15.1	976	US-10-511-937-2423	Sequence 2423, App
32	427	14.9	1006	US-10-511-937-2425	Sequence 2425, App
33	417.5	14.6	1338	US-10-505-928-634	Sequence 634, App
34	417.5	14.6	1338	US-10-505-928-634	Sequence 634, App
35	413	14.4	953	US-11-312-958-56	Sequence 56, App
36	408.5	14.3	1298	US-10-505-928-274	Sequence 274, App
37	403	14.1	369	US-10-953-349-3910	Sequence 3910, App
38	403	14.1	374	US-10-953-349-3909	Sequence 3909, App
39	403	14.1	412	US-10-953-349-3908	Sequence 3908, App
40	397	13.9	648	US-10-511-814-2	Sequence 2, App
41	397	13.9	648	US-10-511-814-14	Sequence 14, App
42	367.5	12.8	272	US-10-370-959-27	Sequence 27, App
43	367.5	12.8	278	US-10-370-959-17	Sequence 17, App
44	367.5	12.8	278	US-10-370-959-31	Sequence 31, App
45	367	12.8	247	US-11-251-465-75	Sequence 75, App

ALIGNMENTS

RESULT 1
US-10-511-937-2991
Sequence 2991, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Klix
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511.937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2991
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2991
Query Match 53.3%; Score 1525.5; DB 6; Length 505;
Best Local Similarity 55.6%; Pred. No. 3e-76;
Matches 299; Conservative 86; Mismatches 116; Indels 37; Gaps 6;
QY 1 MGSNKSXPKXASQRRSLRP...AFLEDYFTSTPQYQENL 542
DB 1 MGSNKSXPKXASQRRSLRP...AFLEDYFTSTPQYQENL 542
QY 61 PKLFGFNSPTVTSPOAGPLAGVTF--VALDYVSRTETDPSFKKGELOIVNTRK 119
DB 61 PKLFGFNSPTVTSPOAGPLAGVTF--VALDYVSRTETDPSFKKGELOIVNTRK 119
QY 41 -----GNSHNSNTPGIR--ACSEDIYVALDYIEIHEDLSFQKGDVVLEBS-- 90
DB 41 -----GNSHNSNTPGIR--ACSEDIYVALDYIEIHEDLSFQKGDVVLEBS-- 90
QY 120 VDVEGDMWLAHSISTGTGTPSNVYAPSDSIOAEEMFYQKTRRESERLLNAENPRG 179
DB 91 -----GEMWKRSLATKREKGTIPSNVYARVDSLETETEMFPGISRKQAEKQLAPGNMIG 145

Qy	180	IFLVARSESTTKGAYCCLSVSDPDMNAGLANKYHKIRKLDSCGFITTRTQPNLSLOLVAY	239
Db	146	SFMIRDSSETTKGSYSLSVADYDPRQDDYKHKIRKRLDNGGFYSISPRSTFSTLOELVDHY	205
Qy	240	SKHADGLCHRLTLTYVTPTSKPTQGLAKDAMEI.PRESLRLLEVKLGGOCFGFVMNGTNGTT	299
Db	206	KKGNDGLCOOKLSVPCMSKRPQ--KPEMKDAMEI.PRESLKLKJLGAAGOFGEVMAATYTKAT	264
Qy	300	RVALITKLPGTMSPAFLQEOAVMKKLREHKLVQLTAAVAVSEBPIYIVTEWMSKGSLLDFL	359
Db	265	KVAVETMKRPGMSVSEAFLEAVAVMKTLGHDKLVKLAAVVTKEPIYIITEEMAGSLLDFL	324
Qy	360	KGETGKYLRLPOLVDMAAQIASGMAYVERPNYVHRDLRAANILVGNLVCKVAFGLIARL	419
Db	325	KSEDSKQPL.PRLIDPFSAQIAEGMAFIEQRNYIHRDLRAANILVSAVLCKIADFGIARV	384
Qy	420	IEDNEYTRAQAKFPKTKTAPPAALYGRITISDWSFGILLTELTLTKGAVPPPGVANNRE	479
Db	385	IEDNEYTRAEQAKFPKTKTAPPAALINFGSFTIKSDWSFGILLMEIYTVGRI.PPGGMSNPE	444
Qy	480	VLDQVERAYRMCCEPCEPESLHDMQCMKRKEPEER.PTEYIQAFLFEDVFTSTNEPQO	537
Db	445	VIRALERGRMRPENCPEELYNIMRCKMKNRPEEPTEYIQAFLFEDVFTTATNESQO	502

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RESULT 2
US-10-505-928-353
; Sequence 353, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 29967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 353
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-353

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Query Match	51.0%	Score 1461	DB 6	Length 512
Best Local Similarly	52.5%	Pred. No. 9.4e-73		
Matches 287; Conservative	87	Mismatches 125;	Indels 48;	Gaps 9

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QY 1 MGSNKSXPKDA-----SRRRSLEPAENVHAGGAPASQTPSKPASADGHRPS 51
Db 1 MGCIKSKGKSLSDGDYDKTQPVANTRRTTYVRD-----PTSKKOORPV-----PE 47
QY 52 AAFAPAAAEPLTFGGFNSSDPTVTSFORAGPLAGVTTFVALYDYESRRTETDLSFKKGERL 111
Db 48 SOLLPGR-----FOTYD-----PEEGDDY-----VALPYGIIHPDDLSFKGGEEM 90
QY 112 QIVANTRKVDVREGGMWMLAHSLSTGOTYIIPSNVYAPSDSIQAEEMYPFGKITRRESERL 171
Db 91 KYLE-----EHEGMWAKSLTLTKEGFISNVAKANTLETBEMFKDITRKDAEQOL 143
QY 172 LMAENPRTFLVRESEITTKGAYCULSVSDPDNAKGLNWKHYKIRKLDGSGGYITSTRTOFNS 231
Db 144 LAPENSAGAFILIRESETLKGFSLSVRDFDPYHGVIVIRHYKIRSLDNGGYIISPIITPC 203
QY 232 LOOLVANYSKRADGLCHRLLTVCPFSKRQOTGLANDAMEIPRESIRLAEVLKGGCGFGEW 291
Db 204 ISDMIKHYQKADGICRRLERAKCISPKPO-KPMDKDAEIPRESIKLTVRLGACGFGGEW 262
QY 292 MGTNGTTRVAVIKTLPGTMSPEALFOAQWVKLRHKLQVLAVVS-EBSITYIVTEYM 350
Db 263 MGYVNNSTKVAVKTLPGTMSVQALEBANIMKLTLOHKLVRLAVAVVIREBSITYITEYM 322

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QY 351 BKGSILDLPELKEBTGKCYLLPOLVDMAAQIASMAVYERNNYHRLDRAANIIVGELNCK 410
Db 323 AKGSILDLPELKEDEGGKVLPLKLIIDSAQIAEGMAVIERKNYIYHRLDRAANVLVSSLMCK 362
QY 411 VADFGLARLIEDNETTARQGAKEPIKMTAPKALYGRPTIKSDVMSFGILLTELTLTKGHV 470
Db 383 IADRLANAVIEDNETTAREGAKEFPIKMTAPKALYGRPTIKSDVMSFGILLTELTLTKGHV 442
QY 471 PYGKAVNREVLDOVERGYRMPCCPEPCPSLHDLMOCKWRKEBERPTFYLOAFLEDTFT 530
Db 443 PYPGTADNVMTALSQGYRMPREVNCCPELYIMDMCKWEKAEERPTFDYLOSLVDLFYT 502
QY 531 STEPOYQ 537
Db 503 ATEGOYQ 509

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RESULT 3
US-10-511-937-2492
; Sequence 2492, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 512
; TYPE: FRT
; ORGANISM: Homo sapiens
US-10-511-937-2492

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Query Match	51.0%;	Score 1461;	DB 6;	Length 512;
Best Local Similarity	52.5%;	Pred. No. 9,4e-73;		
Matches 287;	Conservative 87;	Mismatches 125;	Indels 48;	Gaps 9;
Qy	1	MGSNKSPKHA-----SRRRSLEPAENHYAGAGAPASQTSKPASADGHRPS	51	
Db	1	MGCIKSGKSKSLSDGVDLKTQPVNTERITTYAD-----PTSNKKQRPV-----PE	47	
Qy	52	AAFAAPAAEPKLFGGFNSSDPTVTSPPQAGPLAGVTTFFVALDYVESRTEETLSFEKGERLT	111	
Db	48	SQLLPGOR-----FQTKD-----PEQGQDIV-----VALYFDGHPDLSFKKGEKM	90	
Qy	112	QIVNTEKVDVREGDWMVAHSLSTGQTGYIPSNVVAEBSIOAEWYFGKITRRESERLT	171	
Db	91	KVLE-----EHHEMKAKSLILTKKEGFIPSNVVAKLNTLETBEMFPKQITRDQAEQL	143	
Qy	172	LMANEPGTFLVRESFTTKGAYCLISVSDFPDNAGKLANVGHYKIRKLDSCGFYTTSRQNS	231	
Db	144	LAPENSAGAFIIRESEFTLKGSFSLSVADPDPVHGDIVLKHYSIRSLDNGYIISRITRPC	203	
Qy	232	LQQLVAAYSKRADLCHRLTLTVCTSPQVQGLAKDAMEI PRESLRELVKLGOCFCFGEW	291	
Db	204	ISDIIKHYYQKADDLCHRLERAKCISPPKQ-KPMQKDMELPRESLKLVYKRGAAQFGEW	262	

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Qy 292 MGWNGTTRVAIKTLKPGTMSPEAFLOBAQVKKLREKVLQVLAAYVS-EEPIYVTEYM 350
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 MGIYNNSTKVAVKLTKGINSVQAFLEBANIMKTLQHKVLAAYVRESPIYIITEYM 322
Qy 351 SKGSLDLFLKGETGKYLRLPOLVDMAAQIASGMAVVERMNVHDLRAANILVGENLVCK 410
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 323 AKGSLDLFLKSDDEGKVLPLFLIDFSAQIAGEMAYIERKQYIHRDLRAANVLVESLWCK 382
Qy 411 VADPGLARLIEDNEYTARQAKFPKTKTAPPAALYGRFTISDVSFGILLTELTGGRV 470
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 383 IADFGILARVIDNEYTARQAKFPKTKTAPPAALYGRFTISDVSFGILLTELTGGRV 442
Qy 471 PYPGMNVREVLDOVERGYRMPCEPECSLHDLMOCKRKEPEERPFTEYLQAFLEDPFT 530
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 443 PYPGMTADWMTALISQGIKRPVRENCPELTYDMCKCKEKAEREPFTYDQSLVDDEFT 502
Qy 531 STEPQYQ 537
|| :||:|||||
Db 503 ATEGQYQ 509
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RESULT 4

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US-10-511-937-2467
; Sequence 2467, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2467
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2467
```

Query Match 50.9%; Score 1458; DB 6; Length 509;
Best Local Similarity 59.1%; Pred. No. 1.4e-72;
Matches 272; Conservative 80; Mismatches 98; Indels 10; Gaps 3;

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Qy 79 AGPLAGVTTFAVAYDYESRTETDLSFKGGRLOIVNNTRKVDVREGDWMALASLSTGQT 138
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 ASPLQDNLV--IALHSYEPHSDGLGFKGEPKRLIL-----QSGEMWQAQSLTTCQE 108
Qy 139 GYIPSNVAVPDSIQABEWYFGKITRRESERLLINAEPRGTFPLVRESSTTKGAYCLSVS 198
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 GFIPFNVAKANSLSEPEWPFKNLSRKDAERQLLAPGNTGSPFIRESESTAGSFSLSVR 168
Qy 199 DFDNAKGLNVKIRKLDGSGFYITSRTOFNSLQQLVAVYSKADGLCHRLTTVCPGSK 258
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DFDNQGSGVNVKIRKLDGSGFYISPTITPGHLHLVRHTNMSDGLCTRLSRPCQTOK 228
Qy 259 POTOGGLAWMEIPRESILRLLEVKGQGGFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLO 318
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 PQ-KPMWEDKEWEVREFTLKLVERLGAQGFGFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLO 287
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Qy 319 EAQVKKLREKVLQVLAAYVSEEPYIYTEYMSKSLDLFLKGETGKYLRLPOLVDMAAQ 378
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 288 EANIMKQLOHQRVRLAAYVTOEPIYIITEYMEGSLVDPLKTSQGIKTLINKLDMBAQ 347
Qy 379 IASGMAVVERMNVHDLRAANILVGENLVCKVADFGILARLIEDNEYTARQAKFPKTKT 438
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 348 IAEGMATIERNVYIHRDLRAANILVSDTLSCKADFGILARLIEDNEYTARQAKFPKTKT 407
Qy 439 APEALYGRFTIKSDVMSFGILLTELTGGRVPPYPGMNVREVLDOVERGYRMPCEPECE 498
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 408 APEALINGTFTIKSDVMSFGILLTELVTHGRIPYPGMTNPEVIONLERGYRMPVNDNCE 467
Qy 499 SLHDLMOCKRKEPEERPFTEYLQAFLEDPFTSTEPQYQ 538
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 ELYQMLRCKERPEDEPFTDYLRVSLVEDPFTALTEGQYQ 507
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RESULT 5

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US-10-511-937-2593
; Sequence 2593, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2593
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2593
```

Query Match 29.1%; Score 834; DB 6; Length 659;
Best Local Similarity 36.7%; Pred. No. 1e-38;
Matches 184; Conservative 96; Mismatches 184; Indels 38; Gaps 14;

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Qy 40 KPASADGHRGSAFAFAAPKLFGGFNSDVTYSPORAGPLAGVTT-----FVALYD 94
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 KPSS--HRTKKRPLPTPEEDQI-----LKKLPPEPPAAPVSTSLKKVVALYD 224
Qy 95 YESRTETDLSFKKGERLOIVNNTRKVDVREGDWMALASLSTGQGYIPSNVAVPS-DSIQ 153
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 YMPNANNDLQARKDDEYFILEESNL-----PWRARD-KKGQGGYIPSNVTEADESIB 277
Qy 154 ABEWYFGKITRRESERLLINAEPRGTFPLVRESSTTKGAYCLSV--SDFNAKGLNVKAY 211
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 278 MEWYSKMTFSQAEO--LLKQEGEGGFIVADS--SKAGKYVSVFAKSTGDPQGV-IRHY 334
Qy 212 KIRLDSGGFYITSRTOFNSLQQLVAVYSKADGLCHRLTTVCPGSK-----POTGLAK 266
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 335 VVCSTPQGYTLAKKHLFTTIPELINTHONSAGLISRLK--YVSQONKRAPSTAGIGY 392
Qy 267 DAMEIPRESILRLLEVKGQGGFGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOBAQVKKL 326
|| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 GSWIIDPKDLTFLKELGTGGQGVYKYGKMRQGYDVALIKMIEGSMSEDEFTIEAKVMNLT 452
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Oy 327 SHEKTLVOLAAVASEE-PIYIVTEWYKSGSLDFELKGETCKTYRLPOLVMAAQAISGMAY 385
Db 453 SHEKTLVOLYXCCTKCRPFIPIITEYMANGLLWYLR-ENRHRQTOQLCKCDDVCAMEY 511
Oy 386 VERNMYVARDLRANAILVGENLVCKVADFGIARLIEDNEYTAROGAKPEIKXTAPEALY 445
Db 512 LESQOFLHRDLAARNCVLNVDGCVVAKVSDPLGSRVYLDDEYTSVSGKFPVRMSPEVLWY 571
Oy 446 GRPFIKSVWVSFGILLTTELTKGRVPYEGMVRNREVLDOVERGYRMPCCPECEBSLHLMC 505
Db 572 SKFSKSSDIMAFVGLMWEIYISLGMKPYERFTNSEAHLIAGLRILYRPHLASEKYTYWY 631
Oy 506 QCMRKEPEREPTFEYLOAFLED 527
Db 632 SCWEKADERTPTFKLLSNILD 653

RESULT 6
US-11-312-958-60
Sequence 60, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Sinos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
FILE REFERENCE: MP102-027P1RNONIMM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 631
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-60

```

```

Db      KSNLDQEWYCRNNNRKAEQ-LLRSEDKEGFWNRDS-SQPGLYTVSLYTFKGEGSS 295
OY      207 NVKHYKIRKLDSG--GFYITSRTQNSLQOLVAYYSKADGICHLR---TTCPTSKPQT 261
Db      296 GFRHHIHKETTS PKCYVLAEKHAGSIPETIEYHKHNAAGLVTRLRYPVSVGKNAAPT 355
OY      262 QGLKDAWEIRRESLRLEVKLGQGGQGFGEVMGTNGTTRVALKTLKPGMSPEAFLOEQ 321
Db      356 AGFSTEKKEINPSELTTFRLEDSGFLGVVRLCKMAYQYVAIKALREGMNCEDFLFEAK 415
OY      322 VMKLIHRHKLVLQVYAVVSEB--PIYIVTEYMSKSLDFLKGEGTKYLRLPOLVDMAQIA 380
Db      416 VMMLTTHKLVLQVLYVCQOKPIYIVTEFMEHGCLLFLRQGHHSR-DVLLSMQDVC 474
OY      381 SGMAVVERKMYVHRDLRANILVGSNLVCKVADPGLARLLIEDNEYTAROGAKFPIKWTAP 440
Db      475 EGMETLEBNSFLHRDLAARNCLVSBAGVVKVSDPGMARFYLDQYSSGAKFPVVKCP 534
OY      441 EAALYGRITISDWSFGILLTELTKGRVPPFGMVNREVLDOVERGYMPCPECEBSL 500
Db      535 EVFNYSRSPSSKSDWSFGVLMMEVETBGRMPEKTYNEVVTMRGHLVQPKLASNYV 594
OY      501 HDLMQCCWRKSPBEPRTPEYLOAFLE 527
Db      595 YEVMLRCWQEKPEBGRPSFEDLIRITIDE 621

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RESULT 7
US-10-511-937-2959
? Sequence 2959, Application US/10511937
? Publication No. US2006008836A1
? GENERAL INFORMATION:
?   APPLICANT: EXPRESSION DIAGNOSTICS, INC.
?   APPLICANT: Wohlgenuth, Jay
?   APPLICANT: Fry, Kirk
?   APPLICANT: Woodward, Robert
?   APPLICANT: Ly, Ngoc
?   APPLICANT: Prentice, James
?   APPLICANT: Morris, Macdonald
?   APPLICANT: Rosenberg, Steven
?   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
?   TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
?   FILE REFERENCE: 506612000104
?   CURRENT APPLICATION NUMBER: US/10/511,937
?   CURRENT FILING DATE: 2004-10-19
?   PRIOR APPLICATION NUMBER: PCT/US2003/012946
?   PRIOR FILING DATE: 2003-04-24
?   PRIOR APPLICATION NUMBER: US 10/131,831
?   PRIOR FILING DATE: 2002-04-24
?   PRIOR APPLICATION NUMBER: US 10/325,899
?   PRIOR FILING DATE: 2002-12-20
?   NUMBER OF SEQ ID NOS: 3117
?   SOFTWARE: PatentIn version 3.2
?   SEQ ID NO 2959
?   LENGTH: 620
?   TYPE: PRT
?   ORGANISM: Homo sapiens
US-10-511-937-2959

```

```

:      TYPE: PRT
;      ORGANISM: Homo sapiens
US-11-312-958-60

Query Match      29.0%; Score 829.5; DB 7; Length 631;
Best Local Similarity 39.6%; Pred. No. 1.7e-38;
Matches 177; Conservative 90; Mismatches 161; Indels 19; Gaps 11.

QY      90 VALVDYDSRRTDLSFKKGERLQIVNNTRXKYDVREGDWLHLSLSGTGTYIPSYVA-- 147
      ||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      185 VAMVDFAAGHGDRFLRERGQEYLIL--EKDVH---HWRAAD-KYGNEGYIPSYVYTGK 237
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      148 PSDSIQAEEMWFGKITRRESERLLLAENPFGTFLVRESSTTKGAYCLSV--SDPNAGCL 206
      |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

[illegible]

Db 219 GYVPSYLVKSPNNLETFEWNKSI SRDKAEKLLDPT-GKEGAFVWRDSRTA-CTYTVS 276
Qy 197 VSDPDA----KGLNVGHYKIRKIDSG--GFYITSRQFNSLQOLVAVYSGHADGLCHRL 250
Db 277 V--FTKAVSENNPCIRGHYHKEITNDPKRYVAEKVFDSPILLIYHGHNGGLVTRL 334
Qy 251 T-TVC--PTSKPOTQGLAKAMEIPRESLRLEVLGGCGFGEVWGTWNGTTRVAITLK 307
Db 335 RYVCFGRQAPVTAJRLRYKMWIDPSELFTFVOEISGQGLVHLGVLWAKDKVAITIR 394
Qy 308 PGTMSPEAPLOEAQVMMKLRHEKLVOLYAVVSE-PIYIYEVMSKSLDLFLGEGTKY 366
Db 395 EGAMSEEDPIEBEAVWMLSHPLVOLYGVCLQAPCLVFEFMEHGLSDYLAQRGLF 454
Qy 367 LRLEPOLYDMAQIAGNAYVERMYHRDLAANILVGENLVCAVDGRLAILEDNEYT 426
Db 455 -AAETLLGMCLDVECGAYLEACVHIRDLAARNCLVGENQVIVSPFGMTFPLDQYT 513
Qy 427 ARQAKPEIKMTAEALYGRFTIKSDVMSRGLLTLETTKGRVPYGMVREVLDQYR 486
Db 514 SSTGKFPVWASVEVPSFSKSDVMSFGVLMMEVFSBKLPYENRSSEVEDIST 573
Qy 487 GYRMPCEPCEPSLHDMCOCWRKEPERPTEYL 521
Db 574 GFRLYKRLASTHYQIMHCWKERPEDRAFSRL 608

RESULT 8
US-11-302-678-2
; Sequence 2, Application US/11302678
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sileo-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karibeti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 4656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1NM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-2

Query Match 20.6%; Score 589; DB 7; Length 983;
Best Local Similarity 31.3%; Pred. No. 2.8e-25;
Matches 171; Conservative 80; Mismatches 164; Indels 132; Gaps 19;

Qy 61 PKLFGFNSDVTYTPQRAPILAGVYTFVALVDYESTETDLSFKKGBRLQIVNNTRKV 120
Db 384 PRQGLTNTVTYI-----DLANTNTYFEI 409
Qy 121 DVREGDWMLASHSTGQGY----IPSNVAPSDSIQAEWYFGKITRRESERLLNAEN 176
Db 410 DAVNG-----VSELSPPRQAAVSIITNQAPSVLTIKK---DRTSRNISIISMQPEH 462
Qy 177 PRGTF-----VBSSETKAYCLSVDFNAGLNVK-----HKIRLDSGGF 221
Db 463 PNGIILDEVKYKQOEFTSYTL-----RAGTNTVITSLKPDITVVOIRARTAGY 517
Qy 222 YITSRT-QFNS-----LQOLVAYYSKH-AD 244
Db 518 GYNSRKEFEFTSPDSFISGESSQVVMIAISAAVAIILLTVIVYVLIGRFGYKSKGAD 577
Qy 245 -----GLCHRLTTVCP--TSKPOTQGLAKAMEIPRESLRLEVLGGCGFGE 289
Db 578 EKRLHFGNGLKLPGL---RTYVDPHYEDPTQAVHEFAKELDATNISIDKVVAGSFG 634
Qy 290 VMNGTWNGTTR---VAIKTLKPTMSPEA--FLQEAQVKKLRHEKLVOLYAVVSE-EP 342
Db 635 VCSGRLKLPKKEISVAIKTLKGYTEKQRDFEGEASINGQFDHPNIIIRLEGVYTKSKP 694
Qy 343 IYIVTEYMSKSLDPLKGETGKYLRPLQVMDMAQIAGMAYVERMYHRDLAANIL 402
Db 695 VMIVTEYMSKSLDPLKGETGKYLRPLQVMDMAQIAGMAYVERMYHRDLAANIL 753
Qy 403 VGENLVCKVADFGIARLIEDN---EYARQAKPEIKMTAPEALYGRFTIKSDVMSFGI 459
Db 754 INSNLVCKVADFGIARLIEDNPEAAITTR--GKIPIMTSPALAYAKFTSASVSYGI 812
Qy 460 LTELTTKGRVYPYGMVNRVLDQVGRYMPCEPCEPSLHDMCOCWRKEPERPTE 519
Db 813 VLMEVMSYGRPYWMSNGQVIAVDEGYRLPPMDCPALYOLMDCMQKDRNBRKFE 872
Qy 520 YLQAFLE 526
Db 873 QIVSILD 879

RESULT 9
US-11-303-935-12
; Sequence 12, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closssek, Thomas
; APPLICANT: Ullrich, Axel
; APPLICANT: Millauef, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Filth Street
; Suite 4700
; City: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303,935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435


```

QY 203 AKGLNVAHKYIRKLDSCG-----FYTSRTPQNSLQOLVAVYSKADGLCH 248
D 573 ---IGRHCGYSKADQGBDELYHFHFKPGTKTYIDET-YEDNRVAHQPAKELDSC- 627
QY 249 RLTVCPSTSPQOTGLAKDAMEIPRESIRLEVKLGOCFGEVWVG---TWNGTTRVAIK 304
D 628 -----IKIERVIGAEFGEVCSGRKLKPGQDVAVAIAIK 660
QY 305 TLKPGTMSPEA--FLQDAQVKKLRHEKLVQIYAVSE-EPIYIVTEYMSKGLDPLKG 361
D 661 TLKGYVTEKORRDLCEASIMGCFDHPNVVLEGVVTRGKVMVIEFMENGALDAFLRK 720
QY 362 ETGKYLRLPOLVMAAIIASGMAYVERMYVRDLRANILVGENLVCKVADFGALRIE 421
D 721 HDGQFTVI-QLVGMRLRGIAAGMYRLADMGVYHRDLAARNILVNSNLVCKVSDFGLSRVIE 779
QY 422 DNE---YTARQCAKFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPGVAVNR 478
D 780 DDEPAVYTT--TGSKIPTVMTAPEALQYRKFTSADVMSYGIYVMWEVMSYGERPYMDMSNQ 838
QY 479 EVIDQVERGYRMPCCPEBSLDMQCQWKEKEPERPTEFYLOAFLE 526
D 839 DVIAIEGVRLLPAPMDCPAGLHQMLDMCQKDBAERPKFQIYGLD 886

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RESULT 11
US-11-303-935-2
; Sequence 2, Application US/11303935
; Publication No. US20060099708A1

```

```

GENERAL INFORMATION:
APPLICANT: Closeek, Thomas
            Ullrich, Axel
            Millaer, Birgit

```

```

TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MXL
SIGNAL TRANSDUCTION
DISORDERS

```

```

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
          Suite 4700

```

```

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

```

ZIP: 90071-2066

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

```

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/303,935
FILING DATE: 19-Dec-2005

```

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/073,064

```

```

FILING DATE: 12-Feb-2002
APPLICATION NUMBER: US/08/438,265

```

```

FILING DATE: MAY 9, 1995
APPLICATION NUMBER: US/08/368,776

```

```

FILING DATE: January 3, 1995
APPLICATION NUMBER: <Unknown>

```

```

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

```

```

REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-303-935-2

```

```

Query Match 19.3%; Score 569; DB 7; Length 998;
Best Local Similarity 28.7%; Pred. No. 3.5e-24;
Matches 180; Conservative 84; Mismatches 196; Indels 168; Gaps 22;

```

```

QY 31 AFAASQTPSPAPANDG-HRQPS-----AFAAPAARKEKLEFGNSSTPTVSPQAGPLAG 84
D 300 SFEDRESSHCECEDGYRAPSDPPYACTRPSAPQNL--FNINQTVLSLEMSPADN 357
QY 85 GVTFVALVYRESRTETDLSPFKKE-----RLQIVANTR 118
D 358 GGRNDVYRILCKR---CSWQGEVCYPCGSNIGMPOQTLEDNYTVNDLHANVTF 413
QY 119 KVDV-----REGDWMLAHSLSGTQGYIPSNVAPS--DSIQAEWYFGKTRRESE 168
D 414 EEAIVNGVSDLSRSQRLFAVSLITGQ-----AAPQVSGVWKE-----RVLAGRSVQ 460
QY 169 RLILMAENPRG-----TLVRESERTKAYCLSYSDFNAGGLAVKH 211
D 461 LSWQEPHPNGVITVEYIKYERKQDRETYSTLKTSTS-----ASINLKGTYVVF 513
QY 212 KIRKLDSCGF-YITSRTPQNSLQOLVAVYSKADGLCHRLTV----- 253
D 514 QIRAVTAAGYGNVSPRLDVAITLE-----ASGKMFATVAVSSEONPVITIAVAVAG 565
QY 254 -----CPTSKPOTOG-----LAKDAWEIPRES----- 275
D 566 TILIVFVPGFIIGRHCGYSKADQGBDELYHFHFKPGTKTYIDETPEDPNAVAHQFA 625
QY 276 -----LRLEVKLGOCFGEVWVG---TWNGTTRVAIKTLKPGTMSPEA--FLQDAQV 322
D 626 KELDASCIKIERVIGAEFGEVCSGRKLKPGQDVAVAIAIKTLKGYTEKORRDLCEASI 685
QY 323 MKKLHREKLVQIYAVSE-EPIYIVTEYMSKGLDPLKGBETGKYLRLPOLVMAAIIAS 381
D 686 MGQFDHPNVVLEHGVTRGKVMVIEFMENGALDAFLRHGQFTVI-QLVGMRLRGIAA 744
QY 382 GMAVVERMYVRDLRANILVGENLVCKVADFGALRIEDNE---YTARQCAKFIKMT 438
D 745 GMRYLADMGVYHRDLAARNILVNSNLVCKVSDFGLSRVIEDDEPAVYTT--TGSKIPTVMT 803
QY 439 APEALYGRFTIKSDVMSFGILLTELTTKGRVPGVAVNR-EVIDQVERGYRMPCCPE 498
D 804 APEALQYRKFTSADVMSYGIYVMWEVMSYGERPYMDMSNQDVIAIEGVRLLPAPMDCPA 863
QY 499 SLHDMQCQWKEKEPERPTEFYLOAFLE 526
D 864 GLHQLMLDMCQKDBAERPKFQIYGLD 891

```

```

RESULT 12
US-11-312-958-52
; Sequence 52, Application US/11312958
; Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
            Rosenfeld, Julie Beth
APPLICANT: Sli08-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13424 MOLECULES

```

```
FILE REFERENCE: MP102-027P1RNONMIN
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/11/312,958
PRIOR FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 1130
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-52
```

```

Query Match      19.4% Score 556.5; Db 7; Length 1130;
Best Local Similarity 38.8%; Pred. No. 1.9e-23;
Matches 131; Conservative 39; Mismatches 99; Indels 69; Gaps 7;

QY      268 AMEIPRESRLRYLVGGGCGFGEVMMGTWNGTTR----VAIKTLKPGTMSPEA--FLQEAQ 321
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       717 AKELIDPSRIIRIENRIGANGERFEVCOSRLKTPGRKEIIPAIIKTLKGHMQRORDFLREAS 776

QY      322 VMKKLRHEKVLQLYAVVSF----- 340
          :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       777 IMGFDFHPNIRIRLEGVVTKRSFPALIGEAFCEPGLFRAGFLNSIOADHPVPVGGSLLPRIP 836

QY      341 --EPYIVTEVETYSKSLDFLKGETGKYLTLPOLYMAAQIASGMAYVERMYVHRDLA 398
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       837 AGRPWIMVIEVMENGSLDSFLRKDHGHFTVI-QLVGMKGIASGMKYLSDMGVYHDLAA 895

QY      399 ANILVGENLVCYADVPGCLARLIEDNEYTA--ROGAAPFKMTAPEALYGRTFSKDVS 456
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       896 RNILVNSNLVCKVSDSFLSRVLEDDPEAAVTTTGXKPIRMTPAPEAIAYRKSSASDAWS 955

QY      457 FGLITRLTLTKGRVPPYGVGNREVLDQVEGYMPCBPESBSLHLDMQCCKRKEEERP 516
          ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       956 YGVIMVEMWSYGERPYEMENSNDVIIISIEBGYRLPAPMGCPSALHQLMLCHQKERNNRP 1015

QY      517 TPEYLOAFL-----EDYFTSTPEPYOGGE 540
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1016 KPTDIVSFLLDKLRNPBALHTLVLEDILLVME---SPGE 1050

RESULT 13
US-11-251--465-21
: Sequence 21, Application US/11251465
: Publication NO US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
INFLAMMATORY DISEASES
```

```

; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 894
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-21

```

Query Match	17.1%	Score 489	DB 7	Length 894
Best Local Similarity	28.8%	Pred. No. 6.6e-20		
Matches 162	Conservative	72	Mismatches 216	Indels 112
			Gaps	21
Qy	18	LEPAENVHGA--GGGAPPAAGTPEKPSAD--GHRGPSAPAPAAABPKLFGGNSDDTV	73	
Db	334	LGPPENISATRNGSQAFVHQEPAPAPLOGTLLGVR--LAW-QGQDPPEVLMIDIGLRQEV	389	
Qy	74	TSPQAPGAPLAGYTTFFALVDYBSRTETDLSFKKGELQIVNNTRKYDVREGDMMWHLNST	133	
Db	390	TLELGGDGSVSNLTVCVAAY-----TAAAGGPPSLPVPVL	423	
Qy	134	STGQTGYI-PSNYAPAPDSIOAEEM-----YFGKITRESERLILMAENPRTGLV--RE	185	
Db	424	EAMPPGQAQPHQVLVKRSPSPAPSPMPWYVLGAVNAACVLIL-----ALFLVHRK	476	
Qy	186	SETTKGAYCUSDPDFNAKGLNVKHYIKRLDSCGFYITSRTQFNSLOQLVAYYSKHAQD	245	
Db	477	KETRYG----EVEFPTVERGELVYRVRRKSYSRR--TEATLNSL-----	516	
Qy	246	LCHRLTVCPTRKQTOGLAKDAWE-----IPRESLREVKLGQSGCGEYVMGTWN---	296	
Db	517	-----GISBELKEKRDVWDVDDHKKALGKTLEBGEFGAAMEGQLNDD	559	
Qy	297	GTTVAIKTKLPG--TWSP-EAFLOEAQVMKCLNHEKLVOLVAVV---SEEPYV---IV	346	
Db	560	SILKVAATKMKIACITRSELEDFFLEAVCKMEPFRHVMYRLIGVCFQSGSEBSPPAPVVI	619	
Qy	347	TEYWSKSSLDFL---KGETGYLRLPLQVDMAGQIASGMAVERMNVYHRIIPANIL	402	
Db	620	LPEFKHDDLHSFLLYSRLGDQPVYLLPQMLVKFMADIASGMEYLSSTRFIRHDLAARNCM	679	
Qy	403	VGEVLCKVADFGIARLIDENEYVAROG--AKPFIKTTAPPAALYGRFTIKSDVWSRGIL	460	
Db	680	LNEMWSVCVADFGISKIKIYNGDY-YRQGRIAKMPVKNAIAESLADRYITSKDVWSFGVT	738	
Qy	461	LTELTTGGRAPYPMQVREVLQDQYERGYPMPCEPCESLHMDLCOCKRKEPERPTFEY	520	
Db	739	MMELATNGQPPYEPVENSETYDIHQGNRLKQPADCDGLYALMSRCMELNPQORPSPE	798	
Qy	521	LQAFLEDFYFSTPEPOYPGENTL	542	
Db	799	LREDLENTLKALPPAORPDEIL	820	
RESULT 14				
US-10-505-928-432				
Sequence 432, Application US/10505928				
Publication No. US20060088532A1				
GENERAL INFORMATION:				
APPLICANT: Ludwig Institute for Cancer Research et al.				
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES				
FILE REFERENCE: 28967/39178				
APPLICANT APPLICATION NUMBER: US/10/505,928				
CURRENT FILING DATE: 2004-08-27				
PRIOR APPLICATION NUMBER: US 60/363,019				
PRIOR FILING DATE: 2002-03-07				
NUMBER OF SEQ ID NOS: 866				
SOFTWARE: PatentIn 3.2				
SEQ ID NO 432				

LENGTH: 885
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-432

Query Match 16.9% Score 482.5; DB 6; Length 885;
Best Local Similarity 28.6%; Pred. No. 1.5e-19;
Matches 160; Conservative 72; Mismatches 212; Indels 115; Gaps 20;

QY 18 LEPAENVHGA--GGGAFPASQTPSKPASADGHRGSPSAFAFA---AAEPKLFGEFNSSDT 72
DB 334 LGPPENISATRNGSQAFVHMOEPRAFL-----QCTLLGYRLAYGQDTPRYLMDIGLRQE 388
QY 73 VTSFORAGPLAGVTTTVALYDYESRTETDLSFKKGERLQIVNTRKVDYREGDMWLAHS 132
DB 389 VTLELQDGDGSVSNLTVCAVA---TAAGDGMSPVLPV 422
QY 133 LSTGQGTGIPSNNYVAPSDSIQAEEMV--FGKITRSEERLLNANENRGTFVY--RSET 188
DB 423 LEAMRPVKPES-----TPAFSPMWVYLLGAVVAACVLLI-----ALFLVHRRKKE 470
QY 189 TKGAYCISVDFDNAKLANVGHYKIRKLDGSGFYITSRTQFNSIQOLVAYYSKADGLCH 248
DB 471 RYG---EVEFPTVERBELVVRVRSYSRR--TTEATLNSL----- 507
QY 249 RLTTVCPSTSKPQTQGLAKDAME-----IPRESLRLEVKLGQCGFGEVMGTNN---GTT 299
DB 508 -----GISELKEKLRDVMVDHKKVALGKTIGEGEFGVAMEGQLNQDSDIL 553
QY 300 RVALKTLKPG--TWSP-EAFLQEAQVWKLRHEKLVQLYAVV---SEEPY---IYTEX 349
DB 554 KVAVKTKMIAICTRSELEDFLSEAVCKEFDHPVMMVIGVCFQGSSESPAPAVILPF 613
QY 350 MSKGSLLDFL---KGETGKTLRLPOLVDMAQAQASGMAYVERNNVYHRDLAANIYGE 405
DB 614 MKHGDLSFLYSRLGQPYLLPTQMLVKFMADIASGEYLSYSTRFTHRDIAAENCMLNE 673
QY 406 NLVCKVADFGIARLIEBNEYTARQ--AKPPIKWTAPBAALYGRFTIKSDVMSFGILLTE 463
DB 674 NMSVCVADFGLSKTIYGDY-YRQGRIAKMPVKMIAIESLADRYTTSKSDVMSFGVTWME 732
QY 464 LTTKGRVYPGMVNRVFLDOVERGYRMPCEPECESLHDLQCQWRKEPERPFEVYQA 523
DB 733 IATRGQTPYPGVENSEIYDYLROGNRLKOPADCLDGYALMSRCWELNPODRPSTELRE 792
QY 524 FLEDYFTSTEQVOGENTL 542
DB 793 DLENTLKALPPAQPDEIL 811

RESULT 15
US-11-251-465-20

; Sequence 20, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-251-465-20

Query Match 16.9% Score 482.5; DB 7; Length 885;
Best Local Similarity 28.6%; Pred. No. 1.5e-19;
Matches 160; Conservative 72; Mismatches 212; Indels 115; Gaps 20;

QY 18 LEPAENVHGA--GGGAFPASQTPSKPASADGHRGSPSAFAFA---AAEPKLFGEFNSSDT 72
DB 334 LGPPENISATRNGSQAFVHMOEPRAFL-----QCTLLGYRLAYGQDTPRYLMDIGLRQE 388
QY 73 VTSFORAGPLAGVTTTVALYDYESRTETDLSFKKGERLQIVNTRKVDYREGDMWLAHS 132
DB 389 VTLELQDGDGSVSNLTVCAVA---TAAGDGMSPVLPV 422
QY 133 LSTGQGTGIPSNNYVAPSDSIQAEEMV--FGKITRSEERLLNANENRGTFVY--RSET 188
DB 423 LEAMRPVKPES-----TPAFSPMWVYLLGAVVAACVLLI-----ALFLVHRRKKE 470
QY 189 TKGAYCISVDFDNAKLANVGHYKIRKLDGSGFYITSRTQFNSIQOLVAYYSKADGLCH 248
DB 471 RYG---EVEFPTVERBELVVRVRSYSRR--TTEATLNSL----- 507
QY 249 RLTTVCPSTSKPQTQGLAKDAME-----IPRESLRLEVKLGQCGFGEVMGTNN---GTT 299
DB 508 -----GISELKEKLRDVMVDHKKVALGKTIGEGEFGVAMEGQLNQDSDIL 553
QY 300 RVALKTLKPG--TWSP-EAFLQEAQVWKLRHEKLVQLYAVV---SEEPY---IYTEX 349
DB 554 KVAVKTKMIAICTRSELEDFLSEAVCKEFDHPVMMVIGVCFQGSSESPAPAVILPF 613
QY 350 MSKGSLLDFL---KGETGKTLRLPOLVDMAQAQASGMAYVERNNVYHRDLAANIYGE 405
DB 614 MKHGDLSFLYSRLGQPYLLPTQMLVKFMADIASGEYLSYSTRFTHRDIAAENCMLNE 673
QY 406 NLVCKVADFGIARLIEBNEYTARQ--AKPPIKWTAPBAALYGRFTIKSDVMSFGILLTE 463
DB 674 NMSVCVADFGLSKTIYGDY-YRQGRIAKMPVKMIAIESLADRYTTSKSDVMSFGVTWME 732
QY 464 LTTKGRVYPGMVNRVFLDOVERGYRMPCEPECESLHDLQCQWRKEPERPFEVYQA 523
DB 733 IATRGQTPYPGVENSEIYDYLROGNRLKOPADCLDGYALMSRCWELNPODRPSTELRE 792
QY 524 FLEDYFTSTEQVOGENTL 542
DB 793 DLENTLKALPPAQPDEIL 811

Search completed: June 5, 2006, 17:43:30
Job time : 9.03027 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 117.529 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSXPADASQRRSLP.....AFLEDTFTSTPEQYQENL 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq_8:*
- 2: geneseqp19808:*
- 3: geneseqp19908:*
- 4: geneseqp20008:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*
- 9: geneseqp20068:*
- 10: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2834	100.0	536	2	AAR39706 Human pp6
2	2834	100.0	536	2	ABG95123 Human v-s
3	2834	100.0	536	5	AAU78678 Human SH2
4	2834	100.0	536	6	ABP57260 Human src
5	2834	100.0	536	7	AD120072 Human c-s
6	2834	100.0	536	8	ADL22904 Human MP2
7	2834	100.0	536	8	ADQ88400 Human wll
8	2834	100.0	536	8	ADQ97772 Human can
9	2834	100.0	536	8	ADU04517 Protein t
10	2834	100.0	536	8	ADY84076 Human Src
11	2834	100.0	536	9	ADV94834 Human wll
12	2834	100.0	536	9	AEA35914 Human Src
13	2834	100.0	536	9	ADY84080 Human Src
14	2829	99.8	535	7	ADP45087 Human kin
15	2829	99.8	535	9	AED21154 Human non
16	2821	99.5	542	8	ABB97339 Novel hum
17	2821	99.5	542	8	ADY84075 Human Src
18	2801	98.8	530	8	ADQ88402 Human mut
19	2778.5	98.0	541	6	ADP57261 Mouse src
20	2778.5	98.0	541	8	ADY84077 Murine Src
21	2663.5	94.0	533	3	AAV44447 wild-type
22	2663.5	94.0	533	4	AAAB84661 Amino aci

24	2663.5	94.0	533	9	AEB07192
25	2659.5	93.8	533	3	AAV44449
26	2658.5	93.8	533	2	AAR39705
27	2657.5	93.8	533	3	AAV44451
28	2482	87.6	523	9	AEB07190
29	2408.5	85.0	565	4	ABG23778
30	2225	78.5	423	8	ADQ97769
31	2123.5	74.9	543	4	ABAB84663
32	2123.5	74.9	543	4	ABG10302
33	2123.5	74.9	543	6	ADA00843
34	2123.5	74.9	543	7	ADP45099
35	2123.5	74.9	543	8	ADL22913
36	2123.5	74.9	543	8	ADQ19329
37	2123.5	74.9	543	8	ADQ19331
38	2123.5	74.9	543	8	ADQ26047
39	2123.5	74.9	543	8	ADU06318
40	2123.5	74.9	543	9	ADW78761
41	2123.5	74.9	543	9	ADY19868
42	2123.5	74.9	543	9	AEA35915
43	2123.5	74.9	543	9	AED01122
44	2123.5	74.9	543	9	AED01122
45	2117.5	74.7	541	5	AAU74614

ALIGNMENTS

RESULT 1
ID AAR39706 standard; protein; 536 AA.
AAAR39706;
25-MAR-2003 (revised)
DT 23-DEC-1993 (first entry)
XX Human pp60 c-src protein.
XX Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX Homo sapiens.
XX WO3314193-A1.
XX 22-JUL-1993.
XX 05-JAN-1993; 93WO-US000445.
XX 06-JAN-1992; 92US-00820011.
XX (UYTA) UNIV YALE.
XX Bell L, Madri JA, Warren SL, Luthringer DJ;
XX WPI, 1993-243209/30.
XX P-PSDB; AAR39705.
XX Genetically engineered endothelial cells - which exhibit enhanced cell
XX migration, urokinase-type plasminogen activator activity, and reduced
XX mononuclear cell adhesion and fibronectin prodn.
XX
XX Disclosure; Page 75-77; 91pp; English.
XX The DNA encoding a portion or (more preferably) the entire pp60 c-src
XX polypeptide (Given in AAQ46688) is used to transform endothelial cells.
XX Transformed cells produce increased amounts of pp60 c-src and have
XX improved therapeutic properties. They migrate at faster rates than non-
XX transformed counterparts; have an enhanced ability to inhibit the
XX formation of thrombi and/or dissolve thrombi once they have formed and
XX exhibit reduced mononuclear cell adhesion. They can also be used to
XX improve the success of surgical procedures such as coronary angioplasty,
XX heart bypass surgery, vessel graft and stent implantation. (Updated on 25
XX -MAR-2003 to correct PN field.)


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XX      SQ      Sequence 536 AA;
Query Match      100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGSNKSXPDAQRRLSLPAENVHAGGAGFPAAGTSPKPSADGHRPSAFAFAPAAAE 60
DB      1  MGSNKSXPDAQRRLSLPAENVHAGGAGFPAAGTSPKPSADGHRPSAFAFAPAAAE 60
QY      61  PKLFGFNSSDVTYTSQRAQPLAGVTTFVALYDYESRTETDLSFKKGRRLQIVNTEGD 120
DB      61  PKLFGFNSSDVTYTSQRAQPLAGVTTFVALYDYESRTETDLSFKKGRRLQIVNTEGD 120
QY      121  WMLAHSLSGTQGTGYIPSNVVAAPSDSIQAEEMWFGKITRRESERLLNAENPRGTFIVRES 180
DB      121  WMLAHSLSGTQGTGYIPSNVVAAPSDSIQAEEMWFGKITRRESERLLNAENPRGTFIVRES 180
QY      181  ETTKGAAYCLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYSKADGL 240
DB      181  ETTKGAAYCLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYSKADGL 240
QY      241  CHRLLTVCTPSKPTQOTGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNNGTTRVAIKTL 300
DB      241  CHRLLTVCTPSKPTQOTGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNNGTTRVAIKTL 300
QY      301  KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGETGKY 360
DB      301  KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGETGKY 360
QY      361  LRLPOLVDMAAOIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB      361  LRLPOLVDMAAOIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY      421  AROGAFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDQVER 480
DB      421  AROGAFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDQVER 480
QY      481  GYRMPCPPECPSLHLMCCMRKEPERPTFEYLOAFLEDYFTSTPEYQYQGENL 536
DB      481  GYRMPCPPECPSLHLMCCMRKEPERPTFEYLOAFLEDYFTSTPEYQYQGENL 536

RESULT 2
ABG95123
ID      ABG95123 standard; protein; 536 AA.
AC      ABG95123;
XX      DT      04-DEC-2002 (first entry)
XX      DE      Human v-src isoform.
XX      KW      Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX      KW      proliferative disease; cellular protein isoform; heat shock protein 90;
XX      KW      HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX      KW      T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX      KW      acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX      KW      acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX      KW      papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX      KW      rhabdomyosarcoma; synovial sarcoma; viral infection.
XX      OS      Homo sapiens.
XX      PN      WO200269900-A2.
XX      PD      12-SEP-2002.
XX      PF      01-MAR-2002; 2002WO-US006518.
XX      PR      01-MAR-2001; 2001US-0272751P.
XX

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PA      (CONF-) CONFORMA THERAPEUTICS CORP.
XX      PI      Fritz LC, Burrows FT;
XX      DR      WPI; 2002-698710/75.
XX      N-PSDB; ABS73324.
PT      Treating genetically-defined disease associated with chromosomal
PT      aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT      diseases, involves administering an inhibitor of heat shock protein 90.
XX      PS      Disclosure; Page 310-312; 389pp; English.
XX      CC      The invention describes a method of treating genetically-defined disease
XX      CC      associated with chromosomal aberrations yielding oncogenic fusion
XX      CC      proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX      CC      cell population, treating proliferative diseases associated with mutant
XX      CC      protein or cellular protein isoforms (II) dependent on heat shock protein
XX      CC      (Hsp)-90, or selectively treating cells expressing (II) involving
XX      CC      administering HSP90-inhibitor. The method is useful for treating
XX      CC      genetically-defined disease with chromosomal aberration yielding
XX      CC      oncogenic fusion protein, treating cancerous cells containing fusion
XX      CC      protein in heterogeneous cell population, treating proliferative disease
XX      CC      (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX      CC      cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX      CC      p53), or selectively treating cells expressing mutant protein or cellular
XX      CC      protein isoform in a patient heterozygous for (II). The method is useful
XX      CC      for treating a disease e.g. haematopoietic disorder such as T or B cell
XX      CC      lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX      CC      or a disease characterised by a solid tumour such as papillary thyroid
XX      CC      carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX      CC      synovial sarcoma. The method is also useful for treating viral
XX      CC      infections. This is the amino acid sequence of a human oncogenic protein
XX      SQ      Sequence 536 AA;
Query Match      100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGSNKSXPDAQRRLSLPAENVHAGGAGFPAAGTSPKPSADGHRPSAFAFAPAAAE 60
DB      1  MGSNKSXPDAQRRLSLPAENVHAGGAGFPAAGTSPKPSADGHRPSAFAFAPAAAE 60
QY      61  PKLFGFNSSDVTYTSQRAQPLAGVTTFVALYDYESRTETDLSFKKGRRLQIVNTEGD 120
DB      61  PKLFGFNSSDVTYTSQRAQPLAGVTTFVALYDYESRTETDLSFKKGRRLQIVNTEGD 120
QY      121  WMLAHSLSGTQGTGYIPSNVVAAPSDSIQAEEMWFGKITRRESERLLNAENPRGTFIVRES 180
DB      121  WMLAHSLSGTQGTGYIPSNVVAAPSDSIQAEEMWFGKITRRESERLLNAENPRGTFIVRES 180
QY      181  ETTKGAAYCLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYSKADGL 240
DB      181  ETTKGAAYCLSVSDFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQQLVAAYYSKADGL 240
QY      241  CHRLLTVCTPSKPTQOTGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNNGTTRVAIKTL 300
DB      241  CHRLLTVCTPSKPTQOTGLAKDAWEIPRESLRLEVKLGQCGCFGEVWMTNNGTTRVAIKTL 300
QY      301  KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGETGKY 360
DB      301  KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGETGKY 360
QY      361  LRLPOLVDMAAOIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB      361  LRLPOLVDMAAOIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY      421  AROGAFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDQVER 480
DB      421  AROGAFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDQVER 480
QY      481  GYRMPCPPECPSLHLMCCMRKEPERPTFEYLOAFLEDYFTSTPEYQYQGENL 536

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Db 481 GYRMPCEPCESHDLMCCMKRKEPERPFVEYLQAFLEBYFSTEQYQPGENTL 536

RESULT 3
AAU78678
ID AAU78678 standard; protein; 536 AA.

AAU78678;

18-JUN-2002 (first entry)

Human SH2/SH3 domain containing protein, v-src.

Protein profiling; c-src; SH2; SH3; antibody microarray;
protein microarray; DNA microarray; expression profiling; immunology;
protein analysis; proteome analysis; human; protein expression profiling.

Homo sapiens.

MO200214867-A2.

21-FEB-2002.

13-AUG-2001; 2001WO-US041709.

11-AUG-2000; 2000US-0224939P.

12-APR-2001; 2001US-0283498P.

(AGIL-) AGILIX CORP.

Chait BT, Lattner DR, Lizaldi PM, Kershnar ER, Morrow JS;

Roth ME, Matessich MJ, Mcconnel KJ;

WPI; 2002-304072/34.

Detecting multiple analytes by separating a set of reporter signals
having common property from molecules lacking common property, altering
signal, detecting and distinguishing altered forms of signal from each
other.

Disclosure; Page 224; 341pp; English.

The invention relates to detecting (M1) multiple analytes involving
separating a set of reporter signals (RS), where each RS has a common
property, from molecules lacking the common property, altering the RS,
and detecting and distinguishing the altered forms of the RS from each
other. The method (M1) is useful for detecting multiple analytes M1 is
useful for detection of analytes and biomolecules, (such as proteins,
peptides and protein fragments), preferably for multiplex detection and
analysis of analytes and biomolecules. M1 is useful to detect a specific
analyte (in a specific sample or in multiple samples) or multiple
analytes (in a single sample or multiple samples), and to gather and
catalogue information about unknown analytes. M1 is useful as a detection
system in a number of fields, including antibody or protein microarrays,
DNA microarrays, expression profiling, comparative genomics, immunology,
diagnostic assay and quality control. M1 is useful as a detection and
analysis system for protein analysis, proteome analysis, proteomic,
protein expression profiling, de novo protein discovery, functional
genomics and protein detection. M1 increases the sensitivity and accuracy
of detection of analytes of interest, and allows a complex sample of
analytes to be quickly and easily catalogued in a reproducible manner. M1
is compatible with techniques involving cleavage, treatment or
fragmentation of a bulk sample in order to simplify the sample prior to
introduction into the first stage of a multistage detection system. M1 is
also compatible with any desired sample, including raw extracts and
fractionated samples. The present sequence is human c-src whose SH2/SH3
domains are detected in a sample, using the method of the invention

Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSRPKDASQRRRSLEPENNTHGAGCGAFPSQTPSKRASADGRGSEAAAPAAAE	60
Db	1	MGSNKSRPKDASQRRRSLEPENNTHGAGCGAFPSQTPSKRASADGRGSEAAAPAAAE	60
QY	61	PKLFGFNSDPTVNSPORAGPLAGVTFVVLVDYESFTEFDLSFKGGERIQIVNTEGD	120
Db	61	PKLFGFNSDPTVNSPORAGPLAGVTFVVLVDYESFTEFDLSFKGGERIQIVNTEGD	120
QY	121	WMLAHSLSGTQGYTPSNVYVAPSDIOAEEMVFPKTRRSEERLLNENRGTFLVRES	180
Db	121	WMLAHSLSGTQGYTPSNVYVAPSDIOAEEMVFPKTRRSEERLLNENRGTFLVRES	180
QY	181	ETTKGAYCLSVSDPDNAKGLNVKTKRKLDGSGFYITSRQFNSLQQLVAYYSKADGL	240
Db	181	ETTKGAYCLSVSDPDNAKGLNVKTKRKLDGSGFYITSRQFNSLQQLVAYYSKADGL	240
QY	241	CHRLTTCPTPSKPTQGLADAMEIPRESLLEVKLGQCGEYVMGTMGTTRVAIKTL	300
Db	241	CHRLTTCPTPSKPTQGLADAMEIPRESLLEVKLGQCGEYVMGTMGTTRVAIKTL	300
QY	301	KPGTMSPEAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYTEYMSKSLDPLKGTEGKY	360
Db	301	KPGTMSPEAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYTEYMSKSLDPLKGTEGKY	360
QY	361	LRLPOLVMAAQIASGNAVYERMYVHRDLPAANILVGENIVCYADFGRLRLENDNYT	420
Db	361	LRLPOLVMAAQIASGNAVYERMYVHRDLPAANILVGENIVCYADFGRLRLENDNYT	420
QY	421	AROGAKFPKWTAREALVYGFETIKSDVWSFGILLTETTKGRVYPGMVNRVLDQVER	480
Db	421	AROGAKFPKWTAREALVYGFETIKSDVWSFGILLTETTKGRVYPGMVNRVLDQVER	480
QY	481	GYRMPCEPCESHDLMCCMKRKEPERPFVEYLQAFLEBYFSTEQYQPGENTL 536	
Db	481	GYRMPCEPCESHDLMCCMKRKEPERPFVEYLQAFLEBYFSTEQYQPGENTL 536	

RESULT 4
ABP57260
ID ABP57260 standard; protein; 536 AA.
AC ABP57260;
DT 17-APR-2003 (first entry)
XX Human src-c protein SEQ ID NO:3.
DE Human; src-c; tyrosine kinase; src-c inhibitor; cytosolic; osteopathic;
KW antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
KW antisense oligonucleotide; aberrant bone remodeling; breast cancer;
KW hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
KW ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
KW Kaposi's sarcoma; infection; inflammation; tumour formation.
XX Homo sapiens.
OS MO200295053-A2.
PN MO200295053-A2.
XX 28-NOV-2002.
PD 16-MAY-2002; 2002WO-US015684.
PF 16-MAY-2002; 2002WO-US015684.
PR 18-MAY-2001; 2001US-00860473.
XX (ISIS-) ISIS PHARM INC.
PA (ISIS-) ISIS PHARM INC.
XX Bennett FC, Walt AT;
PI Bennett FC, Walt AT;
XX WPI; 2003-120806/11.
DR N-PSDB; ABZ59382.
XX

PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
 PT useful for diagnosing, treating or preventing diseases associated with
 PT the expression of src-c, e.g. cancer or inflammation, and in research
 PT applications.

XX Example 13; Page 97-100; 137pp; English.

CC The present invention describes a compound (I) that is 8-50 nucleobases
 CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
 CC coding region, intron region, exon region, stop codon, intron-exon
 CC junction, exon-exon junction, or 5' mRNA variant of src-c, and which
 CC specifically hybridizes with and inhibits the expression of src-c. (I)
 CC have cytostatic, antiinflammatory, osteopathic and antibacterial
 CC activities, and can be used in antisense therapy and in vaccines. The
 CC antisense compound (I) can be used for modulating the expression of src-
 CC c and for treating diseases or conditions associated with expression of
 CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
 CC particularly cancer, such as breast cancer, pancreatic cancer, lung
 CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
 CC or Kaposi's sarcoma. (I) are also useful for diagnostic, therapeutic,
 CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 CC formation, as research reagents and kits, and in distinguishing between
 CC functions of various members of a biological pathway. The present
 CC sequence represents human src-c, which is used in an example from the
 CC present invention

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 6; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSQPRDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSQPRDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY 61 PKLFGFNSSDVTYSPQRAGPLAGVYTFVALYDYESRTETDLSFKKGERLQIVNTEGD 120
 DB 61 PKLFGFNSSDVTYSPQRAGPLAGVYTFVALYDYESRTETDLSFKKGERLQIVNTEGD 120
 QY 121 WMLAHSLSGTQGYIPSNVYVAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLYRES 180
 DB 121 WMLAHSLSGTQGYIPSNVYVAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLYRES 180
 QY 181 ETTKGAYCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
 DB 181 ETTKGAYCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
 QY 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTNGTTRVAIKTL 300
 DB 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTNGTTRVAIKTL 300
 QY 301 KEGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
 DB 301 KEGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
 QY 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
 DB 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
 QY 421 AROGAKFPIKMTAPBEALYGRFTIKSDVMSFGILLTELTTKGRVPPGVMNREVLDOVER 480
 DB 421 AROGAKFPIKMTAPBEALYGRFTIKSDVMSFGILLTELTTKGRVPPGVMNREVLDOVER 480
 QY 481 GYRMPCEPCPSGLHLMQCQWRKEPERPTEFYLOAFLEDYTSSTEPQYQGENL 536
 DB 481 GYRMPCEPCPSGLHLMQCQWRKEPERPTEFYLOAFLEDYTSSTEPQYQGENL 536

RESULT 5
 ADI20072
 ID ADI20072 standard; protein; 536 AA.
 XX

AC ADI20072;
 XX
 XX 22-APR-2004 (first entry)
 XX
 DE Human c-Src.
 XX
 KW specific-binding agent; Src; Cytostatic; Cardiant; Src-positive tumor;
 XX heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057238-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 27-DEC-2002; 2002WO-US041564.
 XX
 PR 28-DEC-2001; 2001US-034588P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Schmitt JM, Stork PDS;
 XX
 XX WPI; 2003-587076/55.
 DR N-PSDB; ADI20071.
 XX
 PT New specific-binding agent which specifically binds to Src when Src is
 PT phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
 PT when Ser17 is not phosphorylated, useful for identifying abnormal cell
 PT proliferation.
 PS Disclosure; SEQ ID NO 2; 40pp; English.

CC The present invention relates to a specific-binding agent which
 CC specifically binds to Src when Src is phosphorylated at serine at
 CC position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
 CC phosphorylated. The specific-binding agent is useful as a diagnostic
 CC agent. The agent and the methods may also be used for treating Src-
 CC positive tumors or heart disease. The present sequence represents human c-
 CC Src.

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 7; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSQPRDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
 DB 1 MGSNKSQPRDASQRRSLSPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAAE 60
 QY 61 PKLFGFNSSDVTYSPQRAGPLAGVYTFVALYDYESRTETDLSFKKGERLQIVNTEGD 120
 DB 61 PKLFGFNSSDVTYSPQRAGPLAGVYTFVALYDYESRTETDLSFKKGERLQIVNTEGD 120
 QY 121 WMLAHSLSGTQGYIPSNVYVAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLYRES 180
 DB 121 WMLAHSLSGTQGYIPSNVYVAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLYRES 180
 QY 181 ETTKGAYCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
 DB 181 ETTKGAYCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
 QY 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTNGTTRVAIKTL 300
 DB 241 CHRLLTVCTPSKQTOGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTNGTTRVAIKTL 300
 QY 301 KEGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
 DB 301 KEGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
 QY 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
 DB 361 LRLPOLVDMAAQIASGMAVYERBNVYHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420

CC are useful for treating cancer, to delay or prevent infection,
CC inflammation or tumour formation. The invention is also useful in gene
CC therapy. The present sequence is human wild-type tyrosine kinase protein
CC pp60.

XX Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 8; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPQDASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPQDASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSSDVTSPPRAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
DB 61 PKLFGGNSSDVTSPPRAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENPRGTFIVRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENPRGTFIVRES 180
QY 181 ETTKGAIVCLSVSPDNAGKLVNHYKIRKLDSCGFYITTSRTQFNSLQQLVAIYYSKADGL 240
DB 181 ETTKGAIVCLSVSPDNAGKLVNHYKIRKLDSCGFYITTSRTQFNSLQQLVAIYYSKADGL 240
QY 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCGEGVMGTMGTRVAIKTL 300
DB 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCGEGVMGTMGTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEEPYIYITEYMSKGSLLDFLKGETGKY 360
DB 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEEPYIYITEYMSKGSLLDFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERMNYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERMNYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
QY 421 ARGAKFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVPYPGMNRREVLDOVER 480
DB 421 ARGAKFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVPYPGMNRREVLDOVER 480
QY 481 GYMPCCPECPESLHDMCCMRKEPERPTEFYLOAFLEDYFTSTEPQYQPGENTL 536
DB 481 GYMPCCPECPESLHDMCCMRKEPERPTEFYLOAFLEDYFTSTEPQYQPGENTL 536

RESULT 8
ADQ97772
ID ADQ97772 standard; protein; 536 AA.

XX AC ADQ97772;

DT 07-OCT-2004 (first entry)

DE Human cancer associated sequence HPI0-043, SEQ ID 749.

KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

OS Homo sapiens.

XX PN MO2004060304-A2.

XX PD 22-JUL-2004.

XX PF 22-DEC-2003; 2003MO-US041389.

XX PR 27-DEC-2002; 2002US-00330773.

XX PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2004-543761/52.

XX PT New isolated cancer associated nucleic acids comprising at least 10
XX PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
XX PT cancers such as leukemia and lymphoma.

PS Claim 1; SEQ ID NO 749; 199pp; English.

CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 8; Length 536;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPQDASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPQDASQRRSLLEPAENVHAGGAGFPAASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSSDVTSPPRAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
DB 61 PKLFGGNSSDVTSPPRAGPLAGVTTFPALVDYBSRTETDLSFKKGERLQIVNNTGCD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENPRGTFIVRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYGKTRRESERLLNAENPRGTFIVRES 180
QY 181 ETTKGAIVCLSVSPDNAGKLVNHYKIRKLDSCGFYITTSRTQFNSLQQLVAIYYSKADGL 240
DB 181 ETTKGAIVCLSVSPDNAGKLVNHYKIRKLDSCGFYITTSRTQFNSLQQLVAIYYSKADGL 240
QY 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCGEGVMGTMGTRVAIKTL 300
DB 241 CHRLLTVCPSPKQOTGLADAMEIPRESLRLEVKLGCGCGEGVMGTMGTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEEPYIYITEYMSKGSLLDFLKGETGKY 360
DB 301 KPGTMSPEAFLOEAQVMKLRHEKLVQLYAVVSEEPYIYITEYMSKGSLLDFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERMNYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERMNYVHRDLRAANIIVGENLVCKVADFGIARLIEDNEYT 420
QY 421 ARGAKFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVPYPGMNRREVLDOVER 480
DB 421 ARGAKFPIKWTAPREALYGRFTIKSDVMSFGILLTETTKGRVPYPGMNRREVLDOVER 480
QY 481 GYMPCCPECPESLHDMCCMRKEPERPTEFYLOAFLEDYFTSTEPQYQPGENTL 536
DB 481 GYMPCCPECPESLHDMCCMRKEPERPTEFYLOAFLEDYFTSTEPQYQPGENTL 536

RESULT 9
ADU04517
ID ADU04517 standard; peptide; 536 AA.

XX AC ADU04517;

DT 13-JAN-2005 (first entry)

DE Protein tyrosine kinase Src.

KW Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;

XX KM protein structure; enzyme; EC_2.7.1.112.

XX SQ Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 216 /note= "Tyr phosphorylation site"
 FT Modified-site 419 /note= "Tyr phosphorylation site"
 FT Modified-site 530 /note= "Tyr phosphorylation site"
 FT Modified-site 530 /note= "Tyr phosphorylation site"
 XX
 PN WO2004092703-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 09-APR-2004; 2004WO-US010834.
 XX
 PR 11-APR-2003; 2003US-0462083P.
 PR 11-APR-2003; 2003US-0462472P.
 PR 25-JUL-2003; 2003US-0490057P.
 PR 08-MAR-2004; 2004US-0551311P.
 PR 19-MAR-2004; 2004US-0554701P.
 PR 08-APR-2004; 2004US-00821231.
 XX
 PA (PURD) PURDUE RES FOUND.
 XX
 PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
 XX
 DR WPI; 2004-784629/77.
 XX
 PT Obtaining structural characteristic information for separation and
 PT detection of e.g. proteins comprises irradiating a region formed by
 PT evaporating specimen-containing solvent in a droplet on planar solvo-
 PT phobic sample support.
 XX
 PS Example C; Page 25; 91pp; English.
 XX
 CC The present sequence is that of proto-oncogene protein tyrosine kinase
 CC Src (p60-src, c-src). The invention relates to the combined use of solid
 CC substrates, micro-deposition techniques, spectral imaging methods, and
 CC data processing to facilitate the concentration and separate detection of
 CC biological molecules including proteins, peptides, polysaccharides,
 CC glycans and nucleotides, in a liquid mixture, using spectral analysis
 CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
 CC assisted laser desorption/ionisation (MALDI) time-of-flight mass
 CC spectrometry. The methods were demonstrated in examples from the
 CC invention using peptide fragments of Src. These demonstrated the high
 CC level of analyte discrimination that can be achieved and that the method
 CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
 CC of physiologically important proteins.
 CC
 XX Sequence 536 AA;
 SQ
 Query Match 100.0%; Score 2834; DB 8; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSKPASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSKPASADGHRGSAAPAPAAE 60
 QY 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFVALYBESRTEDLSFKKGERLQIVNTEGD 120
 DB 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFVALYBESRTEDLSFKKGERLQIVNTEGD 120
 QY 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFVALYBESRTEDLSFKKGERLQIVNTEGD 120
 DB 61 PKLFGGNSSDTYTSPORAGPIAGGVTTFVALYBESRTEDLSFKKGERLQIVNTEGD 120
 QY 121 WMLAHSSTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRREBERLLNAENRGTFLVRES 180
 DB 121 WMLAHSSTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRREBERLLNAENRGTFLVRES 180
 QY 121 WMLAHSSTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRREBERLLNAENRGTFLVRES 180
 DB 121 WMLAHSSTGOTGYTIPSNYVAPSDSIQAEEMYPFKITRREBERLLNAENRGTFLVRES 180
 QY 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGGFYITSTRQFNSLQOLVAVYSKADGL 240
 DB 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGGFYITSTRQFNSLQOLVAVYSKADGL 240
 QY 241 CHRLTTCPTSPKPTQGLADAWMEIPRESRLREYKLGQGCPCGEVWMTNGTTRVAIKTL 300
 DB 241 CHRLTTCPTSPKPTQGLADAWMEIPRESRLREYKLGQGCPCGEVWMTNGTTRVAIKTL 300

DB 241 CHRLTTCPTSPKPTQGLADAWMEIPRESRLREYKLGQGCPCGEVWMTNGTTRVAIKTL 300
 QY 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLYAVSEEPYIYEWMSKSLDPLGEGCKY 360
 DB 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLYAVSEEPYIYEWMSKSLDPLGEGCKY 360
 QY 361 LRLPOLVDMANQIASGNAVYERMYVRDRLAANILVGENLVCKVADPGLARLIEDNEYT 420
 DB 361 LRLPOLVDMANQIASGNAVYERMYVRDRLAANILVGENLVCKVADPGLARLIEDNEYT 420
 QY 421 ARQAKPEPIKWTABEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDOYER 480
 DB 421 ARQAKPEPIKWTABEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDOYER 480
 QY 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGNL 536
 DB 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGNL 536
 QY 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGNL 536
 DB 481 GYRMPCEPCEPESLHDMCCMRKEPERPFEYLQAFLEBYFTSTEPQYQNGNL 536
 RESULT 10
 ADY84076
 ID ADY84076 standard; protein; 536 AA.
 XX
 AC ADY84076;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DB Human Src protein isoform 2 SEQ ID NO:2.
 XX
 KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 PN EPI413887-A1.
 XX
 PD 28-APR-2004.
 XX
 PF 22-OCT-2002; 2002EP-00292608.
 XX
 PR 22-OCT-2002; 2002EP-00292608.
 XX
 PA (AVENTIS) AVENTIS PHARMA SA.
 XX
 PI Mercken L, Zambrano N, Rusco T;
 XX
 DR WPI; 2004-332834/31.
 XX
 PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX
 PS Claim 4; SEQ ID NO 2; 45pp; English.
 XX
 CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 2
 CC of human Src protein.
 XX
 SQ Sequence 536 AA;
 Query Match 100.0%; Score 2834; DB 8; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSKPASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSXPDKASQRRSLRPAENVHAGGAFPAASQTPSKPASADGHRGSAAPAPAAE 60

DB 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
QY PKLFGFNSSDVTTSQORAGPLAGVTTFPALVDYESRTTDSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTTSQORAGPLAGVTTFPALVDYESRTTDSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGQGTGYSNVAAPSDSIQAEEMVFGKLTRESEBRLINAEPRGTFIVRES 180
DB 121 WMLAHSLSGQGTGYSNVAAPSDSIQAEEMVFGKLTRESEBRLINAEPRGTFIVRES 180
QY 181 ETTKGAVCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
DB 181 ETTKGAVCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
QY 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTTRVAIKTL 300
DB 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLVAVSEBPIYIVTERMSKSLDPLKGETGKY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLVAVSEBPIYIVTERMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRNREVLDOVER 480
DB 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRNREVLDOVER 480
QY 481 GYRMPCPPECBSLHLMCCQWKKEPERPTFEYLOAFLEDYFTSTEPYOQGENL 536
DB 481 GYRMPCPPECBSLHLMCCQWKKEPERPTFEYLOAFLEDYFTSTEPYOQGENL 536

RESULT 11

ADV94834
ID ADV94834 standard; protein; 536 AA.

XX ADV94834;

XX 10-MAR-2005 (first entry)

XX Human wild type c-Src protein.

XX cytostatic; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
XX breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.

XX Homo sapiens.

XX US2004261142-A1.

XX 23-DEC-2004.

XX 09-JUL-2004; 2004US-00887588.

XX 24-NOV-1999; 99US-00444711.

XX (YEAT/) YEATMAN T J.

XX (IRBY/) IRBY R B.

XX Yeatman TJ, Irby RB;

XX MPI; 2005-038810/04.

XX N-PSDB; ADV94833.

XX New truncated c-Src polypeptide, useful for treating and/or preventing
XX PT clinical conditions associated with or caused by Src mutation, e.g.
XX tumors.

XX Disclosure; SEQ ID NO 2; 28pp; English.

XX The invention relates to a truncated c-Src polypeptide comprising a

CC sequence of 530 amino acids given in the specification. The polypeptide,
CC composition and method are useful for treating and/or preventing clinical
CC conditions associated with or caused by Src mutation e.g. tumors
CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
CC the wild type c-Src protein.

XX SQ Sequence 536 AA;

Query Match 100.0%; Score 2834; DB 9; Length 536;
Best Local Similarity 100.0%; Pred.No.1e-242;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
DB 1 MGSNKGKPDASQRRRSLEPAENVHAGGAFPPASQTPSKPASADGHRGSAFAFAAAE 60
QY 61 PKLFGFNSSDVTTSQORAGPLAGVTTFPALVDYESRTTDSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDVTTSQORAGPLAGVTTFPALVDYESRTTDSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGQGTGYSNVAAPSDSIQAEEMVFGKLTRESEBRLINAEPRGTFIVRES 180
DB 121 WMLAHSLSGQGTGYSNVAAPSDSIQAEEMVFGKLTRESEBRLINAEPRGTFIVRES 180
QY 181 ETTKGAVCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
DB 181 ETTKGAVCISVSPFDNAKGLNVGHYKIRKLDGSGFYITSRTOFNSIQOLVAVYSKADGL 240
QY 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTTRVAIKTL 300
DB 241 CHRLLTVCTPSKQOTGLAKDAWEIPRESLRLEVKLGQCFCGEVWNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLVAVSEBPIYIVTERMSKSLDPLKGETGKY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLVAVSEBPIYIVTERMSKSLDPLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAYVERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAYVERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRNREVLDOVER 480
DB 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYPGMVRNREVLDOVER 480
QY 481 GYRMPCPPECBSLHLMCCQWKKEPERPTFEYLOAFLEDYFTSTEPYOQGENL 536
DB 481 GYRMPCPPECBSLHLMCCQWKKEPERPTFEYLOAFLEDYFTSTEPYOQGENL 536

RESULT 12

AEA35914
ID AEA35914 standard; protein; 536 AA.

XX AEA35914;

XX 25-AUG-2005 (first entry)

XX Human Src kinase amino acid sequence SEQ ID NO:1.

XX Src family kinase; Src kinase.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 298 /note= "constant amino acid K in domain SH2"

XX FT Misc-difference 341 /note= "constant amino acid T in domain SH2"

XX FT Misc-difference 530 /note= "constant amino acid Y in domain SH1"

XX EP1541694-A1.

PD 15-JUN-2005.
 XX
 PF 12-DEC-2003; 2003EP-00028713.
 XX
 PR 12-DEC-2003; 2003EP-00028713.
 XX
 PA (SIRE-) SIRENADE PHARM AG.
 XX
 PI Obermeier A, Bieger B;
 XX WPI; 2005-428084/44.
 DR
 XX
 PT Identifying compound which modulates Src family kinase (SFK) activity by
 PT contacting cells expressed with SFK or mutated SFK with test compound,
 PT where change in phenotype of cells indicates that test compound modulates
 PT SFK activity.
 PS
 PS Disclosure; SEQ ID NO 1; 114pp; English.
 XX
 CC The invention relates to a method (M1) for identifying, selecting and/or
 CC characterizing a compound which modulates Src family kinase (SFK)
 CC activity, by expressing nucleic acids encoding SFK or mutated SFK in
 CC cells, contacting cells with test compound and determining whether
 CC phenotype of cells is changed as compared with phenotype of cells not
 CC expressed with above nucleic acids, where difference in phenotype
 CC indicates that test compound modulate SFK activity. Also described: (1) a
 CC compound (I) identified, selected and/or characterized by (M1); and (2) a
 CC pharmaceutical composition (PCI) containing (1), and a carrier, adjuvant
 CC or vehicle. (1) is useful as a medicament, particularly for the treatment
 CC of diseases, which are at least in part caused by a Src family kinase.
 CC (1) and PCI are useful for producing a medicament for the treatment of
 CC diseases, which are at least in part caused by a Src family kinase,
 CC particularly by a dysfunction of a Src family kinase, in particular
 CC cancer, hypercalcaemia, resection, osteoporosis, osteoarthritis,
 CC symptomatic treatment of bone metastasis, rheumatoid arthritis,
 CC inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
 CC versus host disease, T-cell mediated hypersensitivity disease,
 CC Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
 CC pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
 CC or reperfusion injury, allergic disease, atopic dermatitis, transplant
 CC rejection or allergic rhinitis. The present sequence represents human Src
 CC kinase, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 536 AA;
 Query Match 100.0%; Score 2834; DB 9; Length 536;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPKDASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 DB 1 MGSNKSFKPKDASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 QY 61 PKLFGGNSSDTYTSPQRAPIAGAGVTFVALVYBESRTEDLSFKKGERLQIYNNTGEGD 120
 DB 61 PKLFGGNSSDTYTSPQRAPIAGAGVTFVALVYBESRTEDLSFKKGERLQIYNNTGEGD 120
 QY 121 MWLAHSLSTGOTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 DB 121 MWLAHSLSTGOTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 QY 121 MWLAHSLSTGOTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 DB 121 MWLAHSLSTGOTGYIPSNVYAPSDSIQAEWYFGKTRRESERILLNANRGTFVRES 180
 QY 181 ETTKGAYCLSVSDPNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAVYSKADGL 240
 DB 181 ETTKGAYCLSVSDPNAKGLNVKXKIRKLDGSGFYITTSRTQFNSLQOLVAVYSKADGL 240
 QY 241 CHRLTYVCPTSKPOTQGLADKAWIIPRESILAEVYKLGCGCGEYVWGMGTNTTVAIKTL 300
 DB 241 CHRLTYVCPTSKPOTQGLADKAWIIPRESILAEVYKLGCGCGEYVWGMGTNTTVAIKTL 300
 QY 301 KPGTMSDEAPLQEAQWKKLREKLVOLYAVSEBPIYIVTEVYSKSLIDFLGETGKY 360
 DB 301 KPGTMSDEAPLQEAQWKKLREKLVOLYAVSEBPIYIVTEVYSKSLIDFLGETGKY 360

QY 361 LRLPOLYDMAAQISGMAVYERMYVHRDLRAANILVGENLVCKVADGRLARLIEDNXYT 420
 DB 361 LRLPOLYDMAAQISGMAVYERMYVHRDLRAANILVGENLVCKVADGRLARLIEDNXYT 420
 QY 421 ARQAKFPKWTABEALVGRFTIKSDVWSPGILLTTELTTKGRVYPGMVNRVLDQYER 480
 DB 421 ARQAKFPKWTABEALVGRFTIKSDVWSPGILLTTELTTKGRVYPGMVNRVLDQYER 480
 QY 481 GYRMPCEPCEPSLHDMCCQWRKEPBERPFTFYLQAFLEDYFTSTEQYQGENYL 536
 DB 481 GYRMPCEPCEPSLHDMCCQWRKEPBERPFTFYLQAFLEDYFTSTEQYQGENYL 536
 RESULT 13
 ID ADY84080 standard; protein; 549 AA.
 XX
 AC ADY84080;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human Src cDNA encoded amino acid #1.
 XX
 KW pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 FN EP1413887-A1.
 XX
 PD 28-APR-2004.
 XX
 PF 22-OCT-2002; 2002EP-00292608.
 XX
 PR 22-OCT-2002; 2002EP-00292608.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Mercken L, Zambrano N, Russo T;
 XX WPI; 2004-332834/31.
 DR N-PSDB; ADY84078.
 XX
 FT Identifying therapeutic compound for treating Alzheimer's disease,
 FT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX
 PS Disclosure; SEQ ID NO 4; 45pp; English.
 XX
 CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence is encoded by the
 CC human Src cDNA. The sequence is represented as part of SEQ ID NO:4 in the
 CC sequence listing of the specification.
 XX
 SQ Sequence 549 AA;
 Query Match 100.0%; Score 2834; DB 8; Length 549;
 Best Local Similarity 100.0%; Pred. No. 1e-242;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPKDASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 60
 DB 14 MGSNKSFKPKDASQRRSLPEAENVHAGGAFPPASQTPSKPASADGHRGSAAPAPAAE 73
 QY 61 PKLFGGNSSDTYTSPQRAPIAGAGVTFVALVYBESRTEDLSFKKGERLQIYNNTGEGD 120

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Db      74 PKLGFNNSDVTSPQAGPLAGVTTFVALYDYESTRTDLSFKKGERLQIVNTEGD 133
Qy      121 WMLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRSEERLLNAENPRGTFVRES 180
Db      134 WMLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRSEERLLNAENPRGTFVRES 193
Qy      181 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITTSQFNSLQQLVAAYYSKHADGL 240
Db      194 ETTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITTSQFNSLQQLVAAYYSKHADGL 253
Qy      241 CHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 300
Db      254 CHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 313
Qy      301 KPRTMSPEAPLQEAQWKKLRHEKLVQYVAVSEEPYIYITEVYMSKSLDPLKGETGKY 360
Db      314 KPRTMSPEAPLQEAQWKKLRHEKLVQYVAVSEEPYIYITEVYMSKSLDPLKGETGKY 373
Qy      361 LRLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Db      374 LRLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 433
Qy      421 ARQGAKEPIKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPMVNRREVLDQVER 480
Db      434 ARQGAKEPIKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPMVNRREVLDQVER 493
Qy      481 GYRMPCEPCEPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 536
Db      494 GYRMPCEPCEPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 549

RESULT 14
ADP45087
ID      ADP45087 standard; protein; 535 AA.
AC      ADP45087;
XX      12-FEB-2004 (first entry)
DT      12-FEB-2004 (first entry)
XX      Human kinase SRC.
DE      Human kinase SRC.
XX      Human; protein kinase; enzyme; inhibitor; SRC.
XX      Homo sapiens.
XX      OS
XX      Homo sapiens.
XX      MO2003081210-A2.
XX      PD
XX      02-OCT-2003.
XX      PF
XX      20-MAR-2003; 2003WO-US008725.
XX      PR
XX      21-MAR-2002; 2002US-036692P.
XX      PA
XX      (SUNE-) SUNESIS PHARM INC.
XX      PI
XX      Prescott JC, Braisted A;
XX      WPI; 2003-865136/80.
XX      DR
XX      Identifying ligand binding to inactive conformation of target protein
XX      kinase (T) comprises contacting the conformation modified (T) which
XX      contains reactive group at binding site, with ligands and detecting
XX      PT      kinase-ligand conjugate formation.
XX      PS
XX      Disclosure; SEQ ID NO 56; 260pp; English.
XX      The present invention relates to a method for identifying a ligand (L),
XX      CC      which binds to an inactive conformation of target protein kinase (T). The
XX      CC      method involves contacting inactive conformation of (T), which contains
XX      CC      or is modified to contain a reactive group at or near a binding site of
XX      CC      interest, with one or more ligand candidates capable of covalently
XX      CC      bonding to the reactive group thus forming a kinase-(L) conjugate (C).
XX      The method is useful for identifying protein kinase inhibitors that

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CC      preferentially bind to inactive conformation of a target protein kinase.
CC      The present sequence is a protein kinase which may be modified via an
CC      amino acid substitution, for use in the method of the invention.
XX      SQ      Sequence 535 AA;
XX      Query Match      99.8%; Score 2829; DB 7; Length 535;
XX      Best Local Similarity 100.0%; Pred. No. 2,8e-242;
XX      Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 GSNSKPKDASQRRRSLEPENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAP 61
Db      1 GSNSKPKDASQRRRSLEPENVHAGGAPASQTPSKPASADGHRGSAAPAPAAAP 60
Qy      62 KLGGFNPSSDVTYSPQAGPLAGVTTFVALYYESRTEDLSFKKGERLQIVNTEGDW 121
Db      61 KLGGFNPSSDVTYSPQAGPLAGVTTFVALYYESRTEDLSFKKGERLQIVNTEGDW 120
Qy      122 WMLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRSEERLLNAENPRGTFVRES 181
Db      121 WMLHSLSTGQTGYIPSNYVAPSDSIQAEWYFGKITRRSEERLLNAENPRGTFVRES 180
Qy      182 TTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITTSQFNSLQQLVAAYYSKHADGL 241
Db      181 TTKGAYCLSVSPFDNAKGLNVKHYKIRKLDSSGFFYITTSQFNSLQQLVAAYYSKHADGL 240
Qy      242 HRITTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 301
Db      241 HRITTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNVTTRVAIKTL 300
Qy      302 PGTMSPPEAPLQEAQWKKLRHEKLVQYVAVSEEPYIYITEVYMSKSLDPLKGETGKY 361
Db      301 PGTMSPPEAPLQEAQWKKLRHEKLVQYVAVSEEPYIYITEVYMSKSLDPLKGETGKY 360
Qy      362 RLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPOLVDMMAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 ROGAKEPIKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPMVNRREVLDQVER 481
Db      421 ROGAKEPIKWTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPMVNRREVLDQVER 480
Qy      482 YRMPCEPCEPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 536
Db      481 YRMPCEPCEPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPQYQGENL 535

RESULT 15
AED21154
ID      AED21154 standard; protein; 535 AA.
AC      AED21154;
XX      01-DEC-2005 (first entry)
XX      DE
XX      Human non-receptor protein tyrosine kinase Src protein SEQ ID NO: 4.
XX      XX
XX      Protein interaction; therapeutic; cerebrovascular ischemia;
XX      KW      cerebroprotective; vasotropic; hypoxia; ischemia; multiple sclerosis;
XX      KW      neuroprotective; Huntington's chorea; anticonvulsant; nootropic;
XX      KW      Parkinson's disease; antiparkinsonian; Alzheimer's disease; hyperglycemia;
XX      KW      antidiabetic; diabetes; trauma; tranquilizer; vulnerability; epilepsy;
XX      KW      grand mal seizure; muscle hypertonia; muscle relaxant; paralytic;
XX      KW      muscular-gen.; asthma; antiasthmatic; cardiac arrest; cardiac;
XX      KW      macular degeneration; ophthalmological; psychiatric disorder;
XX      KW      neuroleptic; schizophrenia; AIDS dementia complex; dementia;
XX      KW      inflammation; antiinflammatory; pain; analgesic; opiate dependence;
XX      KW      antidiabetic; cocaine addiction; alcoholism; anticholinic;
XX      KW      anorexia nervosa; anabolic; eating-disorders-gen.; enzyme;
XX      KW      Src tyrosine kinase.
XX      Homo sapiens.

```

PN US2005222042-A1.
XX
XX 06-OCT-2005.
XX 30-MAR-2004; 2004US-00814109.
XX 30-MAR-2004; 2004US-00814109.
XX (HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.
XX
XX Salter MW, Gingrich JR;
XX
XX WPI; 2005-689427/71.
XX N-PSDB; AED21153.
XX
XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor
XX tyrosine kinase Src in cells, comprises administering composition
XX comprising Src-unique domains anchoring protein inhibitor to cells.
XX
XX Example 1; SEQ ID NO 4; 32pp; English.
XX
XX The present invention provides a method for modifying N-methyl-D-
XX aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase
XX Src in cells. The method involves administering a composition including
XX at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to
XX the cells, where modification ameliorates a disease or condition related
XX to NMDAR signaling. Diseases or conditions ameliorated by the invention
XX include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's
XX chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,
XX diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,
XX cerebral palsy, asthma, cardiac arrest, macular degeneration, mental
XX diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS
XX wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,
XX alcohol addiction and other conditions associated with substance abuse
XX and anorexia. The present sequence is the human non-receptor protein
XX tyrosine kinase Src protein.
XX
XX Sequence 535 AA,
SQ

Query Match 99.8%; Score 2829; DB 9; Length 535;
Best Local Similarity 100.0%; Pred. No. 2.8e-242;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSNKSKPKDASQRRRSLEPBNVHGAGGAPPASQTPSKPASADGHRGSAFPAPAAEP 61
DB 1 GSNKSKPKDASQRRRSLEPBNVHGAGGAPPASQTPSKPASADGHRGSAFPAPAAEP 60
QY 62 KLEFGFNSSDPTVTSPOBAGPLAGGVTTFVALVDYESRTEITDLSFKGGERLQIVNTEGDM 121
DB 61 KLEFGFNSSDPTVTSPOBAGPLAGGVTTFVALVDYESRTEITDLSFKGGERLQIVNTEGDM 120
QY 122 WLAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRSESERLILNANPRGTFVRESE 181
DB 121 WLAHSLSTGQTGYIPSNVYAPSDSIQAEWYFGKITRSESERLILNANPRGTFVRESE 180
QY 182 TTKGAYCLSYSDTDNAGLVNKHVKIRKLDGSGFYITSRTQFNSLQQLVAVYSKHADGLC 241
DB 181 TTKGAYCLSYSDTDNAGLVNKHVKIRKLDGSGFYITSRTQFNSLQQLVAVYSKHADGLC 240
QY 242 HRLITVCPSTSKPOTOGIAKDAWEIPRESLBLEVKLGCGCGEYVMGTWNGTTRVAITLK 301
DB 241 HRLITVCPSTSKPOTOGIAKDAWEIPRESLBLEVKLGCGCGEYVMGTWNGTTRVAITLK 300
QY 302 PGTMSPEAFLOEAQVVKLHHEKLVOLYAVVSEPIYVTEYMSKSLDLFLKGETGKYL 361
DB 301 PGTMSPEAFLOEAQVVKLHHEKLVOLYAVVSEPIYVTEYMSKSLDLFLKGETGKYL 360
QY 362 RLFPOLYDMAAQIASGMAVYRRMYVHRDLPAANILVGENLVCKYADFGLARLIEDNEYTA 421
DB 361 RLFPOLYDMAAQIASGMAVYRRMYVHRDLPAANILVGENLVCKYADFGLARLIEDNEYTA 420
QY 422 ROGAKFPPIKWTAPAEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNVREVLDOVERG 481
DB 421 ROGAKFPPIKWTAPAEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNVREVLDOVERG 480

DB 421 ROGAKFPPIKWTAPAEALYGRFTIKSDVWSFGILLTELTTKGRVYPGMVNVREVLDOVERG 480
QY 482 YRMPCEPCEPSLHDMCQCWRKEPERPTEFYLOAFLEDFYFSTEEPOYQGENL 536
DB 481 YRMPCEPCEPSLHDMCQCWRKEPERPTEFYLOAFLEDFYFSTEEPOYQGENL 535

Search completed: June 5, 2006, 17:07:42
Job time : 119.529 secs

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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.5195 Seconds
(without alignments)
2396.538 Million cell updates/sec

Title: US-10-691-079-2
2834

Perfect score: 1 MGSNKSXPKXASQRRSLRP.....AFLEDYFTSTPEYQPGENL 536
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2821	99.5	542	1	TVHUSC protein-tyrosine k
2	2778.5	98.0	541	1	A43610 protein-tyrosine k
3	2661.5	93.9	533	1	TVCHS protein-tyrosine k
4	2621.5	92.5	587	1	TVFVPR protein-tyrosine k
5	2614.5	92.3	568	1	TVFVSL protein-tyrosine k
6	2599.5	91.7	557	1	TVFVS2 protein-tyrosine k
7	2516.5	88.8	526	1	TVFV60 protein-tyrosine k
8	2497.5	88.1	526	2	S20808 protein-tyrosine k
9	2491.5	87.9	526	1	OKFYVR protein-tyrosine k
10	2484.5	87.7	526	2	S15582 protein-tyrosine k
11	2481.5	87.6	526	1	TVFVPR protein-tyrosine k
12	2466.5	87.0	526	2	S6420 protein-tyrosine k
13	2463	86.9	532	1	B34104 protein-tyrosine k
14	2462	86.9	532	1	A34104 protein-tyrosine k
15	2453.5	86.6	545	2	S52313 protein-tyrosine k
16	2446.5	86.3	546	2	S52314 protein-tyrosine k
17	2418	85.3	523	1	TVFVMT protein-tyrosine k
18	2134.5	75.3	537	1	A45501 protein-tyrosine k
19	2123.5	74.9	543	1	TVHUS protein-tyrosine k
20	2121.5	74.9	541	1	TVCHYS protein-tyrosine k
21	2118.5	74.8	541	2	S11645 protein-tyrosine k
22	2065.5	72.9	544	2	S15183 protein-tyrosine k
23	2052.5	72.4	528	1	TVFVGS protein-tyrosine k
24	1978	69.8	534	1	A44991 protein-tyrosine k
25	1960.5	69.2	537	2	I15192 protein-tyrosine k
26	1956	69.0	534	1	S33568 protein-tyrosine k
27	1949	68.8	536	2	S33569 protein-tyrosine k
28	1932.5	68.2	537	1	TVHUSY protein-tyrosine k
29	1929.5	68.1	542	2	A49114 protein-tyrosine k

30	1923	67.9	539	2	B49114 protein-tyrosine k
31	1921.5	67.8	537	1	A43806 protein-tyrosine k
32	1856	65.5	529	1	TVHUPR protein-tyrosine k
33	1845	65.1	517	2	A43807 protein-tyrosine k
34	1813	64.0	517	2	S24547 protein-tyrosine k
35	1600.5	56.5	509	1	TVHAST protein-tyrosine k
36	1594	56.2	663	1	TVHVR protein-tyrosine k
37	1573	55.5	392	2	S04205 protein-tyrosine k
38	1525.5	53.8	505	1	TVHUSC protein-tyrosine k
39	1520.5	53.7	503	1	TVHUSC protein-tyrosine k
40	1515.5	53.5	503	1	TVHUSC protein-tyrosine k
41	1494	52.7	507	1	A39939 protein-tyrosine k
42	1464	51.7	509	1	OKHULK protein-tyrosine k
43	1464	51.7	512	1	TVHULY protein-tyrosine k
44	1456	51.4	512	1	I56160 protein-tyrosine k
45	1455	51.3	509	1	I48845 protein-tyrosine k

ALIGNMENTS

RESULT 1

TVHUSC protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence revision 07-Oct-1994 #text change 05-Oct-2004
C:Accession: A26891, A61083, A23287, A28832, B34704
R:Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 7, 1978-1983, 1987
A:Title: DNA sequence encoding the amino-terminal region of the human c-src protein: imp
A:Reference number: A26891, MUID:87257903; PMID:3299057
A:Accession: A26891
A:Molecule type: mRNA
A:Residues: 1-117,124-191 <TVN>
A:Cross-references: UNIPROT:P12931; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M16
R:Pyper, J.M.; Bolen, J.B.
J. Neurosci. Res. 24, 89-96, 1989
A:Title: Neuron-specific splicing of C-SRC RNA in human brain.
A:Reference number: A61083, MUID:90040822; PMID:2681803
A:Accession: A61083
A:Molecule type: mRNA
A:Residues: 98-145 <PYP>
A:Cross-references: UNIPARC:UPI0000172574
A:Accession: B61083
A:Molecule type: mRNA
A:Residues: 98-117,124-145 <PY2>
A:Cross-references: UNIPARC:UPI0000172574
R:Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 5, 1122-1129, 1985
A:Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of
A:Reference number: A23287, MUID:85213483; PMID:2582238
A:Accession: A23287
A:Molecule type: mRNA
A:Residues: 197-542 <AND>
A:Cross-references: UNIPARC:UPI000016806; GB:X02647; NID:G35588; PIDN:CAA26485.1; PID:G
R:Parke, R.C.; Mardon, G.; Lebo, R.V.; Varnus, H.E.; Bishop, J.M.
Mol. Cell. Biol. 5, 831-838, 1985
A:Title: Isolation of duplicated human C-src genes located on chromosomes 1 and 20.
A:Reference number: A28832, MUID:85187981; PMID:2581127
A:Accession: A28832
A:Molecule type: mRNA
A:Residues: 382-542 <PAR>
A:Cross-references: UNIPARC:UPI000017257D
R:Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A:Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A:Reference number: A34704, MUID:90220588; PMID:1651439
A:Accession: B34704
A:Molecule type: mRNA
A:Residues: 118-123 <PY3>
A:Cross-references: UNIPARC:UPI000017257E
C:Genetics:
A:Gene: GDB:SRC

A:Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A:Introns: 84/1, 117/2, 123/2, 156/2, 191/1, 241/1, 293/1, 353/1, 378/3, 430/1, 474/1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, proto-oncogene src type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pld
F:1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <Mat>
F:1-117,124-542/Product: protein-tyrosine kinase src, short form #status predicted <Mat>
F:91-146/Domain: SH3 homology <SH3>
F:157-254/Domain: SH2 homology <SH2>
F:774-532/Domain: protein kinase homology <KIN>
F:282-290/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:104/Active site: Lys #status predicted
F:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 99.5%; Score 2821; DB 1; Length 542;
Best Local Similarity 98.9%; Pred. No. 7,1e-132;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSDVTSPQAGPLAGVTTFVALYDYSRRTETDLSFKKGERLQIVNNT--- 117
DB 61 PKLFGFNSDVTSPQAGPLAGVTTFVALYDYSRRTETDLSFKKGERLQIVNNTKRV 120
QY 118 ---EGDWMHLAHSLSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLLNAENPRGT 174
DB 121 DVREGWMLAHSLSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLLNAENPRGT 180
QY 175 FLVRESETTKGAYCLSVSDPDNAKGLNVKIKRLDSCGFYITSTRQFNSLQQLVAYYS 234
DB 181 FLVRESETTKGAYCLSVSDPDNAKGLNVKIKRLDSCGFYITSTRQFNSLQQLVAYYS 240
QY 235 KHAADGCHRLTTCPTSPKQTOGLADAMEIPRESRLRLEVKLGCGCGFVWGMGTTR 294
DB 241 KHAADGCHRLTTCPTSPKQTOGLADAMEIPRESRLRLEVKLGCGCGFVWGMGTTR 300
QY 295 VALKTLKPGTMSPEALQEAQVWKLRHEKLVQLYAVSEBPIYITERYMKSGLDPLK 354
DB 301 VALKTLKPGTMSPEALQEAQVWKLRHEKLVQLYAVSEBPIYITERYMKSGLDPLK 360
QY 355 GETGKTLRLPOLVDMAAQLASGMAVYERNNYVRDLRAANILVGENLVCKVADFGIARLI 414
DB 361 GETGKTLRLPOLVDMAAQLASGMAVYERNNYVRDLRAANILVGENLVCKVADFGIARLI 420
QY 415 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYFGMNNREV 474
DB 421 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYFGMNNREV 480
QY 475 LDQVERGYMPCPECPESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYQPG 534
DB 481 LDQVERGYMPCPECPESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYQPG 540
QY 535 NL 536
DB 541 NL 542

RESULT 2
A43610
protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse
N:Alternate names: Rouse sarcoma oncogene
C:Species: Mus musculus (house mouse)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C:Accession: A43610
R:Marines, R.; Mathey-Prevot, B.; Bernard, A.; Baltimore, D.
Science 237, 411-415, 1987
A:Title: Neuronal p60(c-src) contains a six-amino acid insertion relative to its non-mu
A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610
A:Molecule type: mRNA
A:Residue: 1-541
A:Cross-references: UNIPROT:P05480; UNIPARC:UPI0000161D19; GB:M17011; NID:9201056; PIDN.f
C:Comment: The neuronal c-src has an 6 residue insertion of RLNVNR within the amino-termi
C:Genetics:
A:Gene: Src
A:Cross-references: MGI:98397
A:Map position: 2:91.0
C:Superfamily: Tyrosine-protein kinase, proto-oncogene src type; protein kinase homology;
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pld
F:156-253/Domain: SH3 homology <SH3>
F:156-253/Domain: SH2 homology <SH2>
F:273-531/Domain: protein kinase homology <KIN>
F:281-289/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:303/Active site: Lys #status predicted
F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 98.0%; Score 2778.5; DB 1; Length 541;
Best Local Similarity 97.6%; Pred. No. 8,7e-130;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 59
QY 61 PKLFGFNSDVTSPQAGPLAGVTTFVALYDYSRRTETDLSFKKGERLQIVNNT--- 117
DB 60 PKLFGFNSDVTSPQAGPLAGVTTFVALYDYSRRTETDLSFKKGERLQIVNNTKRV 119
QY 118 ---EGDWMHLAHSLSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLLNAENPRGT 174
DB 120 DVREGWMLAHSLSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLLNAENPRGT 179
QY 175 FLVRESETTKGAYCLSVSDPDNAKGLNVKIKRLDSCGFYITSTRQFNSLQQLVAYYS 234
DB 180 FLVRESETTKGAYCLSVSDPDNAKGLNVKIKRLDSCGFYITSTRQFNSLQQLVAYYS 239
QY 235 KHAADGCHRLTTCPTSPKQTOGLADAMEIPRESRLRLEVKLGCGCGFVWGMGTTR 294
DB 240 KHAADGCHRLTTCPTSPKQTOGLADAMEIPRESRLRLEVKLGCGCGFVWGMGTTR 299
QY 295 VALKTLKPGTMSPEALQEAQVWKLRHEKLVQLYAVSEBPIYITERYMKSGLDPLK 354
DB 300 VALKTLKPGTMSPEALQEAQVWKLRHEKLVQLYAVSEBPIYITERYMKSGLDPLK 359
QY 355 GETGKTLRLPOLVDMAAQLASGMAVYERNNYVRDLRAANILVGENLVCKVADFGIARLI 414
DB 360 GETGKTLRLPOLVDMAAQLASGMAVYERNNYVRDLRAANILVGENLVCKVADFGIARLI 419
QY 415 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYFGMNNREV 474
DB 420 EDNEYTARQAGAPFIMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYFGMNNREV 479
QY 475 LDQVERGYMPCPECPESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYQPG 534
DB 480 LDQVERGYMPCPECPESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYQPG 539
QY 535 NL 536
DB 540 NL 541

RESULT 3
TVCHS
protein-tyrosine kinase (BC 2.7.1.112) src - chicken
N:Alternate names: kinase-related transforming protein src
C:Species: Gallus gallus (chicken)
C>Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: A00630; I50217; A41256; C35650; A32432
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983


```
QY 181 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 240
Db 178 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 237
QY 241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 300
Db 238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 297
QY 301 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
Db 298 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 357
QY 361 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRANILVGENLVCKVADFGLARLIENDEYT 420
Db 358 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRANILVGENLVCKVADFGLARLIENDEYT 417
QY 421 AROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDOVER 480
Db 418 AROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDOVER 477
QY 481 GYRMPCPECPESLHDLMCQCKRKEBERPTEYLOAFLEDYFTSTEP 528
Db 478 GYRMPCPECPESLHDLMCQCKRKEBERPTEYLOAFLEDYFTSTEP 525
```

RESULT 5

```
TVEVS1
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
C/Species: avian sarcoma virus S1
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: A25375
R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A/Title: Activation of the cellular src gene by transducing retrovirus.
A/Reference number: A25375; PMID:87064539; PMID:3097513
A/Accession: A25375
A/Molecule type: DNA
A/Residues: 1-568 <IK>
A/Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25
C/Genetics:
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd
F/88-137/Domain: SH3 homology <SH3>
F/148-245/Domain: SH2 homology <SH2>
F/265-523/Domain: protein kinase homology <KIN>
F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: Lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
```

```
Query Match 92.3%; Score 2614.5; DB 1; Length 568;
Best Local Similarity 93.8%; Pred. No. 1.1e-121;
Matches 495; Conservative 12; Mismatches 18; Indels 3; Gaps 1;
QY 1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 60
Db 1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 57
QY 61 PKLFGFNSSDPTVTSPOKAGPLAGVTTFFVALYDYESRRETDLSPFKGERLQIVNTEGD 120
Db 58 PKLFGFNSSDPTVTSPOKAGPLAGVTTFFVALYDYESRRETDLSPFKGERLQIVNTEGD 117
QY 121 NWLAHSLSTGQTGYIPSNVAPSDSIQAEEMWYFGKITRRESRLLLNAPENPGTFPVRES 180
Db 118 NWLAHSLSTGQTGYIPSNVAPSDSIQAEEMWYFGKITRRESRLLLNAPENPGTFPVRES 177
QY 181 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 240
Db 178 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 237
QY 241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 300
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Db 238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 297
QY 301 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
Db 298 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 357
QY 361 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRANILVGENLVCKVADFGLARLIENDEYT 420
Db 358 LRLPOLVDMAAOIASGMAVVERMNYVHRDLRANILVGENLVCKVADFGLARLIENDEYT 417
QY 421 AROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDOVER 480
Db 418 AROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVLDOVER 477
QY 481 GYRMPCPECPESLHDLMCQCKRKEBERPTEYLOAFLEDYFTSTEP 528
Db 478 GYRMPCPECPESLHDLMCQCKRKEBERPTEYLOAFLEDYFTSTEP 525
```

RESULT 6

```
TVEVS2
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
C/Species: avian sarcoma virus S2
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: B25375
R/Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A/Title: Activation of the cellular src gene by transducing retrovirus.
A/Reference number: A25375; PMID:87064539; PMID:3097513
A/Accession: B25375
A/Molecule type: DNA
A/Residues: 1-557 <IK>
A/Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26
C/Genetics:
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F/88-137/Domain: SH3 homology <SH3>
F/148-245/Domain: SH2 homology <SH2>
F/265-523/Domain: protein kinase homology <KIN>
F/273-281/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/295/Active site: Lys #status predicted
F/416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
```

```
Query Match 91.7%; Score 2599.5; DB 1; Length 557;
Best Local Similarity 89.7%; Pred. No. 5.7e-121;
Matches 496; Conservative 14; Mismatches 22; Indels 21; Gaps 2;
QY 1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 60
Db 1 MGSNSKRPDASORRRSLPEAEVNHGAGGAPPASQTPSKPASADGHRGSAFAFAAAE 57
QY 61 PKLFGFNSSDPTVTSPOKAGPLAGVTTFFVALYDYESRRETDLSPFKGERLQIVNTEGD 120
Db 58 PKLFGFNSSDPTVTSPOKAGPLAGVTTFFVALYDYESRRETDLSPFKGERLQIVNTEGD 117
QY 121 NWLAHSLSTGQTGYIPSNVAPSDSIQAEEMWYFGKITRRESRLLLNAPENPGTFPVRES 180
Db 118 NWLAHSLSTGQTGYIPSNVAPSDSIQAEEMWYFGKITRRESRLLLNAPENPGTFPVRES 177
QY 181 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 240
Db 178 ETTKGA YC LSVSPDNAGK LNVKHYKIRKLD SG FYTTSRTOFNSLQQLVAYYSKADGL 237
QY 241 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 300
Db 238 CHRLTVVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTL 297
QY 301 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
Db 298 KEGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 357
```

QY 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLRLIEDNEYT 420
Db 358 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLRLIEDNEYT 417
QY 421 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 480
Db 418 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 477
QY 481 GYRMPCEPCEPSLHDMCCMRKEPERPTEFYLAQFLQEDYF----- 523
Db 478 GYRMPCEPCEPSLHDMCCMRKDPERPFTEFYLAQFLQEDYLGILAVTPMEDKQEGPRG 537
QY 524 -TSTEPQYQGEN 535
Db 538 ETASNKQERDQED 550

RESULT 7

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 22-May-1981 #sequence revision 17-Dec-1982 #text_change 05-Oct-2004
C:Accession: A38017; A00631; S02726; A38018
R:Cernilofsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischner, E.; Goodman, R.; Nature 301, 736-738, 1983
A:Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A:Reference number: A38017; MUID:83141780; PMID:6298633
A:Accession: A38017
A:Molecule type: DNA
A:Residues: 1-526 <CZB>
A:Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J02020
R:Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A:Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A:Reference number: A00630; MUID:83155664; PMID:6299580
A:Accession: A00631
A:Molecule type: DNA
A:Residues: 1-62, 'D', '64'-95, 'T', '97'-123, 'V', '125'-300, 'N', '302'-526 <TAK>
A:Cross-references: UNIPARC:UPI0000172582
A:Experimental source: strain Schmidt-Ruppin
R:Bernier, J.V.; Dezelic, P.; Marx, M.; Calochy, G.
Nucleic Acids Res. 11, 1252, 1983
A:Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom
A:Reference number: S02726; MUID:89160256; PMID:2537953
A:Accession: S02726
A:Molecule type: DNA
A:Residues: 1-9, 'G', '11'-62, 'D', '64'-123, 'V', '125'-319, 'K', '321'-495, 'S', '497'-526 <BAR>
A:Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:961908; PIDN:CAA32012.1; PID
R:Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A:Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucle
A:Reference number: A38018; MUID:83059858; PMID:6292477
A:Accession: A38018
A:Molecule type: DNA
A:Residues: 1-15, 'C', '17'-94, 'RT', '97'-116, 'D', '118'-337, 'T', '339'-526 <TA2>
A:Cross-references: UNIPARC:UPI0000135F24; GB:X00928; NID:9210187; PIDN:AAA42565.1; PID
A:Experimental source: strain RASV441
R:Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A:Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A:Reference number: A38019; MUID:81220979; PMID:6264320
A:Contents: annotation; phosphorylation site
C:Comment: The sequence from the Schmidt-Ruppin strain is shown.
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; blocked amino end; 11popenin; myristylation; onc
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:273-281/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 88.8%; Score 2516.5; DB 1: Length 526;
Best Local Similarity 92.3%; Pred. No. 6.56-117;
Matches 479; Conservative 13; Mismatches 24; Indels 3; Gaps 1;

QY 1 MGSNKSXPCKDASQRRRLPEAENVHAGGAFPAISQTPSKRASADGHRGPAAPAAAE 60
Db 1 MGSSKSKXPCKDPSQRRRLPEPDSTH--HGFFPASQTPNKTAAPDTRTPRSFGVATE 57
QY 61 PKLFGFNSSDPTVTSPPRAGPIAGGVTFVALVYRESRTETDLSFKKGERLQIVNNTGCD 120
Db 58 PKLFGFNSSDPTVTSPPRAGLACGVTFVALVYESMISTDLSFKKGERLQIVNNTGCG 117
QY 121 WMLAHSLSGTQGYTPSNVYAPSDSIQAEWYFPGKTRRESERLLNAENRGTFVYRES 180
Db 118 WMLAHSLSGTQGYTPSNVYAPSDSIQAEWYFPGKTRRESERLLNPNRGTFLVRES 177
QY 181 ETTKGAVCLSVDFDNKAGLVKHYKIRKLDGSGFYITTSRTQFNSLQQLVAYYSKADGL 240
Db 178 ETTKGAVCLSVDFDNKAGLVKHYKIRKLDGSGFYITTSRTQFNSLQQLVAYYSKADGL 237
QY 241 CHRLTYCPNPKPQTQGLADAWERIPRESLREYKLGCGCGEYVMGTNGTTEVAIKTL 300
Db 238 CHRLTYCPNPKPQTQGLADAWERIPRESLREYKLGCGCGEYVMGTNGTTEVAIKTL 297
QY 301 KPGTMSPEAFLOEAQWKKLRHEKLVOLYAVSEEPYIYVENYKSKSLDPLKGENTKY 360
Db 298 KPGTMSPEAFLOEAQWKKLRHEKLVOLYAVSEEPYIYVENYKSKSLDPLKGEMKY 357
QY 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLRLIEDNEYT 420
Db 358 LRLPOLVDMAAQIASGMAVYERMYVHRDLAANILVGENLVCKVADPGLRLIEDNEYT 417
QY 421 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 480
Db 418 ARQAKFPFKMTAEALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLDQYER 477
QY 481 GYRMPCEPCEPSLHDMCCMRKEPERPTEFYLAQFL 519
Db 478 GYRMPCEPCEPSLHDMCCMRKDPERPFTEFYLAQFL 516

RESULT 8

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 05-Oct-2004
C:Accession: S20808; S32774
R:Bobor, J.; Rozkoc, F.; Svoboda, J.
submitted to the EMBL Data Library, May 1990
A:Description: Sequence organization of the adjacent chromosomal flanks the LTR.
A:Reference number: S20808
A:Accession: S20808
A:Molecule type: DNA
A:Residues: 1-526 <BD>
A:Cross-references: UNIPROT:Q06567; UNIPARC:UPI00001068B2; EMBL:X52822; NID:949656; PIDN
A:Experimental source: Mesocricetus auratus (golden hamster) provirus
C:Genetics:
A:Gene: src
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:295/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 88.1%; Score 2497.5; DB 2: Length 526;
Best Local Similarity 91.7%; Pred. No. 5.66-116;

[illegible]

Db 1 MGSSKSRPKDPSQRRRLSEPPDSTH---HGFPAPSQRPDETAAPADARHNRSRSGVATYE 57

Qy 61 PKLFGFNSSDVTYTPSPORAGPLAGGVTTFFVALYDSERTETDLSFKKGERLQIVNNTBGD 120

Db 58 PKLFWGFTSDVTYTPSPORAGPLAGGVTTFFVALYDSESWTETDLSFKKGERLQIVNNTBGD 117

Qy 121 MWLHSLSTGQGTGYIPBNVYAPSDSIQAEEMYPCKTIRRESERLLNAENPRGTELVRES 180

Db 118 MWLHSLSTGQGTGYIPBNVYAPSDSIQAEEMYPCKTIRRESERLLNAENPRGTELVRES 177

Qy 181 ETTKGAAYCLASVSDPDNKKGLNVRKHAKIRKLDGSGFYITSTRQFNSLQQLVAAYYSKHADGL 240

Db 178 ETAGAGACLSVSDPDNKKGRVNVYHYCKLXSGSFYITSTRQFNSLQQLVAAYYSKHADGL 237

Qy 241 CHRLTTCVPTSPKPTQGLADAWEPRESLRLEVKLGQSGFGEVMTGNNGTTRVAIKTL 300

Db 238 CHRLTTCVPTSPKPTQGLADAWEPRESLRLEVKLGQSGFGEVMTGNNGTTRVAIKTL 297

Qy 301 KPGTMSPEAPLQEQVNWKKLRHEKLVOLYAVVSEEPYIYTEVMSKSLDPLKGEHGKY 360

Db 298 KPGTMSPEAPLQEQVNWKKLRHEKLVOLYAVVSEEPYIYTEVMSKSLDPLKGEHGKY 357

Qy 361 LRLPOLVDMAAQISGAAVYERMMYVARDLRAANILVGENLVCKVADFGARLIEDNEYT 420

Db 358 LRLPOLVDMAAQISGAAVYERMMYVARDLRAANILVGENLVCKVADFGARLIEDNEYT 417

Qy 421 ARQAKGPKIKWTABEALYGRFTIKSDVMSFGILLTETTKGRVPYGVNREVLDQVER 480

Db 418 ARQAKGPKIKWTABEALYGRFTIKSDVMSFGILLTETTKGRVPYGVNREVLDQVER 477

Qy 481 GYRMPCEPCEPSLHDMCQCKRKEPERRTFELQAF 519

Db 478 AYRMPCEPCEPSLHDMCQCKRKEPERRTFELQAF 516

RESULT 10

S15582

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)

C|Species: Rous sarcoma virus

A|Variety: strain Prague A

C|Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004

C|Accession: S15582, S09665

R|Lin, Z.; Hackett, P.B.

Nucleic Acids Res. 17, 3986, 1989

A|Title: Sequence variation of the Rous sarcoma virus P1A src gene.

A|Reference number: S15582; PMID:89282411; PMID:2543959

A|Accession: S15582

A|Status: nucleic acid sequence not shown; translation not shown

A|Molecule type: DNA

A|Residues: 1-526 <LIN>

A|Cross-references: UNIPROT:O64994; UNIPROT:O92806; UNIPROT:O60567; UNIPROT:O07461; UNIPROT:O07462

A|Experimental source: strain Prague A

A|Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

A|Note: only a list of differences from sequence S09665 is given; however, the list is 1

C. Fincham, V.J.; Wyke, J.A.

C. Virol. 58, 694-699, 1986

A|Title: Localization of temperature-sensitive transformation mutations and back mutational

A|Reference number: S09665; PMID:86200422; PMID:3009882

A|Accession: S09665

A|Status: nucleic acid sequence not shown

A|Molecule type: DNA

A|Residues: 231-241, 'TH', 244-287, 'G', 289-463, 'P', 465-501, 'N', 503-526 <FIN>

A|Cross-references: UNIPARC:UPI00001755F1

C|Genetics:

A|Gene: src

C|Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type: protein kinase homology

C|Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; onc

F:148-137/Domain: SH3 homology <SH3>

F:148-245/Domain: SH2 homology <SH2>

F:1265-523/Domain: protein kinase homology <KIN>

F:1273-281/Region: protein kinase ATP-binding motif

F:12/Modified site: myristylated amino end (Gly) (19 mature form) #status predicted

F:135/Active site: lys #status predicted

F12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F1295/Active site: Lys #status predicted
F1416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 87.0%; Score 2466.5; DB 2; Length 526;
Best Local Similarity 90.6%; Pred. No. 1.9e-114;
Matches 470; Conservative 13; Mismatches 33; Indels 3; Gaps 1;

QY 1 MGSNKKPDAQGRRSLEPAENVHAGGAGAPASQTPSKRPASADGHRGSAFAFAAAE 60
DB 1 MGSNKKPDRPSPQRSHSLPPDSTH--HGFPASQTPDTPAAPDAHRNRSRFGVATB 57
QY 61 PKLFGFNSSDVTYSQORAGPLAGVTFVALYDERSRTETDLSFKKGERLQIVNTEGD 120
DB 58 PKLFGFNSSDVTYSQORAGPLAGVTFVALYDERSRTETDLSFKKGERLQIVNTEGY 117
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFVRES 180
DB 118 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFVRES 177
QY 181 ETTKGAICYSVDFDNAGKLVNHYKIRKLDGSGFYTSTRQNSLQQLVAIYSKADGL 240
DB 178 ETTKGAICYSVDFDNAGKLVNHYKIRKLDGSGFYTSTRQNSLQQLVAIYSKADGL 237
QY 241 CHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
DB 238 CHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 297
QY 301 KGTMSPEAFLOBQAVMKLRHEKLVQLYAVVSEBPIYVTEBMSKSLDPLKGETGKY 360
DB 298 KGTMSPEAFLOBQAVMKLRHEKLVQLYAVVSEBPIYVTEBMSKSLDPLKGETGKY 357
QY 361 LRLPOLVDMAAQIASMAVYERNNYVHRDLRAANILVGNLVCKVADFGLARLIEDNEYT 420
DB 358 LRLPOLVDMAAQIASMAVYERNNYVHRDLRAANILVGNLVCKVADFGLARLIEDNEYT 417
QY 421 AROGAKFPKMTAPREALVGRFTIKSDVMSFGILLTELTKGVRVPYGMVNEVLDQVER 480
DB 418 AROGAKFPKMTAPREALVGRFTIKSDVMSFGILLTELTKGVRVPYGMVNEVLDQVER 477
QY 481 GYRMPCCPSPESLHDLMOCCWKRKEBERPTEYLAFL 519
DB 478 GYRMPCCPSPESLHDLMOCCWKRKEBERPTEYLAFL 516

RESULT 13
B34104
protein-tyrosine kinase (BC 2.7.1.112) src 2 [similarity] - African clawed frog
N:Alternate names: kinase-related transforming protein (src) ; kinase-related transformin
C:Species: Xenopus laevis (African clawed frog)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C/Accession: B34104; 151563
R:Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A>Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A/Reference number: A34104; PMID:89278134; PMID:2499582
A/Accession: B34104
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-532 <STB>
A/Cross-references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g21
R:Steele, R.E. 1747-1761, 1985
Nucleic Acids Res. 13, 1747-1761, 1985
A>Title: Two divergent cellular src genes are expressed in Xenopus laevis.
A/Reference number: 151563; PMID:85215578; PMID:2987836
A/Accession: 151563
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 439-492 <ST2>
A/Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; P1DN:AAA51644.1; PID:
C/Genes: src
A/Genes: src
A/Introns: 464/1

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
P:87-136/Domain: SH2 homology <SH2>
P:147-244/Domain: SH2 homology <SH2>
F:264-522/Domain: protein kinase homology <KIN>
F:272-280/Region: protein kinase ATP-binding motif
F:/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F1294/Active site: Lys #status predicted
F1415/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 86.9%; Score 2463; DB 1; Length 532;
Best Local Similarity 87.9%; Pred. No. 2.8e-114;
Matches 471; Conservative 24; Mismatches 37; Indels 4; Gaps 3;

QY 1 MGSNKKPDAQGRRSLEPAENVHAGGAGAPASQTPSKRPASADGHRGSAFAFAAAE 60
DB 1 MGATSKKPEGGRRSLDLAAGSH-QPTSLASQTPSK--SLDSHR-PSGQPFQNCND 56
QY 61 PKLFGFNSSDVTYSQORAGPLAGVTFVALYDERSRTETDLSFKKGERLQIVNTEGD 120
DB 57 LPLFGFNSSDVTYSQORAGPLAGVTFVALYDERSRTETDLSFKKGERLQIVNTEGD 116
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFVRES 180
DB 117 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPGTFVRES 176
QY 181 ETTKGAICYSVDFDNAGKLVNHYKIRKLDGSGFYTSTRQNSLQQLVAIYSKADGL 240
DB 177 ETTKGAICYSVDFDNAGKLVNHYKIRKLDGSGFYTSTRQNSLQQLVAIYSKADGL 236
QY 241 CHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
DB 177 ETTKGAICYSVDFDNAGKLVNHYKIRKLDGSGFYTSTRQNSLQQLVAIYSKADGL 236
QY 241 CHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
DB 237 CHRLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 296
QY 301 KGTMSPEAFLOBQAVMKLRHEKLVQLYAVVSEBPIYVTEBMSKSLDPLKGETGKY 360
DB 297 KGTMSPEAFLOBQAVMKLRHEKLVQLYAVVSEBPIYVTEBMSKSLDPLKGETGKY 356
QY 361 LRLPOLVDMAAQIASMAVYERNNYVHRDLRAANILVGNLVCKVADFGLARLIEDNEYT 420
DB 357 LRLPOLVDMAAQIASMAVYERNNYVHRDLRAANILVGNLVCKVADFGLARLIEDNEYT 416
QY 421 AROGAKFPKMTAPREALVGRFTIKSDVMSFGILLTELTKGVRVPYGMVNEVLDQVER 480
DB 417 AROGAKFPKMTAPREALVGRFTIKSDVMSFGILLTELTKGVRVPYGMVNEVLDQVER 476
QY 481 GYRMPCCPSPESLHDLMOCCWKRKEBERPTEYLAFL 536
DB 477 GYRMPCCPSPESLHDLMOCCWKRKEBERPTEYLAFL 532

RESULT 14
A34104
protein-tyrosine kinase (BC 2.7.1.112) src 1 [similarity] - African clawed frog
N:Alternate names: kinase-related transforming protein (src) ; kinase-related transformin
C:Species: Xenopus laevis (African clawed frog)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 31-Dec-2004
C/Accession: A34104; 151564
R:Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A>Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A/Reference number: A34104; PMID:89278134; PMID:2499582
A/Accession: A34104
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-532 <STB>
A/Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g214
R:Steele, R.E.; Choen, R.; Rai, B.B.A.; Winokur, S.T.; Unger, T.F.
Oncogene 7, 2345-2350, 1992
A>Title: Structural organization of a src gene from xenopus laevis.
A/Reference number: 151564; PMID:93064714; PMID:1437158
A/Accession: 151564
A/Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-113 <SH2>
 A:Cross-references: UNIPARC:UPI00000FD97A, GB:M3646; NID:g214808; PIDD:AAA49963.1; PID:
 C:Genetics:
 A:Initiators: 80/1
 C:Superfamily: protein kinase homology; SH2 homology; SH3 homology
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 P:87-116/Domain: SH3 homology <SH3>
 P:147-244/Domain: SH2 homology <SH2>
 P:264-522/Domain: protein kinase homology <KIN>
 P:212-280/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:2/4/Active site: Lys #status predicted
 F:415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 86.9%; Score 2462; DB 1; Length 532;
 Best Local Similarity 87.5%; Pred. No. 3,1e-114;
 Matches 469; Conservative 25; Mismatches 38; Indels 4; Gaps 3;

Qy	1	MGSKSRPKDASQRRRLSPAEVNHGAGGAFPASQTPSKASADGHRGSAAPAAAE	60
Db	1	MGATKSRPKREGSPRSRLDIVEGSH-OPFTSLASQTPNK--SLDSHRPPAQPG-GNCD	56
Qy	61	PKEGGSNDPTVTSPPRAGPLAGVTFVALYDYESRTEITDLSFKKGERLQIVNTEGD	120
Db	57	LTPFGGINSFUTITSPQRTGFLAGGVTFVALYDYESRTEITDLSFKKGERLQIVNTEGD	116
Qy	121	WMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNANRGTFLVRES	180
Db	117	WMLARSLSSGQGYIPSNVYAPSDSIQAEWYLGKITRREARLLLSLENRGTFLVRES	176
Qy	181	ETTGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYISKADGL	240
Db	177	ETTGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYISKADGL	236
Qy	241	CHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGGGEVWGMGTNTTVAIKTL	300
Db	237	CHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGGGEVWGMGTNTTVAIKTL	296
Qy	301	KPGTMSPEAFLOEAQVWKKLHEKLVOLYAVVSEEPYIVTEYMSKSLDPLFGETGKY	360
Db	297	KPGTMSPEAFLOEAQVWKKLHEKLVOLYAVVSEEPYIVTEYMSKSLDPLFGEMGRY	356
Qy	361	LRLPOLYDMAAQISGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLIEDNEYT	420
Db	357	LRLPOLYDMAAQISGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLIEDNEYT	416
Qy	421	ARQAKPPIKWTAPAEALYGRFTIKSDVMSFGILLTETTKGRVPYPMGVAREVLDQVER	480
Db	417	ARQAKPPIKWTAPAEALYGRFTIKSDVMSFGILLTETTKGRVPYPMGVAREVLDQVER	476
Qy	481	GYRMPCEPCEPSLHDLQCCKRKEPERPTEFYLOAFLEDYFTSTEPQYQGENL	536
Db	477	GYRMPCEPCEPSLHDLQCCKRKEPERPTEFYLOAFLEDYFTSTEPQYQGENL	532

RESULT 15
 S52313
 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C:Species: Rous sarcoma virus
 C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
 C:Accession: S52313
 R:Ratovsky, A.; Yatsula, B.; Shutman, M.; Molinova, E.; Kaverina, I.; Musatkina, E.; Lee
 submitted to the EMBL Data Library, January 1995
 A:Description: Two new isoforms of v-src oncogene isolated from low and high metastatic
 A:Reference number: S52313
 A:Accession: S52313
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <TAT>
 A:Cross-references: UNIPROT:O86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:g663083; PID
 C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnd

F:108-157/Domain: SH3 homology <SH3>
 F:168-265/Domain: SH2 homology <SH2>
 F:265-543/Domain: protein kinase homology <KIN>
 F:293-301/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:315/Active site: Lys #status predicted
 F:436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 86.6%; Score 2453.5; DB 2; Length 545;
 Best Local Similarity 87.9%; Pred. No. 8.4e-114;
 Matches 474; Conservative 13; Mismatches 29; Indels 23; Gaps 3;

Qy	1	MGSKSRPKDASQRRRLSPAEVNHGAGGAFPASQTPSK-----PAS---	43
Db	1	MGSKSRPKDASQRRRLSPAEVNHGAGGAFPASQTPSKTAAPLAPRSRRRPAAGHR	57
Qy	44	---ADGHRGSAAPAAAEKLGFGNSDPTVTSPPRAGPLAGVTFVALYDYESRTE	100
Db	58	AAADPTHTRTSPRSRGTVANPEKLGFDPTSDPTVTSPPRARTLAGVTFVALYDYESWIE	117
Qy	101	TDLSFKKGERLQIVNTEGDMWMLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRE	160
Db	118	TDLSFKKGERLQIVNTEGDMWMLAHSVTTGQGYIPSNVYAPSDSIQAEWYFGKITRRE	177
Qy	161	SERLLNANRGTFLVRESFTTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSR	220
Db	178	SGRLLNANRGTFLVRESFTTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSR	237
Qy	221	TOFNSLQQLVAYYSKADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGC	280
Db	238	TOFNSLQQLVAYYSKADGLCHRLTTCPTSPKPTQGLAKDAWEIPRESLRLEVKLGCGC	297
Qy	281	FGEVWGMGTNTTVAIKTLKPGTMSPEAFLOEAQVWKKLHEKLVOLYAVVSEEPYIV	340
Db	298	FGEVWGMGTNTTVAIKTLKPGTMSPEAFLOEAQVWKKLHEKLVOLYAVVSEEPYIV	357
Qy	341	TEYMSKSLDPLFGEGKYLRLPOLYDMAAQISGMAVYERMYVHRDLPAANILVGEN	400
Db	358	TEYMSKSLDPLFGEGKYLRLPOLYDMAAQISGMAVYERMYVHRDLPAANILVGEN	417
Qy	401	LVCVADPGLARLIEDNEYTARQAKPPIKWTAPAEALYGRFTIKSDVMSFGILLTETLT	460
Db	418	LVCVADPGLARLIEDNEYTARQAKPPIKWTAPAEALYGRFTIKSDVMSFGILLTETLT	477
Qy	461	KGRVPYPMGVAREVLDQVERGYRMPCEPCEPSLHDLQCCKRKEPERPTEFYLOAF	519
Db	478	KGRVPYPMGVAREVLDQVERGYRMPCEPCEPSLHDLQCCKRKEPERPTEFYLOAF	536

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 Job time : 22.5195 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 153.616 Seconds
(without alignments)
3227.587 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSFKKASQRRSLRP.....AFLEDYFTSTREPOYQENL 536

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2829	99.8	535	1 SRC_HUMAN	P12931 homo sapien
2	2821	99.5	542	2 Q76P87_HUMAN	Q76P87 homo sapien
3	2799.5	98.8	535	2 Q80XU2_MOUSE	Q80XU2 mus musculu
4	2786.5	98.3	541	2 Q2M414_MOUSE	Q2M414 mus musculu
5	2782.5	98.2	535	2 Q3UKD6_MOUSE	Q3UKD6 mus musculu
6	2781	98.1	542	2 Q9JUI0_RAT	Q9JUI0 rattus norv
7	2773.5	97.9	540	1 SRC_MOUSE	P05480 mus musculu
8	2771	97.8	535	1 SRC_RAT	Q9WUd9 rattus norv
9	2706	95.5	532	2 Q45Q02_RAT	Q45Q02 rattus norv
10	2661.5	93.9	532	1 SRC_CHICK	P00523 gallus gall
11	2616.5	92.3	566	1 SRC_AVIS2	P15054 avian sarco
12	2609.5	92.1	567	1 SRC_AVIS1	P14084 avian sarco
13	2608.5	92.0	587	2 Q64817_PRETR	Q64817 avian sarco
14	2594.5	91.5	556	1 SRC_AVIS1	P14085 avian sarco
15	2528.5	89.2	525	1 SRC_AVISR	P00524 avian sarco
16	2528.5	89.2	525	1 SRC_RSVA	P00524 avian sarco
17	2497.5	88.1	526	2 Q60567_PRETR	Q60567 rous sarcom
18	2486.5	87.7	525	1 SRC_RSVH1	P25020 rous sarcom
19	2486	87.7	532	2 Q5MA59_XENTR	Q5MA59 xenopus tro
20	2485.5	87.7	526	2 Q64994_PRETR	Q64994 rous sarcom
21	2483.5	87.6	523	2 Q93080_PRETR	Q93080 rous sarcom
22	2482	87.6	523	2 Q85477_PRETR	Q85477 rous sarcom
23	2482	87.6	535	2 Q92957_RSVSB	Q92957 rous sarcom
24	2481.5	87.6	526	2 Q92806_PRETR	Q92806 rous sarcom
25	2480.5	87.5	525	1 SRC_RSVSE	P63185 rous sarcom
26	2476.5	87.4	525	1 SRC_RSVS	P00526 rous sarcom
27	2470.5	87.2	526	1 Q64993_RSVSR	Q64993 rous sarcom
28	2466.5	87.0	526	2 Q07461_PRETR	Q07461 rous sarcom
29	2463	86.9	532	2 Q2TAR1_XENLA	Q2TAR1 xenopus lae
30	2458	86.7	531	1 SRC2_XENLA	P13116 xenopus lae
31	2457.5	86.7	537	2 Q7ZX73_XENLA	Q7ZX73 xenopus lae

32	2454	86.6	531	1 SRC1_XENLA	P13115 xenopus lae
33	2453.5	86.6	545	2 Q86352_PRETR	Q86352 rous sarcom
34	2446.5	86.3	546	2 Q86363_PRETR	Q86363 rous sarcom
35	2413	85.1	522	1 SRC_RSVPA	P13163 rous sarcom
36	2318	81.8	534	2 Q6EMH0_BRARE	Q6EMH0 brachydantio
37	2193.5	77.4	527	2 Q91952_XIPXI	Q91952 xiphophorus
38	2137.5	75.4	537	2 Q64089_XENTR	Q64089 xenopus tro
39	2136.5	75.4	537	2 Q6PF70_XENTR	Q6PF70 xenopus lae
40	2129.5	75.1	537	2 Q49863_XENLA	Q49863 xenopus lae
41	2127.5	75.1	541	2 Q99PW1_RAT	Q99PW1 rattus norv
42	2125.5	75.0	536	1 YES_XENLA	P10936 xenopus lae
43	2123.5	74.9	541	2 Q8C762_MOUSE	Q8C762 mus musculu
44	2122	74.9	542	1 YES_HUMAN	P07947 homo sapien
45	2118.5	74.8	540	1 YES_MOUSE	Q04736 mus musculu

ALIGNMENTS

RESULT 1
ID SRC_HUMAN STANDARD; PRT; 535 AA.
AC P12931; Q86VB9; Q9H5A8;
DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-MAR-2006, entry version 79.
DE Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)
DE (C-Src) (pp60c-src).
GN Name=SRC; Synonyms=SRC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1036/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cordley V.B., Collier R.E., Connor R.E., Cordy N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffiths D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.B.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leverhna M.A., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
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RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.",
RL Nature 414:865-871(2001).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=lung, and skin.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

RA Stapleton M., Soares M.B., Bonafide M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantinci P., Prange C.C.,
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 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M.,
 RA Rutherford Y.S.N., Krzywiński M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RP MEDLINE=87257903; PubMed=3299057;
 RX Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.,
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes.",
 RT Mol. Cell. Biol. 7:1978-1983(1987).
 RN [4]
 RN NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RP MEDLINE=85213483; PubMed=2582238;
 RX Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.,
 RT "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT pp60c-src.",
 RT Mol. Cell. Biol. 5:1122-1129(1985).
 RN [5]
 RN NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RP MEDLINE=90040822; PubMed=2681803;
 RX Pyper J.M., Bolen J.B.,
 RT "Neuron-specific splicing of C-SRC RNA in human brain.",
 RT J. Neurosci. Res. 24:89-96(1989).
 RN [6]
 RN NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RP MEDLINE=85187981; PubMed=2581127;
 RX Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.,
 RT "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20.",
 RT Mol. Cell. Biol. 5:831-838(1985).
 RN [7]
 RN ALTERNATIVE SPLICING.
 RP PubMed=1691439;
 RX Pyper J.M., Bolen J.B.,
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain.",
 RT Mol. Cell. Biol. 10:2035-2040(1990).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 85-535.
 RP MEDLINE=97177105; PubMed=9024657; DOI=10.1036/365595a0;
 RX Xu W., Harrison S.C., Eck M.J.,
 RT "Three-dimensional structure of the tyrosine kinase c-Src.",
 RT Nature 385:595-602(1997).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RP MEDLINE=97117069; PubMed=9174343; DOI=10.1021/bi970019n;
 RX Charifson P.S., Shewchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pecofsky G.J., Peel W.R., Rodriguez M., Sternbach D.D.,
 RA Connel T.G.,
 RT "Peptide ligands of pp60(c-src) SH2 domains: a thermodynamic and
 RT structural study.",
 RT Biochemistry 36:6283-6293(1997).
 RN [10]
 RN STRUCTURE BY NMR OF 203-248.
 RP MEDLINE=95161382; PubMed=7532003;
 RX Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.,
 RT "Solution structure of the human pp60c-src SH2 domain complexed with a

RT phosphorylated tyrosine pentapeptide.",
 RT Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC 06NPF1.Centd3 (xeno); NDExp=3; InAct=EBI-621482, EBI-621463;
 CC 09Y6K9.IKKG; NBExp=1; InAct=EBI-621482, EBI-81279;
 CC 060749.khdbsl (xeno); NBExp=1; InAct=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=PI2931-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=PI2931-2; Sequence=VSP_012134;
 CC -1- PTM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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 DR EMBL; AI133293; CAC34523.1; -; Genomic_DNA.
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 DR EMBL; M16461; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16462; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16465; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16466; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16470; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16471; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16472; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16473; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16474; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16475; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16476; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16477; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16478; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16479; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16480; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16481; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16482; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16483; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16484; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16485; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16486; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16488; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16489; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16490; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16491; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16492; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16493; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16494; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16495; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16496; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16497; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16498; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16499; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16500; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16501; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16502; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16503; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16504; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16507; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16508; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16509; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16510; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16511; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16512; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16513; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16516; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16517; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16518; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16519; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16521; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16522; AAA60584.1; JOINED; Genomic_DNA.
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 DR EMBL; M16524; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16525; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16526; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16527; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16528; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16529; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16530; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16531; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16532; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16533; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16534; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16535; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16536; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16537; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16538; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16539; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16540; AAA60584.1; JOINED; Genomic_DNA.
 DR EMBL; M16541; AAA6058

DR PDB; 1O4G; X-ray; A=144-251.
 DR PDB; 1O4H; X-ray; A=144-251.

Query Match 99.8%; Score 2829; DB 1; Length 535;
 Best Local Similarity 100.0%; Pred. No. 1.3e-177;
 Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSNSKPKDASQRRRSLEPENVHAGGAGFPASOTPSKPSADGHRPSAAPPAAAE 61
 DB 1 GSNSKPKDASQRRRSLEPENVHAGGAGFPASOTPSKPSADGHRPSAAPPAAAE 60

QY 62 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 121
 DB 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 120

QY 122 WLAHSLSTGQTGYPSNYVAPSDSIQAEEMVFGKITRRESERLLINAEPRGTFLVRESE 181
 DB 121 WLAHSLSTGQTGYPSNYVAPSDSIQAEEMVFGKITRRESERLLINAEPRGTFLVRESE 180

QY 182 TTYGAYCLSVSDPDMAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYSKHADEL 241
 DB 181 TTYGAYCLSVSDPDMAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYSKHADEL 240

QY 242 HRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCGFGEVMMGTNGTTRVAIKTLK 301
 DB 241 HRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCGFGEVMMGTNGTTRVAIKTLK 300

QY 302 PGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDLPLKGETGKYL 361
 DB 301 PGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDLPLKGETGKYL 360

QY 362 RLPLVYMAAQIASGMAVVERMNVYHDLRAANILVGENLVCKYADFGALILIEDNETA 421
 DB 361 RLPLVYMAAQIASGMAVVERMNVYHDLRAANILVGENLVCKYADFGALILIEDNETA 420

QY 422 ROGAKPFIKMTAPPAALYGRFTIKSDVMSFGILTELTTKGRVPPGVNREVLDQVERG 481
 DB 421 ROGAKPFIKMTAPPAALYGRFTIKSDVMSFGILTELTTKGRVPPGVNREVLDQVERG 480

QY 482 YRMCPPECESLHDLMOQCRKPEBERPTEFYLAFLFEDYFTSTEPQYQGENU 536
 DB 481 YRMCPPECESLHDLMOQCRKPEBERPTEFYLAFLFEDYFTSTEPQYQGENU 535

RESULT 2
 Q76P87_HUMAN PRELIMINARY; PRT; 542 AA.
 AC Q76P87;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DE 07-FEB-2006, entry version 12.
 DT OTTHUMP0000030931.
 GN Name=SRC; ORFNames=RP5-823N20.1-006;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wallis J.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DB EMBL; AL133323; CAC10573.1; -; Genomic_DNA.
 DR HSSP; P12931; 1A09.
 DR SMK; Q76P87; 87-542.
 DR Ensembl; ENSG00000197122; Homo sapiens.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; Tyr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Kinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SEQUENCE 542 AA; 60589 MW; C12D30F8BCD5FF68 CRC64;

Query Match 99.5%; Score 2821; DB 2; Length 542;
 Best Local Similarity 98.9%; Pred. No. 4.5e-177;
 Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MGSNKSFKDASQRRRSLEPENVHAGGAGFPASOTPSKPSADGHRPSAAPPAAAE 60
 DB 1 MGSNKSFKDASQRRRSLEPENVHAGGAGFPASOTPSKPSADGHRPSAAPPAAAE 60

QY 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 117
 DB 61 KLFGGFNSSDTVSPORAGPLAGVTFVALYVESRTETDLSPFKGERLQIVNTEGDM 120

QY 118 ---EGDWLAHSLSTGQTGYPSNYVAPSDSIQAEEMVFGKITRRESERLLINAEPRGT 174
 DB 121 DVREGDWLAHSLSTGQTGYPSNYVAPSDSIQAEEMVFGKITRRESERLLINAEPRGT 180

QY 175 FLVRESSTGAYCLSVSDPDMAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYS 234
 DB 181 FLVRESSTGAYCLSVSDPDMAGLVKHYKIRKLDGSGFYITSRQPNLSIQQLVAYYS 240

QY 235 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCGFGEVMMGTNGTTR 294
 DB 241 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVKLGGCGFGEVMMGTNGTTR 300

QY 295 VAIITKLPGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDLPLK 354
 DB 301 VAIITKLPGTMSPEAFIQEAOVMKKLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDLPLK 360

QY 355 GETGKYRLPLVYMAAQIASGMAVVERMNVYHDLRAANILVGENLVCKYADFGALIL 414
 DB 361 GETGKYRLPLVYMAAQIASGMAVVERMNVYHDLRAANILVGENLVCKYADFGALIL 420

QY 415 EDNEYTA ROGAKPFIKMTAPPAALYGRFTIKSDVMSFGILTELTTKGRVPPGVNREV 474
 DB 421 EDNEYTA ROGAKPFIKMTAPPAALYGRFTIKSDVMSFGILTELTTKGRVPPGVNREV 480

QY 475 LDQVERGYRMPCEPECESLHDLMOQCRKPEBERPTEFYLAFLFEDYFTSTEPQYQGE 534
 DB 481 LDQVERGYRMPCEPECESLHDLMOQCRKPEBERPTEFYLAFLFEDYFTSTEPQYQGE 540

QY 535 NL 536
 DB 541 NL 542

RESULT 3
 Q80XU2_MOUSE

ID Q80XU2_MOUSE PRELIMINARY; PRT; 535 AA.
AC Q80XU2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Rous sarcoma oncogene, isoform 2.
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FWB/N; TISSUE=Salivary gland;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FWB/N; TISSUE=Salivary gland;
RG NIH MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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EMBL: BC039953; AAK39953.1; -; mRNA.
HSSP: P12931; 1043.
DR SMR; Q80XU2; 86-535.
DR Ensembl; ENSMUSG00000027646; Mus musculus.
DR MGI; MGI:98397; Src.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; RCA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000093; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
SQ SEQUENCE 535 AA; 59891 MW; 22CB5CBBE7A061C0 CRC64;
Query Match 98.9%; Score 2799.5; DB 2; Length 535;
Best local similarity 98.9%; Pred. No. 1,2e-175;
Matches 530; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 1 MGSNKKPVDASQRRRLSPAEVHAGAGGAPASQPSKIPASADGHRPSAFAPAALAE 60
DB 1 MGSNKKSPDASQRRRLSPAEVHAGAGGAPASQPSKIPASADGHRPSAFAVPPAAE 59
QY 61 PKLFGFNSDPYTSQRRAGPLAGVTTVALYDYSSRTETDISFFKGRRLQVNNTEGD 120
DB 60 PKLFGFNSDPYTSQRRAGPLAGVTTVALYDYSSRTETDISFFKGRRLQVNNTEGD 119
QY 121 WMLAHLSTGQTYISNVAAPSDSIQAEWYFGKITRRESERLLANENPRTPLVRBS 180
DB 120 WMLAHLSTGQTYISNVAAPSDSIQAEWYFGKITRRESERLLANENPRTPLVRBS 179
QY 181 ETTKGAAYCLSVSDPDNAKGLNVHYKIRKLDGSGFYITSRTPNSIQQLVAYYSKADGL 240
DB 180 ETTKGAAYCLSVSDPDNAKGLNVHYKIRKLDGSGFYITSRTPNSIQQLVAYYSKADGL 239
QY 241 CHRLTVCPSPKQQTQGLAKDAWEIPRESLRLEVLKGGCFEGVMWNTGTTTRVAIKTL 300
DB 240 CHRLTVCPSPKQQTQGLAKDAWEIPRESLRLEVLKGGCFEGVMWNTGTTTRVAIKTL 299
QY 301 KPGTMSPEAFLOBAQYMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGTGKY 360
DB 300 KPGTMSPEAFLOBAQYMKLRHEKLVQLYAVVSEBPIYVTEYMSKSLDPLKGTGKY 359
QY 361 LRLPOLVDMAAQIAGSMAYVERNNYVRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 360 LRLPOLVDMAAQIAGSMAYVERNNYVRDLRAANILVGENLVCKVADFGIARLIEDNEYT 419
QY 421 ARQGAFFPKWPAPEALYGRFTISDVMSRGLITELTTKRVPRPGVNVNEVDQVER 480
DB 420 ARQGAFFPKWPAPEALYGRFTISDVMSRGLITELTTKRVPRPGVNVNEVDQVER 479
QY 481 GYRMPCEPCPSLHLMCCWRKEPEERPTFEYLOAFLEDFYSTEPOQRENL 536
DB 480 GYRMPCEPCPSLHLMCCWRKEPEERPTFEYLOAFLEDFYSTEPOQRENL 535
RESULT 4
Q2M4I4_MOUSE PRELIMINARY; PRT; 541 AA.
AC Q2M4I4;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DE "Characterization of quantitative trait loci influencing growth and
adiposity using congenic mouse strains.";
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CAST/EiJ; TISSUE=Brain;
RA Farber C.R., Corva P.M., Medrano J.F.,
RT "Characterization of quantitative trait loci influencing growth and
adiposity using congenic mouse strains.";
RT Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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EMBL: AY902331; AAX90616.1; -; Genomic DNA.

SQ SEQUENCE 541 AA; 60645 MM; 0534AF027783BCFC CRC64;
 Query Match 98.3%; Score 2786.5; DB 2; Length 541;
 Best Local Similarity 97.8%; Pred. No. 8.5e-175;
 Matches 530; Conservative 3; Mismatches 2; Indels 7; Gaps 2;
 QY 1 MGSNKSXPKDASORRSLSEPAENYHAGAGGAPASQTSKSPASADGHRGSPAAPAAAE 60
 DB 1 MGSNKSXPKDASORRSLSEPAENYHAGAGGAPASQTSKSPASADGHRGSPAAPAAAE 59
 QY 61 PKLFGFNSDPTVTSPOBAPLAGGVTFVALVYESTETDLSFKKGERLQIVNNT--- 117
 DB 60 PKLFGFNSDPTVTSPOBAPLAGGVTFVALVYESTETDLSFKKGERLQIVNNTKV 119
 QY 118 ---BGDWMLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 174
 DB 120 DVREGDWMLAHSLSTGQTGYIPSNVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 179
 QY 175 FLVRESSTKAYCYCLSVDFPNAGLVNKHVKIRKLDGSGFYITSRTGFNSLQOLVAYYS 234
 DB 180 FLVRESSTKAYCYCLSVDFPNAGLVNKHVKIRKLDGSGFYITSRTGFNSLQOLVAYYS 239
 QY 235 KHAAGLCRLTTVCPPTSQPTQGLAKDAMEIPRESLRLEVKLGCGCFGEVMWGTVNGTTR 294
 DB 240 KHAAGLCRLTTVCPPTSQPTQGLAKDAMEIPRESLRLEVKLGCGCFGEVMWGTVNGTTR 299
 QY 295 VAITLKPGTNSPEAFIQEAOVMKKLRHEKLVOLVAVVSEPIYIVTEYMSKSLDLFLK 354
 DB 300 VAITLKPGTNSPEAFIQEAOVMKKLRHEKLVOLVAVVSEPIYIVTEYMSKSLDLFLK 359
 QY 355 GGTGKTYRLPOLVMAAOIASGMAVYEMNVYHDLRAANLNGNLVCKYADRLALIL 414
 DB 360 GGTGKTYRLPOLVMAAOIASGMAVYEMNVYHDLRAANLNGNLVCKYADRLALIL 419
 QY 415 EDNEYTARQAKFPKMTAPBAALYGRFTIKSDVNSFGILLTELTTKGRVYPPGVNREV 474
 DB 420 EDNEYTARQAKFPKMTAPBAALYGRFTIKSDVNSFGILLTELTTKGRVYPPGVNREV 479
 QY 475 LDQYRGYRMPCEPCPSLHDLMCQCRKKEPERPTEYLAQFLDEYFTSTEPYQDGE 534
 DB 480 LDQYRGYRMPCEPCPSLHDLMCQCRKKEPERPTEYLAQFLDEYFTSTEPYQDGE 539
 QY 535 NL 536
 DB 540 NL 541
 RESULT 5
 Q3UKD6_MOUSE PRELIMINARY; PRT; 535 AA.
 AC Q3UKD6;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 12 days pregnant adult female placenta cDNA, RIKEN full-length
 DE enriched library, clone:15302f701 product:Rous sarcoma oncogene, full
 DE insert sequence.
 GN Mus musculus (Mouse).
 GN Name=Src;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RP STRAIN=C57BL/6J; TISSUE=Placenta;

RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kaaukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Kavaei T., Lenhard B., Wells C., Kodaira S., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilmshurst L.G., Aldred S., Allen J.E.,
 RA Amesni-Imbimbato A., Apweiler R., Attalaya R.N., Bailey T.L.,
 RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner M.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guetlich S., Harbers M., Hayashi Y., Henich T.K., Hirokawa N.,
 RA Hill D., Hummelbeck L., Jacome M., Ikeyama A., Iwata T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakanchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tamoczka K., Tan S.L., Tang S.J., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Walsted C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukushima S., Kanamori-Katayama M., Suzuki M., Aoki Y., Araiawa T.,
 RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawaishima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kaaukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saeto R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Batdelti I.R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Girimond S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konoigaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Marchionni L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petosa G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed J.F., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walsted C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmshurst L.G., Wymshurst-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hasehizume W., Imotani K., Ishii Y., Itoh M., Kageawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Ysuntoshi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Maehiro T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barab G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein W.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai J., Kohzuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsumi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Maruoka S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RA Arakawa T., Carninci P., Fukuda S., Hasehizume W., Hayashida K.,
 RA Hori F., Iida Y., Imanura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno H., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.,
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL, AK146056; BAE26665.1; -; mRNA.
 DR MGI, MGI:98397; SFC.
 DR GO, GO:0005515; F:protein binding; IPI.
 DR GO, GO:0004674; F:protein serine/threonine kinase activity; RCA.

DR GO:0004713; F:protein-tyrosine kinase activity; IMP.
 DR GO:0006468; F:protein amino acid phosphorylation; IDA.
 DR InterPro, IPR000719; Prot_kinase.
 DR InterPro, IPR002290; Ser_Thr_kinase.
 DR InterPro, IPR000980; SH2.
 DR InterPro, IPR001452; SH3.
 DR InterPro, IPR001245; Tyr_kinase.
 DR InterPro, IPR008266; Tyr_kinase_AS.
 DR Pfam, PF07714; Kinase_Tyr; 1.
 DR Pfam, PF00017; SH2; 1.
 DR Pfam, PF00018; SH3; 1.
 DR PRINTS, PR00401; SH2DOMAIN.
 DR PRINTS, PR00452; SH3DOMAIN.
 DR PRINTS, PR00109; TYRKINASE.
 DR ProDom, PD000001; Prot_kinase; 1.
 DR ProDom, PD000093; SH2; 1.
 DR ProDom, PD000066; SH3; 1.
 DR SMART, SM00252; SH2; 1.
 DR SMART, SM00326; SH3; 1.
 DR SMART, SM00219; TyrcK; 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE, PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE, PS50001; SH2; 1.
 DR PROSITE, PS50002; SH3; 1.
 SQ SEQUENCE 535 AA; 59995 MW; 0E56EA36892D9715 CRC64;

Query Match 98.2%; Score 2782.5; DB 2; Length 535;
 Best Local Similarity 98.3%; Pred. No. 1,5e-174;
 Matches 527; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 MGSNKKPDASGRSRSLPAENVHAGGAPASQTPSKPASADHRPSAFAFAAAE 60
 DB 1 MGSNKKPDASGRSRSLPAENVHAGGAPASQTPSKPASADHRPSAFAFAAAE 59
 QY PKLFGFNSDPTVTSQPARPLAGVTVTFVALYDYSRTETDLSFKGSRLOIVNTEGD 120
 DB PKLFGFNLDTVTSQPARPLAGVTVTFVALYDYSRTETDLSFKGSRLOIVNTEGD 119
 QY 121 WMLAHSLSGQGYIPSNVVA9SDSIQAEWYFGKTRRESRLINAEENPGTFPVRES 180
 DB 120 WMLAHSLSGQGYIPSNVVA9SDSIQAEWYFGKTRRESRLINAEENPGTFPVRES 179
 QY 181 ETTKAGYCVSPDPAKGLNVHYKRLDSGGFYTSRTQPNLSLOQLVAAYSKADGL 240
 DB 180 ETTKAGYCVSPDPAKGLNVHYKRLDSGGFYTSRTQPNLSLOQLVAAYSKADGL 239
 QY 241 CHRLTVCTPSKPTOTGLAKDAMEIPRESLRLEVLKGGCFGEVVMGTWNGTTRVAIKTL 300
 DB 240 CHRLTVCTPSKPTOTGLAKDAMEIPRESLRLEVLKGGCFGEVVMGTWNGTTRVAIKTL 299
 QY 301 KGTGSPFAFLDPAQVMKRLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGTGKY 360
 DB 300 KGTGSPFAFLDPAQVMKRLRHEKLVQLYAVVSEBPIYIVTEYMSKSLDPLKGTGKY 359
 QY 361 LRLPOLVMAAQTASMAVVERMYVHRDLRAANLVGNLVCCKADPGLARLBENXT 420
 DB 360 LRLPOLVMAAQTASMAVVERMYVHRDLRAANLVGNLVCCKADPGLARLBENXT 419
 QY 421 AROGAKFPKMTAPENALYGRFTIKSDVMSFGILITELTKGRVDPYPCGVNREVLDOVER 480
 DB 420 AROGAKFPKMTAPENALYGRFTIKSDVMSFGILITELTKGRVDPYPCGVNREVLDOVER 479
 QY 481 GYRMPCCPSPSLDLMQCCKRKEPERPTEYIQAFLIEDYFTSTEPQYQGENL 536
 DB 480 GYRMPCCPSPSLDLMQCCKRKEPERPTEYIQAFLIEDYFTSTEPQYQGENL 535
 RESULT 6
 Q9JUI0 RAT PRELIMINARY; PRT; 542 AA.
 AC Q9JUI0;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE Neuronal C-Src tyrosine-specific protein kinase.
 GN Name=Src;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21148003; PubMed=11249956; DOI=10.1016/S0028-3908(00)00185-4;
 RA Linden A., Stortvik M., Lakso M., Haapasalo A., Lee D., Wilkin J.M.,
 RA Sei Y., Caestre E., Wong G.,
 RT "Increased expression of neuronal Src and tyrosine phosphorylation of
 RT NMDA receptors in rat brain after systemic treatment with MK-801."
 RL Neuropharmacology 40:469-481(2001).
 CC [2]
 CC NUCLEOTIDE SEQUENCE.
 RA Linden A.-M., Stortvik M., Lakso M., Wong G., Caestre E.;
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
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 CC
 CC EMBL, AF157016; AAF80335.1; -, mRNA.
 DR HSSP; P12931; 1043.
 DR SMR; Q9J710; 87-542.
 DR Ensembl; ENSRNOG0000009495; Rattus norvegicus.
 DR RGD; 620795; Src.
 DR GO; GO:0016301; P-kinase activity; TAS.
 DR GO; GO:0004713; P-protein-tyrosine kinase activity; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001452; SH2.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Knaae.
 SQ SEQUENCE 542 AA; 60727 MW; 6AC21D6D66B0B39 CRC64;
 Query Match 98.1%; Score 2781; DB 2; Length 542;
 Best Local Similarity 97.8%; Pred. No. 2e-174;
 Matches 531; Conservative 3; Mismatches 1; Indels 8; Gaps 3;

174 TFLVRESEETTKGAYCLSVSPFDNAKGLNWKYKTRKLDSCGFYTSRTQFNSLQOLVAVY 233
 DB TFLVRESEETTKGAYCLSVSPFDNAKGLNWKYKTRKLDSCGFYTSRTQFNSLQOLVAVY 239
 QY SKHADGCHRLTYTCPTSPKPTQGLADAMEIPRESIRLEVKLGQCGFGEVMTGNGTT 293
 DB SKHADGCHRLTYTCPTSPKPTQGLADAMEIPRESIRLEVKLGQCGFGEVMTGNGTT 299
 QY 294 RVAIKTLKPGTMSPEALFQEAQVMKLRHEKLVQLVAVVSEEPYIYVTEYMSKSLDPL 353
 DB RVAIKTLKPGTMSPEALFQEAQVMKLRHEKLVQLVAVVSEEPYIYVTEYMSKSLDPL 359
 QY 354 KGEFGKTLRLPOLYDMAAQTASGMAVYERMMYVRRDLRAANIIVGENLVCKVADPGRL 413
 DB KGEFGKTLRLPOLYDMAAQTASGMAVYERMMYVRRDLRAANIIVGENLVCKVADPGRL 419
 QY 414 IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSPDMSFGILLTELTKGRVPGMVNRE 473
 DB IEDNEYTAROGAKPPIKMTAPEALYGRFTIKSPDMSFGILLTELTKGRVPGMVNRE 479
 QY 474 VLDOVERGYRMPCEPCEPSLHDMCQWKEPBERPTFEXLQAFLEDYFTSTEPQYQPG 533
 DB VLDOVERGYRMPCEPCEPSLHDMCQWKEPBERPTFEXLQAFLEDYFTSTEPQYQPG 539
 QY 534 ENL 536
 DB 540 ENL 542

RESULT 7
 SRC_MOUSE
 ID SRC_MOUSE STANDARD; PRT; 540 AA.
 AC P05480;
 DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-MAR-2006, entry version 65.
 DE Neuronal proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112)
 DE (p60-Src) (C-Src) (pp60c-src).
 DE Name=Src;
 GN Name=Src;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC STRAHLN-BALB/c;
 RX MEDLINE=67263406; PubMed=2440106;
 RA Martinez R., Machey-Prevot B., Bernards A., Baltimore D.;
 RT "Neuronal p60c-src contains a six-amino acid insertion relative to
 RT its non-neuronal counterpart.";
 RL Science 237:411-415(1987).
 RN [2]
 RP INTERACTION WITH DDEF1/ASAP1.
 RX MEDLINE=99038209; PubMed=9819391;
 RA Brown M.T., Andrade J., Radhakrishna H., Donaldson J.G., Cooper J.A.,
 RA Radazzo P.A.;
 RT "ASAP1, a phospholipid-dependent actin GTPase-activating protein that
 RT associates with and is phosphorylated by Src.";
 RL Mol. Cell. Biol. 18:7038-7051(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with DDEF1/ASAP1 via its SH3 domain.
 CC -1- INTERACTION: Interacts with DDEF1/ASAP1 via its SH3 domain.
 CC -1- P7141:Gef1; Nbcxp-2; Inlacc=EBI-298680, EBI-777188;
 CC -1- P7M: Phosphorylated on Tyr-534 by C-Src kinase (CSK). The
 CC phosphorylated form is termed pp60c-src. The phosphorylated tail
 CC interacts with the SH2 domain thereby repressing kinase activity
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.

CC	-1	SIMILARITY: Contains 1 SH3 domain.	CC
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	
CC	Distributed under the Creative Commons Attribution-NonCommercial license	CC	
DR	EMBL; M17031; AAA40135.1; -; mRNA.	DR	
DR	PIR; A43610; A43610.	DR	
DR	HSSP; P12931; 1A09.	DR	
DR	SMR; P05480; 85-540.	DR	
DR	IntAct; P05480; -.	DR	
DR	Ensembl; ENSMUSG00000027646; Mus musculus.	DR	
DR	MGI; MGI:98397; Src.	DR	
DR	GO; GO:0005515; F:protein binding; IPI.	DR	
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IMP.	DR	
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IDA.	DR	
DR	InterPro; IPR00719; Prot_kinase.	DR	
DR	InterPro; IPR002290; Ser_thr_kinase.	DR	
DR	InterPro; IPR000980; SH2.	DR	
DR	InterPro; IPR001452; SH3.	DR	
DR	InterPro; IPR001245; Tyr_kinase.	DR	
DR	InterPro; IPR008266; Tyr_kinase_AS.	DR	
DR	Pfam; PF07714; Kinase_Tyr_1.	DR	
DR	Pfam; PF00017; SH2_1.	DR	
DR	Pfam; PF00018; SH3_1; 1.	DR	
DR	PRINTS; PR00401; SH2DOMAIN.	DR	
DR	PRINTS; PR00452; SH3DOMAIN.	DR	
DR	PRINTS; PR00109; TYRKINASE.	DR	
DR	ProDom; PD000001; Prot_kinase; 1.	DR	
DR	ProDom; PD000093; SH2_1.	DR	
DR	ProDom; PD000066; SH3_1.	DR	
DR	SMART; SM00252; SH2_1.	DR	
DR	SMART; SM00326; SH3_1.	DR	
DR	SMART; SM00219; TyKc; 1.	DR	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	DR	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	DR	
DR	PROSITE; PS50001; SH2_1.	DR	
DR	PROSITE; PS50002; SH3_1.	DR	
KW	ATP-binding; kinase; lipidprotein; Myristate; Nucleotide-binding;	KW	
KW	phosphorylation; proto-oncogene; SH2 domain; SH3 domain; Transferase;	KW	
KW	tyrosine-protein kinase.	KW	
FT	CHAIN	FT	
FT	INIT MET	FT	
FT	1	FT	
FT	540	FT	
FT	0	FT	
FT	0	FT	
FT	By similarity.	FT	
FT	Neuronal proto-oncogene tyrosine-protein	FT	
FT	kinase Src.	FT	
FT	/FtId=PRO_0000088142.	FT	
FT	SH3.	FT	
FT	SH2.	FT	
FT	Protein kinase.	FT	
FT	ATP (By similarity).	FT	
FT	Proton acceptor (By similarity).	FT	
FT	ATP (By similarity).	FT	
FT	ATP (By similarity).	FT	
FT	Phosphotyrosine (by autocatalysis) (By	FT	
FT	similarity).	FT	
FT	Phosphotyrosine (by CSK) (By similarity).	FT	
FT	N-myristoyl glycine (By similarity).	FT	
FT	MOD_RES	FT	
FT	534	FT	
FT	534	FT	
FT	1	FT	
FT	1	FT	
FT	SEQUENCE	FT	
FT	540 AA; 60487 MM; 424BA0EB5D752AA CRC64;	FT	
Query Match	97.9%; Score 2773.5; DB 1; Length 540;	Query Match	
Best Local Similarity	97.6%; Pred. No. 6e-174;	Best Local Similarity	
Matches 528; Conservative	3; Mismatches 3; Indels 7; Gaps 2	Matches 528; Conservative	
QY	2 GSNSKPKDASQRRSLPEAEVNHAGGAPASQSPKPSADGHRGPSAAFAPAAP	QY	61
Db	1 GSNSKPKDASQRRSLPEAEVNHAGGAPASQSPKPSADGHRGPSAAFAPAAP	Db	59
QY	62 KLFPGFNSSDTVTSQPQAGPLAGVTTFFVALYDYBSRTETDLSFKXGRLQIVNNT---	QY	117
Db	60 KLFPGFNSSDTVTSQPQAGPLAGVTTFFVALYDYBSRTETDLSFKXGRLQIVNNTRAKD	Db	119
QY	118 --BEDWMLAHSLSTGCTGYTISNVYABDSIQAEWYRGKTKRRSEKLLLAENPRGTF	QY	175
Db	120 VREDWMLAHSLSTGCTGYTISNVYABDSIQAEWYRGKTKRRSEKLLLAENPRGTF	Db	179

QY	176	LVASESTTGAACVLSDSDPNKAGLVNHYKIKRLDSCGFYTSRTQPNSLQQLVAYYSK	235
DB	180	LVBSSETTTGAACVLSVDPNKAAGLVNHYKIKRLDSCGFYTSRTQPNSLQQLVAYYSK <td>239</td>	239
QY	236	HADGLCHRLTTCPTSPKPTQGLADDAEIPRESILRLKVLKGGCCFGEVMMGTWNGTTRV <td>299</td>	299
DB	240	HADGLCHRLTTCPTSPKPTQGLADDAEIPRESILRLKVLKGGCCFGEVMMGTWNGTTRV <td>299</td>	299
QY	296	AIKTLKPGTMSPEAFLQEAQVKKLRHEKLVQLYAVNSEBPIYYVTEYMSKGSLLDFLKG <td>355</td>	355
DB	300	AIKTLKPGTMSPEAFLQEAQVKKLRHEKLVQLYAVNSEBPIYYVTEYMSKGSLLDFLKG <td>359</td>	359
QY	356	ETKRYLRLPOLVDMMAQIASGMAVYERNNVYHRDLRAANILVGENLVCKVADPEGLALIE <td>415</td>	415
DB	360	ETKRYLRLPOLVDMMAQIASGMAVYERNNVYHRDLRAANILVGENLVCKVADPEGLALIE <td>419</td>	419
QY	416	DNETYARQAGAKPKPKYTAPEALVGRFTIKSDVMSFGILLTELTKGRVPPYGVNREVL <td>475</td>	475
DB	420	DNETYARQAGAKPKPKYTAPEALVGRFTIKSDVMSFGILLTELTKGRVPPYGVNREVL <td>479</td>	479
QY	476	DOVERGYRMPCEPCESLHDMCCOMKKEPERPTFEYLQAFLEDYFTSTEPQYQGEN <td>535</td>	535
DB	480	DOVERGYRMPCEPCESLHDMCCOMKKEPERPTFEYLQAFLEDYFTSTEPQYQGEN <td>539</td>	539
QY	536	L 536 <td></td>	
DB	540	L 540 <td></td>	
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ID	SRC_RAT	STANDARD;	PRT; 535 AA.
AC	Q9WUD9;		
DT	30-MAY-2000,	Integrated into UniProtKB/Swiss-Prot.	
DT	30-MAY-2000,	sequence version 2.	
DT	07-MAR-2006,	entry version 46.	
DE	Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)		
DE	(c-Src) (p60C-Src).		
GN	Name=Src;		
DE	Rattus norvegicus (Rat).		
OS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [mRNA].		
RC	STRAIN=Sprague-Dawley; TISSUE=Testis;		
RA	Stockend J.D., Al-Khalili O., Spier B.J., Batton D.C.;		
RT	"Rattus norvegicus proto-oncogene encoding tyrosine-protein kinase		
RT	p60C-Src";		
RL	Submitted (FE8-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein		
CC	tyrosine phosphate.		
CC	-1 PTM: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The		
CC	phosphorylated form is termed p60C-Src. The phosphorylated tail		
CC	interacts with the SH2 domain thereby repressing kinase activity		
CC	(By similarity).		
CC	-1 SIMILARITY: Belongs to the Tyr protein kinase family. SRC		
CC	subfamily.		
CC	-1 SIMILARITY: Contains 1 SH2 domain.		
CC	-1 SIMILARITY: Contains 1 SH3 domain.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs license		
CC	EMBL; AF130457; AAD24180.1; -; mRNA.		
DR	HSSP; P12931; 1A09.		
DR	SMR; Q9WUD9; 86-535.		
DR	Rfam; ENSRNOC000009495; Rattus norvegicus.		
DR	RGD; 620795; Src.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR000980; SH2.		

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DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; Lipoprotein; Myricate; Nucleotide-binding;
KW Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT CHAIN 1 535
FT INIT MET 0
FT PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
FT BY SIMILARITY.
FT SRC: /FTID=PRO_0000088143.
FT DOMAIN 83 144
FT DOMAIN 150 247
FT DOMAIN 269 522
FT NP_BIND 275 283
FT ACT_SITE 388 388
FT BINDING 297 297
FT MOD_RES 419 419
FT MOD_RES 529 529
FT LIPID 1 1
FT SEQUENCE 535 AA; 59947 MW; AD083DD2357890EC CRC64;
SQ
Query Match 97.8%; Score 2771; DB 1; Length 535;
Best Local Similarity 98.3%; Pred. No. 8.7e-174;
Matches 527; Conservative 4; Mismatches 3; Indels 2; Gaps 2;
QY 2 GSNKSRPKDASQRRRSLEPANTHAGCGAPASQTSKPSADGHRGPSAAR-PAAL 60
DB 1 GSNKSRPKDASQRRRSLEPANTHAGCGAPASQTSKPSADGHRGPSAAR-PAAL 59
QY 61 PKLFGGNSSDVTSPPRAGPLAGGVTTFVALVDYESRTDLSFKKGERLQVNNTEGD 120
DB 60 PKLFGGNSSDVTSPPRAGPLAGGVTTFVALVDYESRTDLSFKKGERLQVNNTEGD 119
QY 121 WMLAHSISTQGTGYPENYVAPSDIOAEEMVFGKIRRESERLLNAENPRGFLVRES 180
DB 120 WMLAHSISTQGTGYPENYVAPSDIOAEEMVFGKIRRESERLLNAENPRGFLVRES 179
QY 181 ETTKGAACLSVSPDNAGKLVKXKTKRLDGGFYITTSRTQNSLQQLVAYSKADGL 240
DB 180 ETTKGAACLSVSPDNAGKLVKXKTKRLDGGFYITTSRTQNSLQQLVAYSKADGL 239
QY 241 CHRLTTCPTSKQTOGLADAMEIPRESLRLEVKGGGCGEYMGTMGTTRVALTKL 300
DB 240 CHRLTTCPTSKQTOGLADAMEIPRESLRLEVKGGGCGEYMGTMGTTRVALTKL 299
QY 301 KPGTMSPEARLQEAQVWKRLRHEKLVOLYAVVSEEPYIYTEVNSKSLDPLKGETGY 360
DB 300 KPGTMSPEARLQEAQVWKRLRHEKLVOLYAVVSEEPYIYTEVNSKSLDPLKGETGY 359
QY 361 LRLPOLVDMAAOIASGAAYVERMYRRDLAANILVGENVVCVADFGIARLIEDNEYT 420
DB 360 LRLPOLVDMAAOIASGAAYVERMYRRDLAANILVGENVVCVADFGIARLIEDNEYT 419
QY 421 ARGGAKEPIKMTAPEALYGRFTIKSDVWSPGILLTETLTKGRVPYGMVNRVTLDOVER 480

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DB 420 ARGGAKEPIKMTAPEALYGRFTIKSDVWSPGILLTETLTKGRVPYGMVNRVTLDOVER 479
QY 481 GYRMPCPECPESLHDMCCQWRKEPERPTEFLQAFLEBYFSTEPQVPGENTL 536
DB 480 GYRMPCPECPESLHDMCCQWRKEPERPTEFLQAFLEBYFSTEPQVPGENTL 535
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ID Q450J2_RAT PRELIMINARY; PRT; 523 AA.
AC Q450J2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Tyrosine protein kinase c-src (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHR, and WKY;
RA Jackson E.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Wistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins."
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial
CC License
DR EMBL: DQ120510; AAC23849.1; -; mRNA.
DR EMBL: DQ120509; AAC23848.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
FT NON_TER 1
FT NON_TER 523
FT SEQUENCE 523 AA; 58672 MW; 8D5D6C2644FDF2FC CRC64;
SQ
Query Match 95.5%; Score 2706; DB 2; Length 523;

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Best Local Similarity 98.3%; Pred. No. 1,6e-169;
Matches 515; Conservative 4; Mismatches 3; Indels 2; Gaps 2;

QY 7 KKKDASQRRRSLEPAENVHAGAGGAPASGTPSKSPASDCHRPASAFA-PAAAEKRLG 65
DB 1 KKKDASQRRRSLEPAENVHAGAGGAPASGTPSKSPASDCHRPASAFA-PAAAEKRLG 59
QY 66 GFNSSTVTSPOBAGPLAGVTFVALDYESTETDLSFKKGERIQIVNTGDMWLAH 125
DB 60 GFNSSTVTSPOBAGPLAGVTFVALDYESTETDLSFKKGERIQIVNTGDMWLAH 119
QY 126 SLSTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLVRESSTKG 185
DB 120 SLSTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLVRESSTKG 179
QY 186 AYCLASVSDPDNAGLVNKHKKIKLDSGCFYITSRQFNSLOOLVAYYSKADGLCHRLT 245
DB 180 AYCLASVSDPDNAGLVNKHKKIKLDSGCFYITSRQFNSLOOLVAYYSKADGLCHRLT 239
QY 246 TVCPSTKPTOTGLAKDAMEIPRESLRELVKLGQCFGEVWMTNGTTRVAIKTLKPGTM 305
DB 240 TVCPSTKPTOTGLAKDAMEIPRESLRELVKLGQCFGEVWMTNGTTRVAIKTLKPGTM 299
QY 306 SPEAFLOEAQVMKKLHHEKLVQLVAVVSEBPIYVTEYNSKSLDLKLGKGTGKYLRLPQ 365
DB 300 SPEAFLOEAQVMKKLHHEKLVQLVAVVSEBPIYVTEYNSKSLDLKLGKGTGKYLRLPQ 359
QY 366 LVDMAQIAGSMAYVERNAVYHRDLAANLVGENLVCKADGLARLIEDNYTARQA 425
DB 360 LVDMAQIAGSMAYVERNAVYHRDLAANLVGENLVCKADGLARLIEDNYTARQA 419
QY 426 KFPKMTAPBAALYGRFTIKSDVMSFGILLTETLTGKRVYPGPMVREVLDOVERGYRMP 485
DB 420 KFPKMTAPBAALYGRFTIKSDVMSFGILLTETLTGKRVYPGPMVREVLDOVERGYRMP 479
QY 486 CPPECESLHDLWCQCRKEPERPTEFYLAFLDYFTSTEPQ 529
DB 480 CPPECESLHDLWCQCRKEPERPTEFYLAFLDYFTSTEPQ 523

RESULT 10
SRC CHICK
ID _SRC CHICK STANDARD; PRT; 532 AA.
AC P00523; Q90992; Q90993; Q91343; Q91345; Q92013; Q98915;
AD 21-JUL-1986. Integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1999. Sequence version 3.
DT 07-MAR-2006. Entry version 78.
DE Proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112) (p60-Src)
DE (c-src) (pp60c-src).
GN Name=SRC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1)
RX MEDLINE=83155664; PubMed=6299580; DOI=10.1016/0092-8674(83)90073-9;
RA Takeya T., Hanafusa H.;
RT "Structure and sequence of the cellular gene homologous to the RSV src
RT gene and the mechanism for generating the transforming virus.",
RL Cell 32:881-890(1983).
RN [2]
RP ERRATUM, AND SEQUENCE REVISION TO 525.
RA Takeya T., Hanafusa H.;
RL Cell 34:319-319(1983).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RX TISSUE=pectoralis muscle; PubMed=2115117;
RA MEDLINE=90318371; PubMed=2115117;
RA Doral T., Wang L.-H.;
RT "An alternative non-tyrosine protein kinase product of the c-src gene
RT in chicken skeletal muscle.",

RL Mol. Cell. Biol. 10:4068-4079(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
RX TYR-435.
RA MEDLINE=97008971; PubMed=8856081;
RA Wejland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
RA Superti-Furga G.;
RT "The purification and characterization of the catalytic domain of Src
RT expressed in Schistosoma cercariae pome. Comparison of unphosphorylated
RT and tyrosine phosphorylated species.",
RL Eur. J. Biochem. 240:756-764(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1-6.
RX MEDLINE=83059861; PubMed=6292480;
RA Takeya T., Hanafusa H.;
RT "DNA sequence of the viral and cellular src gene of chickens. II.
RT Comparison of the src genes of two strains of Avian sarcoma virus and
RT of the cellular homolog.",
RL J. Virol. 44:12-18(1982).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
RX MEDLINE=91304409; PubMed=1712905;
RA Doral T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
RT exon and possible mechanism for the genesis of the 3' end of v-src.",
RL Mol. Cell. Biol. 11:4165-4176(1991).
RN [7]
RP ATP-BINDING SITE.
RX MEDLINE=84270751; PubMed=6431300;
RA Kamp M.P., Taylor S.S., Setton B.M.;
RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
RT dependent protein kinase have homologous ATP-binding sites.",
RL Nature 310:589-592(1984).
RN [8]
RP PHOSPHORYLATION.
RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
RA Hunter T.;
RT "Protein kinase C phosphorylates pp60src at a novel site.",
RL Cell 42:849-857(1985).
RN [9]
RP PHOSPHORYLATION SITE TYR-415.
RX MEDLINE=82082387; PubMed=6273838;
RA Smart J.E., Oppermann H., Czerwikofsky A.P., Purchio A.F.,
RA Erikson R.L., Bishop J.M.;
RT "Characterization of sites for tyrosine phosphorylation in the
RT transforming protein of Rous sarcoma virus (pp60v-src) and its normal
RT cellular homologue (pp60c-src).",
RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
RN [10]
RP PHOSPHORYLATION SITE TYR-526.
RX MEDLINE=86151652; PubMed=2420005;
RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT "Tyrosine 527 is phosphorylated in pp60c-src: implications for regulation.",
RL Science 231:1431-1434(1986).
RN [11]
RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.
RX MEDLINE=89249341; PubMed=2470512; DOI=10.1016/0092-8674(89)90791-5;
RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Waller J.L.,
RA Shalloway D.;
RT "Purified maturation promoting factor phosphorylates pp60c-src at the
RT sites phosphorylated during fibroblast mitosis.",
RL Cell 57:763-774(1989).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
RX MEDLINE=98070614; PubMed=9405157; DOI=10.1006/jmbi.1997.1426;
RA Williams J.C., Wejland A., Gonfloni S., Thompson A.,
RA Courtneidge S.A., Superti-Furga G., Wierenga R.K.;
RT "The 2.35 Å crystal structure of the inactivated form of chicken Src:
RT a dynamic molecule with multiple regulatory interactions.",
RL J. Mol. Biol. 274:757-775(1997).
RN [13]
RP STRUCTURE BY NMR OF 80-139.

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RA MEDLINE:932727385; PubMed:8504663; DOI=10.1016/0014-5793(93)81538-B;
RX Yu H., Rosen M.K., Schreiber S.L.;
RT "H and 15N assignments and secondary structure of the Src SH3
RT domain."
RL FEBS Lett. 324:87-92(1993).
CC -1- FUNCTION: Unknown.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
CC phosphorylation site is not phosphorylated. It can also be
CC activated by point mutations as well as by truncations at the C-
CC terminal end or by other mutations.
CC -1- SUBUNIT: p60c-src forms a complex with polyoma virus middle T
CC antigen.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P00523-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
CC degree of kinase activity, in certain fully differentiated cells
CC such as neurons, platelets and macrophages. Isoform 1 is widely
CC expressed. Isoform 2 is expressed only in the muscle.
CC -1- PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The
CC phosphorylated form is termed p60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: V00402; CAA23696.1; -; Genomic DNA.
DR EMBL: J00908; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL: M57290; AAA49078.1; -; mRNA.
DR EMBL: S43604; AAD13831.1; -; mRNA.
DR EMBL: S43616; AAD13835.1; -; mRNA.
DR EMBL: S43587; AAD13830.1; -; mRNA.
DR EMBL: S43609; AAD13832.1; -; mRNA.
DR EMBL: S43614; AAD13834.1; -; mRNA.
DR EMBL: S43579; AAB13953.2; -; mRNA.
DR PIR: A00630; TVCHS
DR PDB: 1P1W; X-ray; A=144-246.
DR PDB: 1P2F; X-ray; A=144-246.
DR PDB: 1NLQ; NMR; C=80-139.
DR PDB: 1NLP; NMR; C=80-139.
DR PDB: 1P13; X-ray; A/B=144-245.
DR PDB: 1PRL; NMR; C=76-139.
DR PDB: 1PRM; NMR; C=76-139.
DR PDB: 1RLQ; NMR; C=76-139.
DR PDB: 1SRL; NMR; @=76-139.
DR PDB: 1SRM; NMR; @=76-139.
DR PDB: 2PTK; X-ray; @=-.
DR Ensembl: ENSGALG00000003855; Gallus gallus.
DR LinkHub: P00523; -.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF07714; Kinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00019; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.

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ID	SRC	AVIS2	STANDARD;	PRT;	586	AA.
DR	ProdDom:	PD000001;	Prot kinase;	1.		
DR	ProdDom:	PD000093;	SH2_1.			
DR	ProdDom:	PD000066;	SH3_1.			
DR	SMART;	SM00252;	SH2_1.			
DR	SMART;	SM00326;	SH3_1.			
DR	SMART;	SM00219;	TYKc;	1.		
DR	PROSITE;	PS00107;	PROTEIN KINASE ATP;	1.		
DR	PROSITE;	PS50011;	PROTEIN KINASE DOM;	1.		
DR	PROSITE;	PS00109;	PROTEIN_KINASE_TYR;	1.		
DR	PROSITE;	PS50001;	SH2_1.			
DR	PROSITE;	PS50002;	SH3_1.			
KW	3D-structure;	Alternative splicing;	ATP-binding;	Kinase;	Lipoprotein;	
KW	Myristate;	Nucleotide-binding;	Phosphorylation;	Proto-oncogene;		
KW	SH3 domain;	SH3 domain;	Transferase;	Tyrosine-protein kinase.		
FT	INTT MET	0	0	By similarity.		
FT	CHAIN	1	532	Proto-oncogene tyrosine-protein kinase		
FT			/FTid=PRO_000088144.			
FT	DOMAIN	80	141	SH3.		
FT	DOMAIN	147	244	SH2.		
FT	DOMAIN	266	519	Protein kinase.		
FT	NP BIND	272	280	ATP (By similarity).		
FT	ACT_SITE	385	385	Proton acceptor (By similarity).		
Query Match						
Similarity 94.2%; Score 2661.5; DB 1; Length 532;						
Matches 504; Conservative 10; Mismatches 16; Indels 3; Gaps 1;						
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QY	62	KLFGGPNSSDVTVISPOBAGPIAGGVTTFFVALYDESRTEEDLSFKKGERLQIVNNTBGDW	121			
DB	58	KLFGGPNSSDVTVISPOBAGPIAGGVTTFFVALYDESRTEEDLSFKKGERLQIVNNTBGDW	117			
QY	122	WLASLSLTGQGGYIPSNVYVAPSDSIQAEEMVFGKITRRESERLLNMPNPGTELVSE	181			
DB	118	WLASLSLTGQGGYIPSNVYVAPSDSIQAEEMVFGKITRRESERLLNMPNPGTELVSE	177			
QY	182	TTKGAAYCYSVDPFNAGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAYYSKHADEL	241			
DB	178	TTKGAAYCYSVDPFNAGLNVKHYKIRKLDGSGFYITSRTOFNSLQOLVAYYSKHADEL	237			
QY	242	HRLTTVGPPTSKEPTQGLAKDAWEIPRESLRLEVLGGCCFGEVVMGTNGTTRVAIKTLK	301			
DB	238	HRLTNVGPPTSKEPTQGLAKDAWEIPRESLRLEVLGGCCFGEVVMGTNGTTRVAIKTLK	297			
QY	302	PGTMSPEAFLOEADVMKKLRHEKLVQLYAVVSEPIYIVTRYMSKGLDPLKKEFGYTL	361			
DB	298	PGTMSPEAFLOEADVMKKLRHEKLVQLYAVVSEPIYIVTRYMSKGLDPLKKEFGYTL	357			
QY	362	RLPOLVMAAIOASGMAYVERHMYVHDDLRANLIVGENLVCKYADFGLARLIDNEXYA	421			
DB	358	RLPOLVMAAIOASGMAYVERHMYVHDDLRANLIVGENLVCKYADFGLARLIDNEXYA	417			
QY	422	ROGAKFPDKTAPAPAAAYGRTIKSDVMSFGILITELTTKGRVYVPGVNVREVLDQYERG	481			
DB	418	ROGAKFPDKTAPAPAAAYGRTIKSDVMSFGILITELTTKGRVYVPGVNVREVLDQYERG	477			
QY	482	YRMCPPECPESLHDLNCCQWRKKEPERPTEFYLQAFLEDYFTSTEPQYQGENUL	536			
DB	478	YRMCPPECPESLHDLNCCQWRKKEPERPTEFYLQAFLEDYFTSTEPQYQGENUL	532			
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DT	30-AUG-2005,	sequence version 2.				
DT	07-MAR-2006,	entry version 64.				
DE	Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-					

DE Src) (v-Src) (pp60v-src).
 GN Name=V-SRC;
 OS Avian sarcoma virus (strain PR2257).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxId=11879;
 RN NUCLEOTIDE SEQUENCE (GENOMIC RNA).
 RP MEDLINE=89094972; PubMed=2463376;
 RX Geryk J., Dezelee P., Barnier J.V., Svoboda J., Nehyba J., Karakoz I.,
 RA Ryndtch A.V., Yatsula B.A., Calothy G.;
 RT "Transduction of the cellular src gene and 3' adjacent sequences in
 avian sarcoma virus PR2257.";
 RL J. Virol. 63:481-492(1989).
 CC [2]
 CC NUCLEOTIDE SEQUENCE (GENOMIC RNA).
 RA Yatsula B.A., Geryk J., Svoboda J., Ryndtch A.V., Calothy G.,
 RA Dezelee P.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 CC -! FUNCTION: This phosphoprotein, required for both the initiation
 and the maintenance of neoplastic transformation, is a protein
 kinase that catalyzes the phosphorylation of tyrosine residues in
 vitro.
 CC -! CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 tyrosine phosphate.
 CC -! PTM: The phosphorylated form is termed pp60v-src.
 CC -! SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 subfamily.
 CC -! SIMILARITY: Contains 1 SH2 domain.
 CC -! SIMILARITY: Contains 1 SH3 domain.
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
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 CC EMBL: M21526; AAA42583.1; -; Genomic RNA.
 CC EMBL: X51863; CAA36156.1; -; Genomic RNA.
 CC PIR: A30174; TVFVPR.
 CC HSSP: P00523; 2PTK.
 CC SMR: P15054; 83-524.
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 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR Pfam: PF00714; PKinase_Tyr; 1.
 DR Pfam: PF00018; SH3_1; 1.
 DR PRINTS: PR00401; SH3DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KM Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
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 FT Tyrosine-protein kinase transforming
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 FT ATP (By similarity).

FT ACT SITE 385 385 Proton acceptor (By similarity).
 FT BINDING 294 294 ATP (By similarity).
 FT MOD_RES 415 415 Phosphotyrosine (By autocatalysis) (By
 FT similarity).
 FT LIPID 1 1 N-myristoyl glycine (by host) (By
 FT similarity).
 SQ SEQUENCE 586 AA; 65670 MW; 76520EF485B5CD02 CRC64;
 Query Match 92.3%; Score 2616.5; DB 1; Length 586;
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 Matches 496; Conservative 10; Mismatches 18; Indels 3; Gaps 1;
 QY 2 GSNVSKPKDASGRRRSLPEAVNVHAGGAFAPASQTPSPASADGHRGSAAPAPAAP 61
 DB 1 GSKSKPKDPSQRRSLPEPDSTH--HGFPASQTPNKTAAADPTKTRTSRSFGVATBP 57
 QY 62 KLFGGNSDVTYSPQAPPLAGVTFVALYDYSRTTDLSPKKGERLQIVNTEGDM 121
 DB 58 KLFGGNTSDVTYSPQAPALAGVTFVALYDYSRTTDLSPKKGERLQIVNTEGDM 117
 QY 122 WLAHSLSTGQGYISNTYASBDSIOAEWYFGKTRRSERLLNAENPRGFLVRES 181
 DB 118 WLAHSLTTGQGYISNVYAPSDSIOAEWYFGKTRRSERLLNPNPRGFLVRES 177
 QY 182 TTKGAYCLSDPFDNAKGLNVKTKRKLDGSGFYTSRQNSLQQLVAYYSKADGIC 241
 DB 178 TTKGAYCLSDPFDNAKGLNVKTKRKLDGSGFYTSRQNSLQQLVAYYSKADGIC 237
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 AC P14084;
 DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DE 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-
 DE Src) (v-Src) (pp60v-src).
 GN Name=V-SRC;
 OS Avian sarcoma virus (strain S1).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
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 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87064539; PubMed=3097513;
 RX Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RA "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -! FUNCTION: This phosphoprotein, required for both the initiation
 and the maintenance of neoplastic transformation, is a protein
 kinase that catalyzes the phosphorylation of tyrosine residues in
 vitro.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed pG0v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC PIR; A25375; TYVVS1.
 CC HSP; P00523; 2PTK.
 CC SMR; P14084; 83-524.
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 DR Pfam; PF00018; SH3_1; 1.
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 DR PRINTS; PR00452; SH3DOMAIN.
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 DR SMART; SM00252; SH2; 1.
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 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 KM Tyrosine-protein kinase.
 FT INIT MET 0
 FT CHAIN 1 567
 FT By similarity.
 FT Tyrosine-protein kinase transforming
 FT protein Src.
 FT /FTid=PRO_0000088150.
 FT SH3.
 FT SH2.
 FT Protein kinase.
 FT ATP (By similarity).
 FT Proton acceptor (By similarity).
 FT ACT_SITE 385 385
 FT BINDING 294 294
 FT MOD_RES 415 415
 FT Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT N-myristoyl glycine (by host).
 FT LIPID 1 1
 FT SEQUENCE 567 AA; 63501 MW; EA4FC38195A098D CRC64;
 SQ
 Query Match 92.1%; Score 2609.5; DB 1; Length 567;
 Best Local Similarity 93.7%; Pred. No. 4e-163;
 Matches 494; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

DR 178 TTGAGVCLSVSDPDNAGLVKHKIKRLDGGFYITSRTOFSSLAQQLVAAYSKHADGLC 237
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 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 28.
 DE Protein-tyrosine kinase.
 GN Name=src;
 OS Avian sarcoma virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Alpharetrovirus; unclassified Alpharetrovirus.
 OX NCBI_TaxID=11876;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PR2257/16;
 RX MEDLINE=95016532; PubMed=7931166;
 RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
 RA Dezelle P.;
 RT "Evolution and origin of virus PR2257, a recent C-src transducing
 RT virus.";
 RL J. Gen. Virol. 75:2777-2781 (1994).
 CC -----
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 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
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 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR000980; SH2.
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 DR Pfam; PF07714; Pkinase_Tyr; 1.
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Qy 362 RLPLVMAAQAISGMAVVERMYVHDLRAANLIVGSENLCKYADFGALRLIDNEXYA 421
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Qy 422 ROGAKPFIKWTAPBALYGRFTIKSDVWSFGILLTELTTKGRVPEPGVNVREVLDOYERG 481
Db 418 ROGAKPFIKWTAPBALYGRFTIKSDVWSFGILLTELTTKGRVPEPGVNVREVLDOYERG 477
Qy 482 YRHPCPPECPESLHDLNCCCKRKEPERPTEFYLAFLDYF----- 523
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DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 72.
DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
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GN Name=v-Src;
OS Avian sarcoma virus (strain RASV1441).
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OC Alpharetrovirus; unclassified Alpharetrovirus.
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RP NUCLEOTIDE SEQUENCE (GENOMIC RNA).
RX MEDLINE=83059858; Pubmed=6292477;
RA Takeya T., Feldman R.A., Hanafusa H.;
RT "DNA sequence of the viral and cellular src gene of chickens. 1.
RT Complete nucleotide sequence of an EcoRI fragment of recovered avian
RT sarcoma virus which codes for gp37 and pp60src."
RN J. Virol. 44:1-11(1982).
RL [2]
RP PHOSPHORYLATION SITE TYR-415.
RX MEDLINE=81220979; Pubmed=6264320;
RA Neil J.C., Ghysdahl J., Vogt P.K., Smart J.E.;
RT "Homologous tyrosine phosphorylation sites in transformation-specific
RT gene products of distinct avian sarcoma viruses."
RL Nature 291:675-677(1981).
RN [3]
RP STRUCTURE BY NMR OF 84-139.
RX MEDLINE=95063992; Pubmed=7526465;
RA Peng S., Chen J.K., Yu H., Simon J.A., Scheeher S.L.;
RT "Two binding orientations for peptides to the Src SH3 domain:
RT development of a general model for SH3-ligand interactions."
RL Science 266:1241-1247(1994).
CC -1- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- PTM: The phosphorylated form is termed pp60v-src.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC

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CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
CC EMBL: K00928; AAA42565.1; -; Genomic_RNA.
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CC LinkHub; P00525; -.
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QY 242 HRLTTVCPTSKPOTOGIAXDAWEIPRESRLREYKLGCGCFGEVWMTGWTGTRVAIKTLK 301
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Job time : 155.616 secs

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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 30.7894 Seconds

(Without alignments)
1523.786 Million cell updates/sec

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
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1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep:*
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4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCTUS.COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RA.COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2834	100.0	536	1 US-07-820-011A-4	Sequence 4, Appli
2	2834	100.0	536	2 US-08-426-509A-13	Sequence 13, Appli
3	2834	100.0	536	2 US-08-232-545-13	Sequence 13, Appli
4	2834	100.0	536	2 US-09-444-711A-2	Sequence 2, Appli
5	2834	100.0	536	2 US-09-929-266-10	Sequence 10, Appli
6	2834	100.0	536	2 US-09-977-261-13	Sequence 13, Appli
7	2834	100.0	536	5 PCT-US93-00445-4	Sequence 4, Appli
8	2834	100.0	536	5 PCT-US95-05008-13	Sequence 13, Appli
9	2834	100.0	537	2 US-09-949-016-10282	Sequence 10282, A
10	2801	98.8	530	2 US-09-444-711A-4	Sequence 4, Appli
11	2663.5	94.0	533	1 US-07-820-011A-2	Sequence 2, Appli
12	2660.5	93.9	533	2 US-07-820-011A-2	Sequence 3, Appli
13	2660.5	93.9	533	5 PCT-US93-00445-2	Sequence 2, Appli
14	2123.5	74.9	543	2 US-08-426-509A-14	Sequence 14, Appli
15	2123.5	74.9	543	2 US-08-232-545-14	Sequence 14, Appli
16	2123.5	74.9	543	2 US-09-470-881-8	Sequence 8, Appli
17	2123.5	74.9	543	2 US-09-538-092-870	Sequence 870, Appli
18	2123.5	74.9	543	2 US-09-977-261-14	Sequence 14, Appli
19	2123.5	74.9	543	5 PCT-US95-05008-14	Sequence 14, Appli
20	2121.5	74.9	541	2 US-08-864-281-20	Sequence 20, Appli
21	1949	68.8	536	2 US-08-426-509A-12	Sequence 12, Appli
22	1949	68.8	536	2 US-08-232-545-12	Sequence 12, Appli
23	1949	68.8	536	2 US-09-977-261-12	Sequence 12, Appli
24	1949	68.8	536	5 PCT-US95-05008-12	Sequence 12, Appli
25	1944	68.6	532	1 US-08-594-447-1	Sequence 1, Appli
26	1944	68.6	532	1 US-08-665-647-1	Sequence 1, Appli

27	1932.5	68.2	537	2 US-08-426-509A-11	Sequence 11, Appli
28	1932.5	68.2	537	2 US-08-232-545-11	Sequence 11, Appli
29	1932.5	68.2	537	2 US-09-977-261-11	Sequence 11, Appli
30	1932.5	68.2	537	5 PCT-US95-05008-11	Sequence 11, Appli
31	1932	68.2	536	2 US-09-538-092-859	Sequence 859, App
32	1924.5	67.9	537	2 US-09-771-161A-212	Sequence 212, App
33	1924.5	67.9	537	2 US-09-771-161A-213	Sequence 213, App
34	1856	65.5	529	2 US-08-426-509A-15	Sequence 15, Appli
35	1856	65.5	529	2 US-08-232-545-15	Sequence 15, Appli
36	1856	65.5	529	2 US-09-538-092-885	Sequence 885, App
37	1856	65.5	529	2 US-09-977-261-15	Sequence 15, Appli
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41	1528.5	53.9	505	2 US-08-426-509A-17	Sequence 17, Appli
42	1528.5	53.9	505	2 US-08-232-545-17	Sequence 17, Appli
43	1528.5	53.9	505	2 US-09-977-261-17	Sequence 17, Appli
44	1528.5	53.9	505	5 PCT-US95-05008-17	Sequence 17, Appli
45	1464	51.7	508	2 US-09-862-154-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-820-011A-4
Sequence 4, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.

AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: pp60c-src
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

Query Match 100.0%; Score 2834; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 KEGTMSPEAFLOBAQVMKLRHEKLVQLYAVVSEEPITYETEMSGSLDPLKGETGKY 360
361 LRLPOLVDMAAOASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLIENEXT 420
361 LRLPOLVDMAAOASGMAYVERMYVHRDLRAANILVGENLVCKVADFGLARLIENEXT 420
421 ABOGAFPIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYPGWNRREVLDOVER 480
421 ABOGAFPIKMTAPEALYGRFTIKSDVWSFGILLTELTTKGRVPYPGWNRREVLDOVER 480
481 GYRMPCEPCPSLHLMLCCQCKEPEERPTFEYLOAFLEDYTSSTBPOYQPEENT 536
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RESULT 2
US-08-426-509A-13
Sequence 13, Application US/08426509A
Patent No. 6326469

GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gilelsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 536 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: No. 6326469e

US-08-426-509A-13

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 WMLAHSLSGTQGYIPSNVVA PSDSIOAEEMVFGKITRRESRLLNAMENPGTFLYRES 180
121 WMLAHSLSGTQGYIPSNVVA PSDSIOAEEMVFGKITRRESRLLNAMENPGTFLYRES 180
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Db 301 KPGTMSBEALFQEQVWKLRHEKLVOLYAVVSEEPITYIVTEVMSKSLDPLGEGTCKY 360
Qy 361 LRLPQLVDMAAQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
Db 361 LRLPQLVDMAAQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
Qy 421 ARQAKKPKIKWTAEALYGRFTIKSDVWSFGILLTELTTKGRVPYFGMVNREVLDOVER 480
Db 421 ARQAKKPKIKWTAEALYGRFTIKSDVWSFGILLTELTTKGRVPYFGMVNREVLDOVER 480
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Db 481 GYRMPCEPCEPSLHDMCCMRKPEBERPTEFYLOAFLEDFYFSTEPQYQGENL 536

RESULT 3

US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Axel
; APPLICANT: Gishizaky, Mikhail
; APPLICANT: Sures, Iman G.
; TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-232-545-13

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGSNKSXPXKASQRRSLRPAENVHAGGAFPAASQTPSKRPAADGHRGSPAAAPAAAE 60
Qy 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIYNNTEGD 120
Db 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIYNNTEGD 120
Qy 121 WMLAHSISTGOTGIIIPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFVRES 180

|||||
Db 121 WMLAHSISTGOTGIIIPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFVRES 180
Qy 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGFTYTSRTQFNSLOQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGFTYTSRTQFNSLOQLVAYYSKADGL 240
Qy 241 CHRLTYCPSKPTQGLADAMEIPRESLRLEVKLGCGCGEVMGWNQTTVAIKTL 300
Db 241 CHRLTYCPSKPTQGLADAMEIPRESLRLEVKLGCGCGEVMGWNQTTVAIKTL 300
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Db 301 KPGTMSBEALFQEQVWKLRHEKLVOLYAVVSEEPITYIVTEVMSKSLDPLGEGTCKY 360
Qy 361 LRLPQLVDMAAQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
Db 361 LRLPQLVDMAAQIASGMAVYERNYVHRDLRAANILVGENLVCKVADFGRLIEDNEYT 420
Qy 421 ARQAKKPKIKWTAEALYGRFTIKSDVWSFGILLTELTTKGRVPYFGMVNREVLDOVER 480
Db 421 ARQAKKPKIKWTAEALYGRFTIKSDVWSFGILLTELTTKGRVPYFGMVNREVLDOVER 480
Qy 481 GYRMPCEPCEPSLHDMCCMRKPEBERPTEFYLOAFLEDFYFSTEPQYQGENL 536
Db 481 GYRMPCEPCEPSLHDMCCMRKPEBERPTEFYLOAFLEDFYFSTEPQYQGENL 536

RESULT 4

US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764833
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Irdy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-7136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-09-444-711A-2

Query Match 100.0%; Score 2834; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSNKSXPXKASQRRSLRPAENVHAGGAFPAASQTPSKRPAADGHRGSPAAAPAAAE 60
Db 1 MGSNKSXPXKASQRRSLRPAENVHAGGAFPAASQTPSKRPAADGHRGSPAAAPAAAE 60
Qy 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIYNNTEGD 120
Db 61 PKLFGFNSSDPTVTSPPRAGPLAGGVTTFVALYDYESRTEITDLSFKKGERLQIYNNTEGD 120
Qy 121 WMLAHSISTGOTGIIIPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFVRES 180
Db 121 WMLAHSISTGOTGIIIPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFVRES 180
Qy 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGFTYTSRTQFNSLOQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPDNAKGLNVKHYKIRKLDSSGFTYTSRTQFNSLOQLVAYYSKADGL 240
Qy 241 CHRLTYCPSKPTQGLADAMEIPRESLRLEVKLGCGCGEVMGWNQTTVAIKTL 300

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Db 241 |||||CHLTTVCPTSKPQTGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTGNNGTTRVAIKTL 300
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Db 301 |||||KPGTMSPEALFQEAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
Qy 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Db 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Qy 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
Db 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
Qy 481 |||||GYMPCPEPCPSLHDMCCWKKEPERPTFEYLQAFLEDYFTSTREPOQPENT 536
Db 481 |||||GYMPCPEPCPSLHDMCCWKKEPERPTFEYLQAFLEDYFTSTREPOQPENT 536
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RESULT 5

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US-09-929-266-10
; Sequence 10, Application US/09929266
; Patent No. 6824981
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matthesich
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 100.0%; Score 2834; DB 2; Length 536;

Best Local Similarity 100.0%; Pred. No. 2.6e-215;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 |||||MGSNKSXPDAQSORRSLPEAENVHAGAGGAPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 |||||MGSNKSXPDAQSORRSLPEAENVHAGAGGAPASQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 |||||PKLFGGFNSSDVTYTSPOKRAPIAGVTTFPALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Db 61 |||||PKLFGGFNSSDVTYTSPOKRAPIAGVTTFPALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Qy 121 |||||WMLAHLSTGQGYIIPSNVVAAPSDSIQAEEMVFGKITTRESERLLANENPGTFIVRES 180
Db 121 |||||WMLAHLSTGQGYIIPSNVVAAPSDSIQAEEMVFGKITTRESERLLANENPGTFIVRES 180
Qy 181 |||||ETTGAAYCISVDFDPAKGLNVGHYKIRKLDGSGFYITSTRTOFNSIQOLVAIYYSKADGL 240
Db 181 |||||ETTGAAYCISVDFDPAKGLNVGHYKIRKLDGSGFYITSTRTOFNSIQOLVAIYYSKADGL 240
Qy 241 |||||CHRLTTVCPTSKPQTGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTGNNGTTRVAIKTL 300
Db 241 |||||CHRLTTVCPTSKPQTGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTGNNGTTRVAIKTL 300
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Qy 301 |||||KPGTMSPEALFQEAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
Db 301 |||||KPGTMSPEALFQEAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
Qy 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Db 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Qy 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
Db 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
Qy 481 |||||GYMPCPEPCPSLHDMCCWKKEPERPTFEYLQAFLEDYFTSTREPOQPENT 536
Db 481 |||||GYMPCPEPCPSLHDMCCWKKEPERPTFEYLQAFLEDYFTSTREPOQPENT 536
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RESULT 6

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US-09-977-261-13
; Sequence 13, Application US/09977261
; Patent No. 6908984
; GENERAL INFORMATION:
; APPLICANT: ULTRICH, AXEL
; APPLICANT: GISHIZKI, MIKHAEL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; CURRENT APPLICATION NUMBER: US/09/977,261
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/332,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 100.0%; Score 2834; DB 2; Length 536;

Best Local Similarity 100.0%; Pred. No. 2.6e-215;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 |||||MGSNKSXPDAQSORRSLPEAENVHAGAGGAPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 |||||MGSNKSXPDAQSORRSLPEAENVHAGAGGAPASQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 |||||PKLFGGFNSSDVTYTSPOKRAPIAGVTTFPALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Db 61 |||||PKLFGGFNSSDVTYTSPOKRAPIAGVTTFPALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Qy 121 |||||WMLAHLSTGQGYIIPSNVVAAPSDSIQAEEMVFGKITTRESERLLANENPGTFIVRES 180
Db 121 |||||WMLAHLSTGQGYIIPSNVVAAPSDSIQAEEMVFGKITTRESERLLANENPGTFIVRES 180
Qy 181 |||||ETTGAAYCISVDFDPAKGLNVGHYKIRKLDGSGFYITSTRTOFNSIQOLVAIYYSKADGL 240
Db 181 |||||ETTGAAYCISVDFDPAKGLNVGHYKIRKLDGSGFYITSTRTOFNSIQOLVAIYYSKADGL 240
Qy 241 |||||CHRLTTVCPTSKPQTGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTGNNGTTRVAIKTL 300
Db 241 |||||CHRLTTVCPTSKPQTGLAKDAWEIPRESLRLEVKLGQCFCFGEVWMTGNNGTTRVAIKTL 300
Qy 301 |||||KPGTMSPEALFQEAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
Db 301 |||||KPGTMSPEALFQEAQVWKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDPLKGETGKY 360
Qy 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Db 361 |||||LRLPOLVDMAAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
Qy 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
Db 421 |||||AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTETTKGRVPYPGMVNREVLDOVER 480
```

Db 421 ARGAKFPKMTAPREALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
QY 481 GYRMPCCPECEPSLHDLMOCCMKRKEPERPFTFEYLQAFLEDFYFTSTEPQYQGENL 536
Db 481 GYRMPCCPECEPSLHDLMOCCMKRKEPERPFTFEYLQAFLEDFYFTSTEPQYQGENL 536

RESULT 7
PCT-US93-00445-4
Sequence 4, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luchtinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820, 011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kund, Heinz-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.

AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kund, Heinz-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
PCT-US93-00445-4

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No.2,6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSFKPKDASQRRRLSEPAENVHAGGAFPPASQTPSKRPSADGHRGSPAAAPAAAE 60
Db 1 MGSNKSFKPKDASQRRRLSEPAENVHAGGAFPPASQTPSKRPSADGHRGSPAAAPAAAE 60
QY 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
Db 61 PKLFGFNSSDVTYSPQAGPLAGVTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTGTGYIPSNYVAPSDSIOAEWYFQKTRRESERLLNANRGTFLVRES 180
Db 121 WMLAHSLSGTGTGYIPSNYVAPSDSIOAEWYFQKTRRESERLLNANRGTFLVRES 180
QY 121 WMLAHSLSGTGTGYIPSNYVAPSDSIOAEWYFQKTRRESERLLNANRGTFLVRES 180
Db 121 WMLAHSLSGTGTGYIPSNYVAPSDSIOAEWYFQKTRRESERLLNANRGTFLVRES 180
QY 181 ETTKGAYCLSVSDPNAGKLVNRYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
Db 181 ETTKGAYCLSVSDPNAGKLVNRYKIRKLDGSGFYITSRTQFNSLQQLVAYYSKADGL 240
QY 241 CHRLTYVCPSPKPTQGLADAWKIPRESLRLEFKLDGCGCEGVMGMNCTTVAIKTL 300
Db 241 CHRLTYVCPSPKPTQGLADAWKIPRESLRLEFKLDGCGCEGVMGMNCTTVAIKTL 300
QY 241 CHRLTYVCPSPKPTQGLADAWKIPRESLRLEFKLDGCGCEGVMGMNCTTVAIKTL 300
Db 241 CHRLTYVCPSPKPTQGLADAWKIPRESLRLEFKLDGCGCEGVMGMNCTTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVWKKLRHEKLYLVAVSSEPIYIVTEVYSKSLDPLKGSTGY 360
Db 301 KPGTMSPEAFLOEAQVWKKLRHEKLYLVAVSSEPIYIVTEVYSKSLDPLKGSTGY 360
QY 301 KPGTMSPEAFLOEAQVWKKLRHEKLYLVAVSSEPIYIVTEVYSKSLDPLKGSTGY 360
Db 301 KPGTMSPEAFLOEAQVWKKLRHEKLYLVAVSSEPIYIVTEVYSKSLDPLKGSTGY 360
QY 361 LRLPOLVMAAQIASGNAVYERNYVARDLRAANILVGENLVCKVADFGLARLLIDNEYT 420
Db 361 LRLPOLVMAAQIASGNAVYERNYVARDLRAANILVGENLVCKVADFGLARLLIDNEYT 420
QY 421 ARGAKFPKMTAPREALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
Db 421 ARGAKFPKMTAPREALYGRFTIKSDVWSFGILLTELTGKRVYPYGMVNRVLDQVER 480
QY 481 GYRMPCCPECEPSLHDLMOCCMKRKEPERPFTFEYLQAFLEDFYFTSTEPQYQGENL 536
Db 481 GYRMPCCPECEPSLHDLMOCCMKRKEPERPFTFEYLQAFLEDFYFTSTEPQYQGENL 536

RESULT 8
PCT-US93-05008-13
Sequence 13, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Miesenchaffen E.V.
APPLICANT: Holzgarten Str. 2
APPLICANT: Muenchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:


```

ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match      100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPXDASGRRSLSLEPAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKKPXDASGRRSLSLEPAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDPTYSQORAGPLAGVTTFAALDYESTRTDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDPTYSQORAGPLAGVTTFAALDYESTRTDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGTGYIPSNVYAPSDSIQAEEMWFGKLTTRRESERLLNAENPRGTFLVRES 180
DB 121 WMLAHSLSGTQGTGYIPSNVYAPSDSIQAEEMWFGKLTTRRESERLLNAENPRGTFLVRES 180
QY 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYSKADGL 240
DB 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYSKADGL 240
QY 241 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 300
DB 241 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 300
QY 241 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 300
DB 241 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
DB 301 KPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIIDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIIDNEYT 420
QY 421 ARQGAPEPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPVPGMNRREVLDQVER 480
DB 421 ARQGAPEPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPVPGMNRREVLDQVER 480
QY 481 GYRMPCEPCEBSLHDLMCQWRKEPERPTFEYLQAFLEDYFTSTEPQYQPGENTL 536
DB 481 GYRMPCEPCEBSLHDLMCQWRKEPERPTFEYLQAFLEDYFTSTEPQYQPGENTL 536

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DB 481 GYRMPCEPCEBSLHDLMCQWRKEPERPTFEYLQAFLEDYFTSTEPQYQPGENTL 536
RESULT 9
US-09-949-016-10282
; Sequence 10282, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match      100.0%; Score 2834; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.6e-215;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKKPXDASGRRSLSLEPAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAE 60
DB 2 MGSNKKPXDASGRRSLSLEPAENVHAGGAGFAPASQTPSKPASADGHRGSAAPAPAAE 61
QY 61 PKLFGFNSSDPTYSQORAGPLAGVTTFAALDYESTRTDLSFKKGERLQIVNTEGD 120
DB 62 PKLFGFNSSDPTYSQORAGPLAGVTTFAALDYESTRTDLSFKKGERLQIVNTEGD 121
QY 121 WMLAHSLSGTQGTGYIPSNVYAPSDSIQAEEMWFGKLTTRRESERLLNAENPRGTFLVRES 180
DB 122 WMLAHSLSGTQGTGYIPSNVYAPSDSIQAEEMWFGKLTTRRESERLLNAENPRGTFLVRES 181
QY 181 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYSKADGL 240
DB 182 ETTKGAICYLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRTOFNSLQOLVAYYSKADGL 241
QY 241 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 300
DB 242 CHRLTTCPTSKQOTGGLAKDAWEIPRESLRLEVKLGOCGFGVWMTGNNGTTRVAIKTL 301
QY 301 KPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 360
DB 302 KPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLLDFLKGETGKY 361
QY 361 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIIDNEYT 420
DB 362 LRLPOLVDMAAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIIDNEYT 421
QY 421 ARQGAPEPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPVPGMNRREVLDQVER 480
DB 422 ARQGAPEPIKMTAPBALYGRFTIKSDVMSFGILLTELTKGVPVPGMNRREVLDQVER 481
QY 481 GYRMPCEPCEBSLHDLMCQWRKEPERPTFEYLQAFLEDYFTSTEPQYQPGENTL 536
DB 482 GYRMPCEPCEBSLHDLMCQWRKEPERPTFEYLQAFLEDYFTSTEPQYQPGENTL 537

RESULT 10
US-09-444-711A-4
; Sequence 4, Application US/09444711A

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Patent No. 6764833
GENERAL INFORMATION:
APPLICANT: Yeatman, Timothy J.
APPLICANT: Iddy, Rosalyn B.
TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
FILE REFERENCE: USF-T136
CURRENT APPLICATION NUMBER: US/09/444,711A
CURRENT FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 530
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(530)
OTHER INFORMATION: amino acid sequence of the mutant c-src polypeptide encoded
OTHER INFORMATION: by the mutant c-src coding region
US-09-444-711A-4

Query Match 98.8%; Score 2801; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPXKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
DB 1 MGSNKSXPXKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDSERTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDSERTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
DB 121 WMLAHSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
QY 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
DB 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
QY 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
DB 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
QY 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
DB 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYITVETYSKSGSLDFLKGEGKY 360
DB 301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYITVETYSKSGSLDFLKGEGKY 360
QY 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLPAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLPAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKRPIMKTAPBALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVREVLDOVER 480
DB 421 ARQAKRPIMKTAPBALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVREVLDOVER 480
QY 481 GYRMPCEPCEPSLHDLMCQMKRPEPERPTEYLQAFLEDPYFSTEPQY 530
DB 481 GYRMPCEPCEPSLHDLMCQMKRPEPERPTEYLQAFLEDPYFSTEPQY 530

RESULT 11
US-09-470-861-3
Sequence 3, Application US/09470861
Patent No. 6685938
GENERAL INFORMATION:
APPLICANT: CHERESH, David A.
APPLICANT: ELICERI, Brian
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
TITLE OF INVENTION: YES TYROSINE KINASES
FILE REFERENCE: TSRI 651.2

CURRENT APPLICATION NUMBER: US/09/470,861
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US99/11780
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,220
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 533
TYPE: PRT
ORGANISM: Chicken
US-09-470-861-3

Query Match 94.0%; Score 2663.5; DB 2; Length 533;
Best Local Similarity 94.0%; Pred. No. 7.4e-202;
Matches 504; Conservative 11; Mismatches 18; Indels 3; Gaps 1;

QY 1 MGSNKSXPXKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
DB 1 MGSNKSXPXKASQRRSLPEAENVHAGGAFPASQTPSKPASADGHRGSAAPAAAE 60
QY 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDSERTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSSDPTVTSPPRAGLAGVTTFFVALYDSERTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
DB 121 WMLAHSSTGQTGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENRGTFVRES 180
QY 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
DB 181 ETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQQLVAYYSKADGL 240
QY 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
DB 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
QY 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
DB 241 CHRLTYCPTSPKPTQGLADAMEIPRESLRLRYKLGQCGCGEYMGTMGTNITTVAIKTL 300
QY 301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYITVETYSKSGSLDFLKGEGKY 360
DB 301 KPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEEPYITVETYSKSGSLDFLKGEGKY 360
QY 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLPAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAAQIASGNAVYERNYVHRDLPAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKRPIMKTAPBALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVREVLDOVER 480
DB 421 ARQAKRPIMKTAPBALYGRFTIKSDVMSFGILLTELTTGKRVYPCGMVREVLDOVER 480
QY 481 GYRMPCEPCEPSLHDLMCQMKRPEPERPTEYLQAFLEDPYFSTEPQY 536
DB 481 GYRMPCEPCEPSLHDLMCQMKRPEPERPTEYLQAFLEDPYFSTEPQY 536

RESULT 12
US-07-820-011A-2
Sequence 2, Application US/07820011A
Patent No. 533615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasmidogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield

```

STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 254 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
TITLES: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
US-07-820-011A-2

Query Match 93.9%; Score 2660.5; DB 1; Length 533;
Best Local Similarity 93.8%; Pred. No. 1.3e-201;
Matches 503; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

Qy 1 MGSNSKPRDASQRRSLSPAENVHAGAGGAPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNSKPRDPSQRRSLSPDSTH--HGCFPASQTPNKTAAPDTHRTSRSGFTVATE 57
Qy 61 PTLFGFNSSDVYTSQRAQPLAGVTTTPALYDYSRTETDLSFKKGERLQIVNTEGD 120
Db 58 PTLFGGFNSDVTYTSQRAQALAGVTTTPALYDYSRTETDLSFKKGERLQIVNTEGD 117
Qy 121 MWLAHSLTGTGQCYISNTVVAAPSDSIQAEEMVFGKTRRESEKLLANAENPRGTPLVRES 180
Db 118 MWLAHSLTGTGQCYISNTVVAAPSDSIQAEEMVFGKTRRESEKLLANAENPRGTPLVRES 177
Qy 181 ETTKGAYCLSVSDFDNAGKLVNHYKIRKLDGSGFYITSRTQFNSLQQLVAVYSKADGL 240
Db 178 ETTKGAYCLSVSDFDNAGKLVNHYKIRKLDGSGFYITSRTQFNSLQQLVAVYSKADGL 237
Qy 241 CHRLLTVCTSKRQTOGLAKDAWEIPRESLRLEVKGGCGFGVNMGTWGTTRVAIKTL 300
Db 238 CHRLLTVCTSKRQTOGLAKDAWEIPRESLRLEVKGGCGFGVNMGTWGTTRVAIKTL 297
Qy 301 KRGTSPPAFLOBAQVKKLRHEKLVOLYAVVSEBPYIYVTEYMSKSLDPLKSGTGKY 360
Db 298 KRGTSPPAFLOBAQVKKLRHEKLVOLYAVVSEBPYIYVTEYMSKSLDPLKSGTGKY 357
Qy 361 LRLPOLVDMAAOIASGMAYVERNNYVHRLDRAANILVGENLVCKVADFGIARLIENDEYT 420
Db 358 LRLPOLVDMAAOIASGMAYVERNNYVHRLDRAANILVGENLVCKVADFGIARLIENDEYT 417

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Qy 421 ARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVLDOVER 480
Db 418 ARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVLDOVER 477
Qy 481 GYRMPCCPECSLHDMCQWRKEBERPTPEYLQAFLEDYFTSTPEYQPGENTL 536
Db 478 GYRMPCCPECSLHDMCQWRKEBERPTPEYLQAFLEDYFTSTPEYQPGENTL 533

RESULT 13
PCT-US93-00445-2
Sequence 2, Application PC/TUS9300445
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madril, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 254 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
TITLES: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-2

Query Match 93.9%; Score 2660.5; DB 5; Length 533;
Best Local Similarity 93.8%; Pred. No. 1.3e-201;
Matches 503; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

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Search completed: June 5, 2006, 17:18:20
Job time : 31.7894 secs

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COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-232-545-14

Query Match      74.9%; Score 2123.5; DB 2; Length 543;
Best Local Similarity 74.5%; Pred. No. 3.3e-159;
Matches 407; Conservative 51; Mismatches 75; Indels 13; Gaps 4;

QY      1 MGSNKSXP-KDASQRRSLRPAENVHAGG--GAPPASQTPSKPAGDGHGSPSAAPAPA 57
DB      1 MGCISKENKSPAIKRYRPENTPEPVSTSVSHYGAEPVSPCPSSSA---KGTAVNFS 57
QY      58 AAEP-----KLFGEFNSDVTSPQRAQPLAGVTFVALYDYESRTETDLSFKKGER 110
DB      58 SMTPEGGSSGVTPFGGASSSFVSPSSYPAGLTGVTIFVALYDYERATTEDELSFKKGER 117
QY      111 LOIVNNTBGDWMIAHSLSSTGQTYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAEN 170
DB      118 FOIINTBGDWMFARSIATGKNGYIPSNVYAPADSIQAEEMVFGKMGKDAERLLNPGN 177
QY      171 PRGTPLVRSSETTKGAYCLSVSPDNAKLNVGHYKIRKLDSCGFYITTSRTQNSLQOLY 230
DB      178 ORGIFLVRSSETTKGAYSLIRDMDEIRGDNVGHYKIRKLDNGGYITTRAQPDLOKLV 237
QY      231 AYSKKAADGICHRLLTVCPFSKPTQGLAKDAWEIPRESLRLLEVKLGGCGFGEVMNGTNN 290
DB      238 KHTEHADGICHLITVCPYKPTQGLAKDAWEIPRESLRLLEVKLGGCGFGEVMNGTNN 297
QY      291 GTTRVAIKTLKPGTMSPEAFLOEAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKGSLL 350
DB      298 GTTKVAIKTLKPGTMMPEAFLOEAQIMKLRHDKLVPLVAVVSEBPIYIVTEFMSKGSLL 357
QY      351 DFLKSGTGYTLRPLQVLDMAAQASGMAYVERMNYVHRDLRANILVGENLVCKVADFG 410
DB      358 DFLKSGDGYTLRPLQVLDMAAQIADGMAYIERMNYIHRDLRANILVGENLVCKIADFG 417
QY      411 ARLIENEXTAROGAKPRTKWTPEALVGRFTIKSDVMSFGILLTELTKGRVPPGMV 470
DB      418 ARLIENEXTAROGAKPRTKWTPEALVGRFTIKSDVMSFGILLTELTKGRVPPGMV 477
QY      471 NREVLDOVERGYMPCPPECPSLSIDLMSCKMRKEPERPTPEYLOAFLEDYFTSTEPQY 530
DB      478 NREVLQOVERGYMPCPPECPSLSIDLMSCKMRKEPERPTPEYLOAFLEDYFTATERQY 537
QY      531 QPGENTL 536
DB      538 QPGENTL 543
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QY 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
|
|
|
Db 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
|
|
|
Db 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
QY 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
|
|
|
Db 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
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RESULT 2

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US-09-929-266-10
; Sequence 10, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kezrenat
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew B. Roth
; APPLICANT: Martin J. Matteesich
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-929-266-10
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Query Match 100.0%; Score 2834; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGSNKSXPDAQSORRSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
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|
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Db 1 MGSNKSXPDAQSORRSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYTSQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLOIVNTEGD 120
|
|
|
Db 61 PKLFGFNSSDVTYTSQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLOIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLYRES 180
|
|
|
Db 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLYRES 180
QY 181 ETTKGAYCISVSDFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQQLVAAYSKADGL 240
|
|
|
Db 181 ETTKGAYCISVSDFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQQLVAAYSKADGL 240
QY 241 CHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNTTTRVAIKTL 300
|
|
|
Db 241 CHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNTTTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQYMKLRHEKLVOLYAVVSEBEPIYIVTEYMSKSLDLFLKGETGKY 360
|
|
|
Db 301 KPGTMSPEAFLOEAQYMKLRHEKLVOLYAVVSEBEPIYIVTEYMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
|
|
|
Db 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
```

```
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
|
|
|
Db 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
QY 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
|
|
|
Db 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
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RESULT 3

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US-09-977-261-13
; Sequence 13, Application US/09977261
; Publication No. US20030045427A1
; GENERAL INFORMATION:
; APPLICANT: ULIRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-977-261-13
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Query Match 100.0%; Score 2834; DB 3; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGSNKSXPDAQSORRSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
|
|
|
Db 1 MGSNKSXPDAQSORRSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTYTSQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLOIVNTEGD 120
|
|
|
Db 61 PKLFGFNSSDVTYTSQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLOIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLYRES 180
|
|
|
Db 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNANPRGTFLYRES 180
QY 181 ETTKGAYCISVSDFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQQLVAAYSKADGL 240
|
|
|
Db 181 ETTKGAYCISVSDFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQQLVAAYSKADGL 240
QY 241 CHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNTTTRVAIKTL 300
|
|
|
Db 241 CHRLTTCPTSKPQTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTGNTTTRVAIKTL 300
QY 301 KPGTMSPEAFLOEAQYMKLRHEKLVOLYAVVSEBEPIYIVTEYMSKSLDLFLKGETGKY 360
|
|
|
Db 301 KPGTMSPEAFLOEAQYMKLRHEKLVOLYAVVSEBEPIYIVTEYMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
|
|
|
Db 361 LRLPOLVDMAAQAISGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
|
|
|
Db 421 AROGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNREVLDQVER 480
QY 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
|
|
|
Db 481 GYRMPCEPPECPSLHDMCCWKKEPERPTEFYLOAFLEDYFTSTPEYQOGENL 536
```



```
RESULT 4
US-10-691-079-2
; Sequence 2, Application US/10691079
; Publication No. US2004017631A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA S.A.
; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
; FILE REFERENCE: PAAV2002/0030
; CURRENT APPLICATION NUMBER: US/10/691,079
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-691-079-2

Query Match      100.0%; Score 2834; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSDDTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGGNSDDTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
DB 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
QY 181 ETTKGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSKADGL 240
DB 181 ETTKGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSKADGL 240
QY 241 CHRITTCPTSKPQTQGLADAMEIPRESLRLEVYLGQGCFCGEVWMTGNTTVAIKTL 300
DB 241 CHRITTCPTSKPQTQGLADAMEIPRESLRLEVYLGQGCFCGEVWMTGNTTVAIKTL 300
QY 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLYAVVSEEPYIYIYEVMSKSLDLFLGEGTKY 360
DB 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLYAVVSEEPYIYIYEVMSKSLDLFLGEGTKY 360
QY 361 LRLPOLVDMAAQIASGMAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREVLDQVER 480
DB 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREVLDQVER 480
QY 481 GYRMPCEPCEPESLHDMCCQWKREPERPTEFYLOAFLEDFYFSTEPQYOPGENL 536
DB 481 GYRMPCEPCEPESLHDMCCQWKREPERPTEFYLOAFLEDFYFSTEPQYOPGENL 536

RESULT 5
US-10-887-588-2
; Sequence 2, Application US/10887588
; Publication No. US2004026114A1
; GENERAL INFORMATION:
; APPLICANT: Idby, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-1136
; CURRENT APPLICATION NUMBER: US/10/887,588
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/444,711
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 7
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SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-10-887-588-2

Query Match      100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPDKASQRRSLRLEPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGGNSDDTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGGNSDDTVTSPPRAGPLAGGVTTFVALYDSESTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
DB 121 WMLAHSISTGQTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENRGTFLVRES 180
QY 181 ETTKGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSKADGL 240
DB 181 ETTKGAAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRQFNSLQOLVAVYSKADGL 240
QY 241 CHRITTCPTSKPQTQGLADAMEIPRESLRLEVYLGQGCFCGEVWMTGNTTVAIKTL 300
DB 241 CHRITTCPTSKPQTQGLADAMEIPRESLRLEVYLGQGCFCGEVWMTGNTTVAIKTL 300
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DB 301 KPGTMSPEAFLOEQVWKKLRHEKLVOLYAVVSEEPYIYIYEVMSKSLDLFLGEGTKY 360
QY 361 LRLPOLVDMAAQIASGMAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVYERMYVARDLRAANILVGENLVCKVADFGRLLEDNEYT 420
QY 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREVLDQVER 480
DB 421 ARQAKPEPIKWTABEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRREVLDQVER 480
QY 481 GYRMPCEPCEPESLHDMCCQWKREPERPTEFYLOAFLEDFYFSTEPQYOPGENL 536
DB 481 GYRMPCEPCEPESLHDMCCQWKREPERPTEFYLOAFLEDFYFSTEPQYOPGENL 536

RESULT 6
US-10-497-641-2
; Sequence 2, Application US/10497641
; Publication No. US20050037446A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt and Stork
; TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
; FILE REFERENCE: 65064-02
; CURRENT APPLICATION NUMBER: US/10/497,641
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/41564
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/345,888
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-497-641-2

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPXDAQRRLSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPXDAQRRLSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSDPVTSPQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSDPVTSPQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRTFLVRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRTFLVRES 180
QY 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
DB 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
QY 241 CHRLLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCFCFGEVWNGTNGTTRVAIKTL 300
DB 241 CHRLLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCFCFGEVWNGTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLFLKGETGKY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFP1KMTAPBALYGRFTIKSDVWSFGILLTELTKGRVVPYPGVNNREVLDOVER 480
DB 421 AROGAKFP1KMTAPBALYGRFTIKSDVWSFGILLTELTKGRVVPYPGVNNREVLDOVER 480
QY 481 GYRMPCEPCPSLHLMQCCKRKEBERPTEYLOAFLEDYFTSTEPYQGENL 536
DB 481 GYRMPCEPCPSLHLMQCCKRKEBERPTEYLOAFLEDYFTSTEPYQGENL 536
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RESULT 7

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US-10-825-568-10
; Sequence 10, Application US/10825568
; Publication No. US2005006916A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Lattimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matcesalch
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/10/825,568
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-825-568-10
```

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1,1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGSNKSXPXDAQRRLSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPXDAQRRLSLEPAENVHAGGAGFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSDPVTSPQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
DB 61 PKLFGFNSDPVTSPQRAGPLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNTEGD 120
QY 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRTFLVRES 180
DB 121 WMLAHSLSGTQGYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRTFLVRES 180
QY 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
DB 181 ETTKGA YCLSVSDFDNAGKLANVHYKIRKLDGSGFYITSRTQFNSLQQLVAAYSKHADGL 240
QY 241 CHRLLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCFCFGEVWNGTNGTTRVAIKTL 300
DB 241 CHRLLTVCPSTSKPQTQGLAKDAWEIPRESLRLEVKLGQCFCFGEVWNGTNGTTRVAIKTL 300
QY 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLFLKGETGKY 360
DB 301 KPGTMSPEAFLOBAQVMKLRHEKLVOLYAVVSEBPIYIVTEYMSKSLDLFLKGETGKY 360
QY 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRLPOLVDMAAQIASGMAVVERMNYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFP1KMTAPBALYGRFTIKSDVWSFGILLTELTKGRVVPYPGVNNREVLDOVER 480
DB 421 AROGAKFP1KMTAPBALYGRFTIKSDVWSFGILLTELTKGRVVPYPGVNNREVLDOVER 480
QY 481 GYRMPCEPCPSLHLMQCCKRKEBERPTEYLOAFLEDYFTSTEPYQGENL 536
DB 481 GYRMPCEPCPSLHLMQCCKRKEBERPTEYLOAFLEDYFTSTEPYQGENL 536
```

RESULT 8

```
US-10-821-231C-1
; Sequence 1, Application US/10821231C
; Publication No. US20050275637A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongman
; APPLICANT: Ben-Amotz, Dor
; APPLICANT: Xie, Yong
; APPLICANT: Davison, Vincent J.
; APPLICANT: Mrozek, Melissa
; TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
; FILE REFERENCE: 12264/17
; CURRENT APPLICATION NUMBER: US/10/821,231C
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/462,083
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/462,472
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/490,057
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/554,701
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/551,311
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 536
; TYPE: PRT
```

ORGANISM: Homo sapiens
US-10-821-231C-1

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFFVALDYESTRTDLSFKKGERLOIYNNTEGD 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTTFFVALDYESTRTDLSFKKGERLOIYNNTEGD 120
QY 121 WMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
DB 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
QY 241 CHRLTYCPTSKPOTQGLADAMEIPRESIRLEVKLGQCGCFGEVWMTNGTTRVAIKTL 300
DB 241 CHRLTYCPTSKPOTQGLADAMEIPRESIRLEVKLGQCGCFGEVWMTNGTTRVAIKTL 300
QY 301 KPGTMSPEARLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLKGETGY 360
DB 301 KPGTMSPEARLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLKGETGY 360
QY 361 LRIPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRIPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPYGMVNRREVLDQVER 480
DB 421 AROGAKFPKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPYGMVNRREVLDQVER 480
QY 481 GYMPCEPPECESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPYOQPGENTL 536
DB 481 GYMPCEPPECESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPYOQPGENTL 536
```

RESULT 9
US-10-469-469-273

Sequence 273, Application US/10469469
Publication No. US20060079493A1
GENERAL INFORMATION:
APPLICANT: FRITZ, LAWRENCE C.
APPLICANT: BURROWS, FRANCIS J.
TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
TITLE OF INVENTION: DISORDERS WITH HSP90 INHIBITORS
FILE REFERENCE: CON-0010-USN
CURRENT APPLICATION NUMBER: US/10/469,469
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: PCT/US02/06518
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/272,751
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 330
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 273
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-10-469-469-273

Query Match 100.0%; Score 2834; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60

DB 1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60

```
QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFFVALDYESTRTDLSFKKGERLOIYNNTEGD 120
DB 61 PKLFGFNSSDVTSPORAGPLAGVTTFFVALDYESTRTDLSFKKGERLOIYNNTEGD 120
QY 121 WMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFVRES 180
DB 121 WMLAHSISTGQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFVRES 180
QY 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
DB 181 ETTKGAYCLSVSPDNAGKLVNHYKIRKLDGSGFYITTSRTQFNSLQOLVAAYSKADGL 240
QY 241 CHRLTYCPTSKPOTQGLADAMEIPRESIRLEVKLGQCGCFGEVWMTNGTTRVAIKTL 300
DB 241 CHRLTYCPTSKPOTQGLADAMEIPRESIRLEVKLGQCGCFGEVWMTNGTTRVAIKTL 300
QY 301 KPGTMSPEARLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLKGETGY 360
DB 301 KPGTMSPEARLOEAQVWKLRHEKLVQLYAVVSEBPIYITEYMSKSLDPLKGETGY 360
QY 361 LRIPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
DB 361 LRIPOLVDMAAOJASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLIEDNEYT 420
QY 421 AROGAKFPKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPYGMVNRREVLDQVER 480
DB 421 AROGAKFPKMTAPEALYGRFTIKSDVMSFGILITELTTKGRVPYGMVNRREVLDQVER 480
QY 481 GYMPCEPPECESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPYOQPGENTL 536
DB 481 GYMPCEPPECESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTEPYOQPGENTL 536
```

RESULT 10
US-11-233-510-24

Sequence 24, Application US/11233510
Publication No. US20060063190A1
GENERAL INFORMATION:
APPLICANT: Fischer, Timothy J.
APPLICANT: Whitehead, Clark M.
APPLICANT: Malinowski, Douglas P.
APPLICANT: Marcello, Raphael
TITLE OF INVENTION: Methods and Compositions for Evaluating
TITLE OF INVENTION: Breast Cancer Prognosis
FILE REFERENCE: 46143/296738
CURRENT APPLICATION NUMBER: US/11/233,510
CURRENT FILING DATE: 2005-09-22
PRIOR APPLICATION NUMBER: 60/612,073
PRIOR FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: 60/611,965
PRIOR FILING DATE: 2004-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-11-233-510-24

Query Match 100.0%; Score 2834; DB 6; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
DB 1 MGSNKSXPKASQRRSLBPENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
QY 61 PKLFGFNSSDVTSPORAGPLAGVTTFFVALDYESTRTDLSFKKGERLOIYNNTEGD 120
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Db      61 PKLFGFNSSDVTYSPORAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGD 120
Qy      121 WMLAHLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 180
Db      121 WMLAHLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 180
Qy      181 ETTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 240
Db      181 ETTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 240
Qy      241 CHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
Db      241 CHRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTL 300
Qy      301 KPGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 360
Db      301 KPGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 360
Qy      361 LRLPOLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Db      361 LRLPOLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      421 ARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVER 480
Db      421 ARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVER 480
Qy      481 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTPOQPGENTL 536
Db      481 GRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTPOQPGENTL 536

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RESULT 11

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US-10-394-322A-56
/ Sequence 56, Application US/10394322A
/ Publication No. US20030232391A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNESIS PHARMACEUTICALS, INC.
/ APPLICANT: Prescott, John C.
/ TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
/ FILE REFERENCE: 39750-0006 US
/ CURRENT APPLICATION NUMBER: US/10/394,322A
/ PRIOR FILING DATE: 2003-03-30
/ PRIOR APPLICATION NUMBER: US 60/366,892
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PaedSeq for Windows Version 4.0
/ SEQ ID NO 56
/ LENGTH: 535
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-394-322A-56

```

```

Query Match      99.8%; Score 2829; DB 4; Length 535;
Best Local Similarity 100.0%; Pred. No. 2,3e-174;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 GSNKSKPKDASQRRSLLEPAENVHGAAGGAFPASQTPSKPASADGHRGSAAPAPAAAP 61
Db      1 GSNKSKPKDASQRRSLLEPAENVHGAAGGAFPASQTPSKPASADGHRGSAAPAPAAAP 60
Qy      62 KLFGFNSSDVTYSPORAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 121
Db      61 KLFGFNSSDVTYSPORAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 120
Qy      122 WLAHSLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 181
Db      121 WLAHSLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 180
Qy      182 TTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 241
Db      181 TTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 240
Qy      242 HRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 301

```

```

Db      241 HRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 300
Qy      302 PGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 361
Db      301 PGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 360
Qy      362 RLPLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 ROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 481
Db      421 ROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 480
Qy      482 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTPOQPGENTL 536
Db      481 YRMPCPECPESLHDMCCMKRKEPERPTFEYLOAFLEDYFTSTSTPOQPGENTL 535

```

RESULT 12

```

US-10-814-109-4
/ Sequence 4, Application US/10814109
/ Publication No. US20050222042A1
/ GENERAL INFORMATION:
/ APPLICANT: GlaxoSmithKline
/ APPLICANT: Salter, Michael
/ TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of St
/ FILE REFERENCE: 2560.004
/ CURRENT APPLICATION NUMBER: US/10/814,109
/ PRIOR FILING DATE: 2004-03-30
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 535
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-814-109-4

```

```

Query Match      99.8%; Score 2829; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 2,3e-174;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 GSNKSKPKDASQRRSLLEPAENVHGAAGGAFPASQTPSKPASADGHRGSAAPAPAAAP 61
Db      1 GSNKSKPKDASQRRSLLEPAENVHGAAGGAFPASQTPSKPASADGHRGSAAPAPAAAP 60
Qy      62 KLFGFNSSDVTYSPORAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 121
Db      61 KLFGFNSSDVTYSPORAGPLAGVTTFVALYDYESRTEITDLSFKKGERLQIVNTEGDM 120
Qy      122 WLAHSLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 181
Db      121 WLAHSLSTGQGTGYTISNYYAPSDSIOAEWYFGKITTRESERLLLNAENRGTFLVRES 180
Qy      182 TTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 241
Db      181 TTKGAACSVSPFDNAKGLNVGHYKIRKLDGSGFYITTSRTQNSLQOLVAAYYSKADGL 240
Qy      242 HRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 301
Db      241 HRLTTCPTSKPOTQGLADAMEIPRESLRLEVKLGQCGFGEVWMTNGTTRVAIKTLK 300
Qy      302 PGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 361
Db      301 PGTMSPEALQEAQWKKLRHEKLVOLYAVVSEEPYIYTEYMSKSLDFLKGETGKYL 360
Qy      362 RLPLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 421
Db      361 RLPLVDMAAOJASGMAVERNNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYT 420
Qy      422 ROGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGVMNREVLDOVERG 481

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Db 421 ROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVLDQVERG 480
Qy 482 YRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQYQGENL 536
Db 481 YRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQYQGENL 535

RESULT 13

US-10-691-079-1
; Sequence 1, Application US/10691079
; Publication No. US20040176313A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA S.A.
; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
; FILE REFERENCE: FRAY2002/0030
; CURRENT APPLICATION NUMBER: US/10/691,079
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-691-079-1

Query Match 99.5%; Score 2821; DB 4; Length 542;

Best Local Similarity 98.9%; Pred. No. 7.8e-174;
Matches 536; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 MGSNKSFKPDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 PKLFGFNSSDYTSPPQAPPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNTGCD 117
Db 61 PKLFGFNSSDYTSPPQAPPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNTKRV 120
Qy 118 ---EGDWMALHSLSTQGTGYTPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 174
Db 121 DVREGMWMLHSLSTQGTGYTPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGT 180
Qy 175 FLVRESSETTGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFYTTSRTQFNSLQOLVAYYS 234
Db 181 FLVRESSETTGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFYTTSRTQFNSLQOLVAYYS 240
Qy 235 KHAADGLCHRLTTYCPTSKPQTQGLADAMEIPRESRLLEVKLGGCGFGEVWMTNGTTR 294
Db 241 KHAADGLCHRLTTYCPTSKPQTQGLADAMEIPRESRLLEVKLGGCGFGEVWMTNGTTR 300
Qy 295 VAIKITLKPQTMSPBEAFLOEAQVMKRLRHEKLVOLYAVVSEEPYITVTEYMSKSLDLFLK 354
Db 301 VAIKITLKPQTMSPBEAFLOEAQVMKRLRHEKLVOLYAVVSEEPYITVTEYMSKSLDLFLK 360
Qy 355 GENGKTLRLPOLVDMAAQJASGMAYVERMYVHRDLRAANILVGENLVCKVADFGRLARLI 414
Db 361 GENGKTLRLPOLVDMAAQJASGMAYVERMYVHRDLRAANILVGENLVCKVADFGRLARLI 420
Qy 415 EDNEYTAROGAKFPKMTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 474
Db 421 EDNEYTAROGAKFPKMTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREV 480
Qy 475 LDQVERGYRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQYQGE 534
Db 481 LDQVERGYRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQYQGE 540

Qy 535 NL 536
Db 541 NL 542

RESULT 14

US-10-887-588-4
; Sequence 4, Application US/10887588

; Publication No. US20040261142A1
; GENERAL INFORMATION:
; APPLICANT: Yeastman, Timothy J.
; APPLICANT: Ildy, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-T136
; CURRENT APPLICATION NUMBER: US/10/887,588
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/444,711
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(530)
; OTHER INFORMATION: amino acid sequence of the mutant c-Src polypeptide encoded
; OTHER INFORMATION: by the mutant c-Src coding region
US-10-887-588-4

Query Match 98.8%; Score 2801; DB 5; Length 530;

Best Local Similarity 100.0%; Pred. No. 1.5e-172;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSNKSFKPDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Db 1 MGSNKSFKPDASQRRSLBPAENVHAGGAFPASQTPSKPASADGHRGSAAPAPAAE 60
Qy 61 PKLFGFNSSDYTSPPQAPPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Db 61 PKLFGFNSSDYTSPPQAPPLAGGVTFVALYDYESRTETDLSFKKGERLQIVNNTGCD 120
Qy 121 WMLHSLSTQGTGYTPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFLVRES 180
Db 121 WMLHSLSTQGTGYTPSNYVAPSDSIQAEEMYPFKITRRESERLLNAENPRGTFLVRES 180
Qy 181 ETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFYTTSRTQFNSLQOLVAYYSKHAADGL 240
Db 181 ETTKGAYCLSVSDPDNAKGLNVGHYKIRKLDGSGFYTTSRTQFNSLQOLVAYYSKHAADGL 240
Qy 241 CHRLTTYCPTSKPQTQGLADAMEIPRESRLLEVKLGGCGFGEVWMTNGTTRVAIKTL 300
Db 241 CHRLTTYCPTSKPQTQGLADAMEIPRESRLLEVKLGGCGFGEVWMTNGTTRVAIKTL 300
Qy 301 KPQTMSPBEAFLOEAQVMKRLRHEKLVOLYAVVSEEPYITVTEYMSKSLDLFLKGETGKY 360
Db 301 KPQTMSPBEAFLOEAQVMKRLRHEKLVOLYAVVSEEPYITVTEYMSKSLDLFLKGETGKY 360
Qy 361 LRLPOLVDMAAQJASGMAYVERMYVHRDLRAANILVGENLVCKVADFGRLARLIENDEYT 420
Db 361 LRLPOLVDMAAQJASGMAYVERMYVHRDLRAANILVGENLVCKVADFGRLARLIENDEYT 420
Qy 421 AROGAKFPKMTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREVLDQVER 480
Db 421 AROGAKFPKMTAPAEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRREVLDQVER 480
Qy 481 GYRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQY 530
Db 481 GYRMPCEPECESLHDLMOCCMRKEPERPTEFYLAFLIEDYFTSTEPQY 530

RESULT 15

US-10-732-923-13447
; Sequence 13447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13447
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13447

Query Match 98.1%; Score 2781; DB 5; Length 542;
Best Local Similarity 97.8%; Pred. No. 3e-171;
Matches 531; Conservative 3; Mismatches 1; Indels 8; Gaps 3;

QY 1 MGSNKSXPXASQRRSLPEAENVHAGGAPASQTPSKPASADGHRGSAAPA--PAA 59
DB 1 MGSNKSXPXASQRRSLPEAENVHGA-CGAPPASQTPSKPASADGHRGPAAAFVPPAA 59
QY 60 EPKLPGFNSSDVTVTSPORAGPLAGGVTFVALYDYSRTETDLSFKKGRLOIVNNT-- 117
DB 60 EPKLPGFNSSDVTVTSPORAGPLAGGVTFVALYDYSRTETDLSFKKGRLOIVNNTRK 119
QY 118 ---EGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRG 173
DB 120 VDVREGDWMLAHSLSGTQGYIPSNVYAPSDSIQAEEMYPGKITRRESERLLNAENPRG 179
QY 174 TFLVRESETTKAYCISVSDPDNAKGLNVHYKIRKLDSCGFYITSTRQFNSLQOLVAY 233
DB 180 TFLVRESETTKAYCISVSDPDNAKGLNVHYKIRKLDSCGFYITSTRQFNSLQOLVAY 239
QY 234 SKRADLCHRLTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQGFGEVMNGTNGTT 293
DB 240 SKRADLCHRLTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQGFGEVMNGTNGTT 299
QY 294 RVAIKTLKPGTMSPEAFLOEAQVMKDLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDFL 353
DB 300 RVAIKTLKPGTMSPEAFLOEAQVMKDLRHEKLVQLYAVVSEEPYIYVTEYMSKSLDFL 359
QY 354 KGETGYLRLPOLVDMAQIASGMAYVERNNYVHRDLRAANIIVGENLVCKVADFGIARL 413
DB 360 KGETGYLRLPOLVDMSAQIASGMAYVERNNYVHRDLRAANIIVGENLVCKVADFGIARL 419
QY 414 IEDNEYTAOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNRE 473
DB 420 IEDNEYTAOGAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVNRE 479
QY 474 VLDQVERGYRMPCCPECPESLHDMCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYQPG 533
DB 480 VLDQVERGYRMPCCPECPESLHDMCCMRKEPEERPTFEYLQAFLEDYFTSTEPQYQPG 539
QY 534 ENL 536
DB 540 ENL 542

Search completed: June 5, 2006, 17:43:04
Job time : 108.266 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 6.95244 Seconds

(without alignments)
891.618 Million cell updates/sec

Title: US-10-691-079-2

Perfect score: 2834
Sequence: 1 MGSNKSXPKDASQRRSLRP.....AFLEDYFTSTPQYQGENL 536Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1528.5	53.9	505	US-10-511-937-2991	Sequence 2991, App
2	1464	51.7	512	US-10-505-928-353	Sequence 353, App
3	1464	51.7	512	US-10-511-937-2492	Sequence 2492, App
4	1461	51.6	509	US-10-511-937-2467	Sequence 2467, App
5	845	29.8	659	US-10-511-937-2593	Sequence 2593, App
6	838.5	29.6	631	US-11-312-958-60	Sequence 60, App
7	800.5	28.2	620	US-10-511-937-2859	Sequence 2859, App
8	586	20.7	983	US-11-302-678-2	Sequence 2, App
9	573	20.2	994	US-11-303-935-12	Sequence 12, App
10	571	20.1	998	US-11-303-935-2	Sequence 2, App
11	569.5	20.1	993	US-11-303-935-11	Sequence 11, App
12	558.5	19.7	1130	US-11-312-958-52	Sequence 52, App
13	492	17.4	894	US-11-251-465-21	Sequence 21, App
14	485.5	17.1	885	US-10-505-928-432	Sequence 432, App
15	485.5	17.1	885	US-11-251-465-20	Sequence 20, App
16	482	17.0	343	US-11-255-147-6	Sequence 6, App
17	481	17.0	806	US-11-251-465-22	Sequence 22, App
18	477.5	16.8	346	US-11-255-147-4	Sequence 4, App
19	477.5	16.8	348	US-11-255-147-2	Sequence 2, App
20	476.5	16.8	422	US-11-251-465-67	Sequence 67, App
21	476.5	16.8	422	US-11-251-465-70	Sequence 70, App
22	469	16.5	972	US-11-255-147-8	Sequence 8, App
23	459	16.2	1308	US-11-248-132-2	Sequence 2, App
24	448	15.8	999	US-10-196-749-434	Sequence 434, App
25	442	15.6	391	US-11-223-945-38	Sequence 38, App

26	442	15.6	1259	US-11-223-945-40	Sequence 40, App
27	441	15.6	550	US-10-538-066-757	Sequence 757, App
28	441	15.6	1255	US-10-538-066-364	Sequence 364, App
29	441	15.6	1255	US-11-223-945-43	Sequence 43, App
30	439	15.5	993	US-10-511-937-2463	Sequence 2463, App
31	436	15.4	976	US-10-511-937-2423	Sequence 2423, App
32	427	15.1	1006	US-10-511-937-2425	Sequence 2425, App
33	417.5	14.7	1338	US-10-505-928-634	Sequence 634, App
34	417.5	14.7	1338	US-10-505-928-857	Sequence 857, App
35	408.5	14.4	1298	US-10-505-928-274	Sequence 274, App
36	408	14.4	953	US-11-312-958-56	Sequence 56, App
37	403	14.2	369	US-10-953-349-3910	Sequence 3910, App
38	403	14.2	374	US-10-953-349-3909	Sequence 3909, App
39	403	14.2	412	US-10-953-349-3908	Sequence 3908, App
40	397	14.0	344	US-10-511-814-2	Sequence 2, App
41	397	14.0	648	US-10-511-814-14	Sequence 14, App
42	367.5	13.0	272	US-10-370-959-27	Sequence 27, App
43	367.5	13.0	278	US-10-370-959-17	Sequence 17, App
44	367.5	13.0	278	US-10-370-959-31	Sequence 31, App
45	367	12.9	247	US-11-251-465-75	Sequence 75, App

ALIGNMENTS

RESULT 1
US-10-511-937-2991
; Sequence 2991, Application US/10511937
; Publication No. US20060088836m1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2991
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2991
Query Match 53.9%; Score 1528.5; DB 6; Length 505;
Best Local Similarity 56.4%; Pred. No. 2.4e-76;
Matches 300; Conservative 84; Mismatches 117; Indels 31; Gaps 6;
QY 1 MGSNKSXPKDASQRRSLRPENYHAGGAFPAQSOTPSKPADGHRGSPAAPAAAE 60
DB 1 MGSNKSX-----FLQVGQNFSTKSTASPHCEVYVDPSTIKP----- 40
QY 61 PKLGGFSSDPTVTSFQAGLAGVYTF-VALDYESRTETDLSFKKGELOVNNTEG 119
DB 41 -----GPNSHNSNTPGIRE--AGSEDTIVVALDYERAIHHEDLSFQAGDM-VLBSG 91
QY 120 DWMLAHSLSQGTQYIYSNYVAPSDSIQAEHMFCKITRRESRLLLAENPRTFLVRE 179
DB 92 EMMFARSLATKKEQYIYSNYVAPSDSIQAEHMFCKITRRESRLLLAENPRTFLVRE 151

[illegible]

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RESULT 2
US-10-505-928-353
; Sequence 353, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 353
; LENGTH: 512
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-505-928-353

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Query Match	51.7%;	Score 1464;	DB 6;	Length 512;
Best Local Similarity	53.0%;	Pred. No. 7.4e-73;		
Matches 287;	Conservative 87;	Mismatches 125;	Indels 42;	Gaps 9

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QY 1 MGSNNKSKRFD-----SORRSLSBEAENVHAGGAGAPASQSPSPKSPASADGHRGP 51
D 1 MGC1KSKKKDLSDDGVLDKTPVNTERTITYRD-----PSNKGQRV-----PE 47
QY 52 AAFAPAAAPKPLFGGFNSSDVYTSQORAGPLAGVTFVALYDYSRTEITDLSFKKGERL 111
D 48 SOLPGOR-----FOTKD-----PEEGQDIV-----VALPYDDIHDDLSFFKKGEX 90
QY 112 QIVNNTEGDWMLAHSLSTGQGTGYIPSNVYAPASDSIOAEEMYPCKIRRSERLLNAEP 171
D 91 KVLBE--HEMMKAKSLLTKGSEFIPSNVAKANTLETBEMFDDITRKQAEKRLAPGMS 149
QY 172 RGTPLVRESFTTKGAYCLUSVSDFDNAKGLNVHKKIRKLDGGFYITSRTQNSLQOLVA 231
D 150 AGAPLIRSESLTKGSPSLSVDPDVGIVIKHYKIRSLDNGGYIISPRTIPCISDMIK 209
QY 232 YYSKADLDCRLTLTVCPSTKQOTOGIADAMEIPRESLRLKVLQGGFGEVWMTWNG 291
D 210 HYQKQADSLCRLERKACISPKQ--KPMDDAMEIPRESIKLVRLGAGQGFGEVWMTWYNN 268
QY 292 TTRVALIKLKGTGMSPEAFLOEAQWKKLREKLYOLVAVS--EETIYVTEYMSKSL 350
D 269 STKVAVKTLKGTGMSVQAFLEBANIMKTLQHKLVAVLVVVRBEPIYIITEEMAGSLL 328

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QY 351 FFLKGEKTEKYLRLPOLYMAAOAISGMYVEEMVNVHDLRAANTIUGENLVCKVADFGI 410

Db 329 DFLSDBSGKVLPLKLDIPSAOIAEGMAYIEKXNTIHRDLRAANVLVSLSMCKIADFGI 388

QY 411 ARLIEDNEYTAROGAKFPIKWTAPENALYGRFTIKSDVMSFGILLTELTTKGRVPYGMV 470

Db 389 ARVIEDNEYTARREGAKFPIKWTAPENALNFGCTIKSDVMSFGILLYEIVTYGKIPIRGRT 448

QY 471 NREVLIDQVGRYRMCPEPCESLSLHDMCQCKRKRPDEERPTREYLOAFLEDFYTSIEPOY 530

Db 449 NADVMTALSOGYRMRPVENCEDELIDMKMCWEKAERPTPDYLOSVLADPYTATGEOY 508

QY 531 Q 531

Db 509 Q 509

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, RESULT 3
, US-10-511-997-2492
, Sequence 2492, Application US/10511937
, Publication No. US2006008836A1
, GENERAL INFORMATION:
, APPLICANT: EXPRESSION DIAGNOSTICS, INC.
, APPLICANT: Wohlgenuth, Jay
, APPLICANT: Fry, Kirk
, APPLICANT: Woodward, Robert
, APPLICANT: Ly, Ngoc
, APPLICANT: Prentice, James
, APPLICANT: Morris, MacDonald
, APPLICANT: Rosenberg, Steven
, TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
, TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
, FILE REFERENCE: 506612000104
, CURRENT FILING DATE: US/10/511,937
, CURRENT FILING DATE: 2004-10-19
, PRIOR APPLICATION NUMBER: PCT/US2003/012946
, PRIOR FILING DATE: 2003-04-24
, PRIOR APPLICATION NUMBER: US 10/131,831
, PRIOR FILING DATE: 2002-04-24
, PRIOR APPLICATION NUMBER: US 10/325,899
, PRIOR FILING DATE: 2002-12-20
, NUMBER OF SEQ ID NOS: 3117
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 2492

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; TYPE: prt
; ORGANISM: Homo sapiens
US-10-511-937-2492

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Query Match      51.7%; Score 1464; DB 6; Length 512;
Best Local Similarity 53.0%; Pred. No. 7,4e-73;
Matches 287; Conservative 87; Mismatches 125; Indels 42; Gaps 9;

Oy 1 MGSNKSXPKA-----SQRRSLSPAEVNHGAGGAPASQTSKPASADGHRCS 51
Db 1 MGCSKSKGKSLSDGDYDLKTQIPVNRTERITYVD-----PTSNKQQRV-----PE 47

Oy 52 AAFAPALAPRLFCGFNSDPVTQSPQAPAGLVTTFVALYDRESRNETQLSPFKGERL 111
Db 48 SQLPQGR-----FQTKD-----PEEGQDIV-----VALYIPDGIHPDLSKKGKGM 90

Oy 112 QIVNTEGDWMLAHSLSGTQGTGVIIPSNVYAPSDSIQAEWYFGKITRRESERLLLAENP 171
Db 91 KVLVEE-HGEWVKAKSLLTKEGFIIPSNVYALNTLREWEFFKQITRQDARQLLAPGNS 149

Oy 172 RGTFLVRESSETTKAYCLISVDIPNAKGLNVKHGKIRLDSGGFYTSRTPGNSIQQLVA 231
Db 150 AGALILNESETLKQSPFLSVRDPFPHGVGDVYKHKKISLNDGCGYIISRIRIIPPCSDMIX 209

Oy 232 YYSKADQGLCHRLTTCVPTSKPQTQGLAKDAWEIPRESLRILEVKLGQCGCFGEVWNGTWNG 291
Db 210 HYQKQAGLQCRRLKEKACISPPQK-KPMDKQAMEIPRESILKLVKLGAGQFGEVWNGYNN 268

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Qy 292 TTRVAITLKPGTMSPEAFLOEAOVMKKLREHKLVOIYAAVS-REPIYIYEMSKSL 350
Db 269 STKVAATLTPGTMVSQAFLEBANLTKLQHDKLVRLAAYVTRREPIYIYEMAKSSL 328
Qy 351 DFLKSGTKYRLRQPLVDMAAOIASGMAVERNNYVHRDLRAANILVGENLVCKVADFG 410
Db 329 DFLKSDGKVLPLKLDPSAQIAEGMAVIERKVIHRDLRAANVIVSESLMCKIADPGL 388
Qy 411 ARLIEDNEYARQAKFPPIKTAPEALYGRFTIKSDWMSFGILLTELTKGRVPIYGMV 470
Db 389 ARVEDNEYARBEAKFPPIKTAPEALINFCFTIKSDWMSFGILLTELTKGRVPIYGMV 448
Qy 471 NRKVLDOVERGYMRPCPECSLHDLMOCKMRKEPERPFEYLOAFLEBYFTSTEROY 530
Db 449 NADVTMLSGYRMRPVENCPELDYIMKCMKEAERPTFYLOSVLDDPYATBGOY 508
Qy 531 Q 531
Db 509 Q 509

RESULT 4
US-10-511-937-2467
; Sequence 2467, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2467
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2467

Query Match 51.6%; Score 1461; DB 6; Length 509;
Best Local Similarity 59.9%; Pred. No. 1.1e-72;
Matches 272; Conservative 80; Mismatches 98; Indels 4; Gaps 3;
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Qy 319 KLAREKLVYAAVSEPIYIYTEMKSGSLDPLKSGTKYRLRQPLVDMAAOIASGMA 378
Db 294 QLOHQLVRLAAYVTRREPIYIYTEMKSGSLDPLKSGTKYRLRQPLVDMAAOIASGMA 353
Qy 379 YVERNNYVHRDLRAANILVGENLVCKVADFGALRIEDNEYARQAKFPPIKTAPEAL 438
Db 354 FIERERNYHRDLRAANILVSDTISCKIADFGALRIEDNEYARQAKFPPIKTAPEALIN 413
Qy 439 YGRFTIKSDWMSFGILLTELTKGRVPIYGMVNRKVLDOVERGYMRPCPECSLHDL 498
Db 414 YGRFTIKSDWMSFGILLTELTKGRVPIYGMVNRKVLDOVERGYMRPCPECSLHDL 473
Qy 499 CQCKRKEPERPFEYLOAFLEBYFTSTEROY 532
Db 474 RLCWKEPERPFEYLOAFLEBYFTSTEROY 507

RESULT 5
US-10-511-937-2593
; Sequence 2593, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2593
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2593

Query Match 29.8%; Score 845; DB 6; Length 659;
Best Local Similarity 37.1%; Pred. No. 2.8e-39;
Matches 184; Conservative 96; Mismatches 184; Indels 32; Gaps 13;
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Qy      327 ULVAVSSE--PIYIYTEMSKSLDPLFKGEFGTKLRLEPOLVDMAOIQSGAAVVRMY 385
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Db       459 QLVGCTKRGRIFITTEYMANCCLNYLR-ERHRFOTQQLLMECDVCVEAMEYLESKPF 517
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Qy      386 VHRDLRAANILVGENTLCKVADFGFLARLLIEDNEYTAROGAKEPFIKTATBEAALYGRFTIK 445
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Db       518 LHRDLAANCILVNDGGVVKVSDFGLSRVYLDDDEYTSSVGSKEPVWRSPEVLWYSKFSBK 577
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Qy      446 SDWSFGLLTBELTTKGAVPYPGMWREVLDDOVEGYRNPCEPCRESLHDMCCORKE 505
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Db       578 SDIAFGLMWEIYSLGKMPYRFNTSEAHEIAOGLRLYRPHLASKEYTYTIMYSCMBEK 637
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Qy      506 PEERPFEYLOAFLED 521
          :|||||||:::|||||||
Db       638 ADERTPKILLSNILD 653
          :|||||||:::|||||||

RESULT 6
US-11-312-958-60
Sequence 60, Application US/11312958
Publication No. US20060100152N1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Sinos-Santlida, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13424 MOLECULES
FILE REFERENCE: MP102-027P1BONMINM
CURRENT APPLICATION NUMBER: US/11/312, 958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369, 022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360, 495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370, 121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373, 010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373, 908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377, 717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379, 949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382, 409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385, 280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386, 879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 631
TYPE: PR1
ORGANISM: Homo sapiens
US-11-312-958-60

Query Match      29.6%; Score 838.5; DB 7; Length 631;
Best Local Similarity   39.5%; Pred. No. 6.1e-39;
Matches 174; Conservative 91; Mismatches 163; Indels 13; Gaps 9;

Qy      90 VALYDESRTETDSFKKGERLQIVNNTGDMWLASLSGTGTGYIPSNYYA--PSDSIQ 147
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Db       185 VAMVPDFOALEGHDLRLRGGOEYLLIEKRDVHWWRARD-KYGNEGVIPTSYVTGKKSNIND 243
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||
Qy      148 AEEVFYFCGITRRESRRLLINENPFGTVLVRSSETTKAACLSV--SDPNAGLANVKNRK 206
          |||:::|||||||:::|||||||:::|||||||:::|||||||:::|||||||

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244 QYEWYCRMNRSKAEQ-LLRSEDEKCGFMVBD5-SQPGLYTVSLYTKFGGEGSSGFRHYH 301
Qy 207 IRKLD5G--GGYITSRTQFN5LQOQVAYYSKADQLCHRL---TTCPSFKSPQTOGLAD 261
Db 302 IKETTTSPKKYYLLEKHAFGSIPELIEYHKHMAALVTRLRYPVSVKGNAPFTTAGFSYE 361
Qy 262 AMEIPRESLRLLEVKLGGCGCFGEVMMGTNRVVAIKTLKPGTMSPEARLQEAQVKKLR 321
Db 362 KHEINPSLTLTMRRLHSGSLFGVYRLGKRRAQYKAIKAIAREAMCEBEDIIEBAKVMKLT 421
Qy 322 HEKLVQLVAVVSEE-PIYIVTEYMSKSGLLDFLKGETGKYLRLPOLVDMAAQIASGMAYV 380
Db 422 HPKLVQLVGVCCTQCKPFIYIVTEFMSRGCCLNFRORGHFSR-DVLISMCDQCEBMEYL 480
Qy 381 ERMNYVHDLDAANILVGENLVCKRADGLARLIDNETYARQAKFPKIXMPARPAALVG 440
Db 481 ERNSFIRHDLAARCLVSEAGVAVKSDFGMAAYFLDDQYTS5GAKFPKWCQPEYFNS 540
Qy 441 RFTKSDVMSFGILLTELTGKRVYPCMVNVREVLDOYGERGYRMCPCPECPESLHDLMCQ 500
Db 541 RFSKSDVMSGVLMEVFTSGRMPEFKTYIEVVTMYTRGHRLVQPKLASVYVEVMLR 600
Qy 501 CWKKEPERPTEFYLOAFLE 521
Db 601 CWQEKPEGRPSFEDLLRTIDE 621

RESULT 7
US-10-511-937-2959
; Sequence 2959, Application US/10511937
; Publication No. US20060088936A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morrie, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2959
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2959

Query Match 28.2%; Score 800.5; DB 6; Length 620;
Best Local Similarity 34.6%; Pred. No. 6.7e-37;
Matches 176; Conservative 93; Mismatches 181; Indels 59; Gaps 14

Qy 19 EPAENVHAGAGGAPASQTPSKPASAADGHRGSAFAFAAAEPKLGFGFNSSDVTYTSPOR 78
Db 147 DPTGN-----ASKKLPRLPRBEDRR-----PLMEPEE 173

Qy 79 AGPLAGVTFVALYDYESRTETDLSFKKGERLQVNTNTEGDWMLAHSISTQGTGYP5N 138
Db 174 -----TVVIALYQYDNPQELALRNBEYCLDSSSEIHMMVQD-RNGHEGVPS5 224

Qy 139 YVAS--DSIOAEMYPCKITRRBSERLLLAENRGTFIVRESRTTGAYCLVSDPN 196
Db 139 YVAS--DSIOAEMYPCKITRRBSERLLLAENRGTFIVRESRTTGAYCLVSDPN 196

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Db      225 YLVEKSPNNLETYEWYKNSISRDKAEKLLDT-GKEGAFWVRDSRTA-GTYTVSV--FTK 280
Qy      197 A-----KGLANYKHYKIRLDSG--GFYITSTRQFNSLQOLVAYYSKHADG-CHRLT-TYC- 248
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      281 AVSSENNPCIKHAIKTDNDPKRYIAEKVPSISLILNYHGHNGGLVTRLRVYCF 340
Qy      249 -PTSKPOTOGIAXDAMEIPRESLRLEVKGCGCFGEVWMTWGTTRVAIKTLKPTMSP 307
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      341 GRQKAPTAGLRGKWTVIDSELPFVQEISGCGFGLVHLGWLKDKVAIKTIEGAMSE 400
Qy      308 EAPLOAQVWKLRHEKLVOLYAVVSEE-PIYITVEYMSKGLDLFLKGETGYLRPLQ 366
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      401 EDPIEAEFVWVKLSHPILVOLYGVCLGQAPICLVFEEMEGCLSDYLRTQGLF-AAETL 459
Qy      367 VDMAAQASGMAYVERNNYVHRDLRANILVGENLVCKVADFGLARLIENDEYTAQGA 426
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      460 LGNCCLDCEGMAALEACVIRDLAARNCLVGENQVIRKVSDFGMRTRVLDDQYTSYGTG 519
Qy      427 FPIKMTAPEALYGRFTIKSDVMSFGILTELTTKGHVPYPGVNRVLDQVERGYMPC 486
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      520 FPKMASPEVFSRYSKSDVMSFVLMVEVSEBGKIPYENRNSVEVEDISTGFRLLYX 579
Qy      487 PPECPSLHDMCOCWKEPEBERPTPEYL 515
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      580 PRLASTHYQIMNHCMKREPEDRPAPFRL 608

RESULT 8
US-11-302-678-2
; Sequence 2, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Sileo-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MEI02-012P1NM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-2

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```

Qy      61 PKLFGFNSSDVTYSPQAPPLAGVTTFVALYDSESTETDLSFKKGERLQIVNNTGD 120
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      384 PRQGLINTVVTY-----DLAHTNNTFE-----IDAVNGVS-- 416
Qy      121 WMLHSLSTGQTCY----IPSNVAPSDSIQABEWYFGKTTRESEKLLNAENPRTFL 176
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      417 -----ELSSPPROFPAVSIITNOAAPSPLVTLIK---DRTSRNSISISWQEPHEPNQIIL 468
Qy      177 -----VSEETTGAYCLSVSDPDMAKGLVK-----HKIRKLDGCGFYIISRT 221
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      469 DYEKKYKEKQOETSYTIL-----RARGTNVTISSLKPDITTYVQIARTPAGYGTMSRK 523
Qy      222 -OFNS-----LOOLVAYSKH-AD----- 238
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      524 FEFETSPDSISIGESSQVMMIAISAVALIILTVIYVLIGRFGYKSHGADKRLHF 583
Qy      239 -----GLCHRLTYVCP-TSKPOTGLAKDAMEIPRESLRLEVKGCGCFGEVWMTW 289
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      584 GNGLKLPGL---RTYVDPTHYEDPTQAVHEFAKELDATNISIIDKVAGABFGEVCSGRL 640
Qy      290 NGTTR---VAITLKRGTMSPFA--FLOAQVWKLRHEKLVOLYAVVSE-BPIYIYTE 342
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      641 KLPSSKEISVAIYITLKVGYTEKORRDFLGASIMGQPDHNIIRLBSGVVTKSKPMIYTE 700
Qy      343 YMSKGSLLDFLKGETGYLRPLQOLVDMAAQIASGMAYVERNNYVHRDLRANILVGENLV 402
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      701 YMNGSLDSFLRGHDAQFTVI-QLVGMLRGIASGMKYLSDMGYVHRDLAARNILINSNV 759
Qy      403 CKVADFGLARLIEDN---EYTAQGAKEPPIKMTAPEALYGRFTIKSDVMSFGILTEL 459
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      760 CKVSDRGLSVLDDPEAAVTTTR-GGKIPIMTSPFAIAVRKFTSADSVSYGLVBEVM 818
Qy      460 TKGRVYPYGVNRVLDQVERGYRMPCCPESLHDMCOCWKEPEBERPTPEYLOAF 519
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      819 SYGRPRYPMWNSNDVIRKAVDEGYRLPPMDCPALYOLMDCQKORNNRPKFOIVSIL 878
Qy      520 E 520
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      879 D 879

RESULT 9
US-11-303-935-12
; Sequence 12, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Closssek, Thomas
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
; DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/303,935
; FILING DATE: 19-Dec-2005
; CLASSIFICATION: 435

```

Query Match 20.7%; Score 586; DB 7; Length 983;
 Best Local Similarity 31.4%; Pred. No. 4.3e-25;
 Matches 170; Conservative 82; Mismatches 163; Indels 126; Gaps 20;

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/073,064
 FILING DATE: 12-Feb-2002
 APPLICATION NUMBER: US/08/438,265
 FILING DATE: MAY 9, 1995
 APPLICATION NUMBER: US/08/368,776
 FILING DATE: January 3, 1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Wardburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEEX: 67-3510
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 994 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-11-303-935-12

Query Match 20.2%; Score 573; DB 7; Length 994;
 Best Local Similarity 28.4%; Pred. No. 2,8e-24;
 Matches 179; Conservative 82; Mismatches 187; Indels 182; Gaps 23;
 31 APPASQPSKPAADG-HRGS-----AAPAPAAEKLFGGNSDPTVS----- 75
 300 SFSDRSGSSKCECEGYRAPSDPPYACTRPPAPONTL--FYNQTVSLEKSPADN 357
 76 -----PORAGPLAGVYTFVAL-----YDYESRT 99
 358 GGRNDVYRILCKRCSWEGECVPCGSGNIGMPQGTLENNVYVMMLAHANTTFEVEA 417
 100 ETDLS-FKKGRLQIVNNTGDMWLAHSLSTGQTGYIPSNVAPS--DSIOAEWYFGKI 156
 418 VNGVSDLSRSQRL-----FAAVSITTGQ-----AAPSQVSGWKE-----RV 454
 157 TRRESERLLMANPRG-----TLVRESERTKAYCISVSDFDNAGK 199
 455 LQRSVOLSWOEPHPNGVITEYEIKYYEKQRERTYSTLTKSTIS-----ASINLKP 507
 200 LANKHYKIRLDSGGF-YITSRTQFNSLQOLVAVYSGHADGLCHRLTTV----- 247
 508 GIVYVQIRAVTAVAGVGNISPRLDVATLEE-----ASGKMFETAVSSEQNPIIITA 559
 248 -----CPTSKPQTQ-----LAKDAMEIPRES--- 269
 560 VVAVAGTIIIVFWFGIIRBRGYSKADQEGDBELYFCHTKYIDPEYEDPNRAVHQ 619
 270 -----LRLVVLKGGCFGEYWMG-----TANGTTRVAKITLKPTMSPEA--FIQEA 314
 620 FAKELDASCIKIRIVGAGEFGEVCSGRLLPGORDVAVAKITLKGYTEKQRDFCEA 679
 315 QVKKLRLHEKLYOLYAVNSE-EPYIYITEYMSKSLDFLKGEGTKRLRLOLVDAAOI 373
 680 SINGQDHPVNVILLEGVYTRGKFMVYIEFMENGALDAFLRKIDGQTVV--QLVGMIRGI 738
 374 ASGMAYERNMNVYHRLRAANILVGENLYCKVADFGIARLLIEDNE--YTARQAKFPIK 430
 739 AAGMRVLADMGVYHRLDAARNILVNSLYCKVSDFGLSRIYEDDPEAVYTT-TGSKIPIVR 797
 431 WTRPEALGRFTIKSDVMSFGILLTELTTKGAVPIPGVNNREYLDQVERGCMPCBPBC 490
 798 WTRPEALQVRKFTSASDVMSYGIWMVMSYGERPYWDMGNQVIAIEBGRFLRAPMDC 857
 491 PESTLHLMCCMRKEPERPTEFYLAFL 520

DB 858 PAGIHLMLDCWQKDRAPRPFQIVGILD 887
 RESULT 10
 US-11-303-935-2
 Sequence 2, Application US/11303935
 Publication No. US20060099708A1
 GENERAL INFORMATION:
 APPLICANT: Ciosek, Thomas
 Ulrich, Axel
 Millauer, Birgit
 TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 AND TREATMENT OF MDK1
 SIGNAL TRANSDUCTION
 DISORDERS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/303,935
 FILING DATE: 19-Dec-2005
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/073,064
 FILING DATE: 12-Feb-2002
 APPLICATION NUMBER: US/08/438,265
 FILING DATE: MAY 9, 1995
 APPLICATION NUMBER: US/08/368,776
 FILING DATE: January 3, 1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Wardburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 998 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-11-303-935-2
 Query Match 20.1%; Score 571; DB 7; Length 998;
 Best Local Similarity 30.3%; Pred. No. 2,8e-24;
 Matches 164; Conservative 76; Mismatches 165; Indels 137; Gaps 19;
 76 PORAGPLAGVYTFVAL-----YDYESRTETDLS-FKKGRLQIVNNTGDMWLAHSLSTG 130
 390 POGTGEDNVYVVMDLAHANTTFEVEAVNGVSDLSRSQRL-----FAAVSITTG 439
 131 QTCGYIPSNVAPS--DSIOAEWYFGKITRRESERLLMANPRG----- 173
 440 Q-----AAPSQVSGWKE-----RVLQRSVOLSWOEPHPNGVITEYEIKYYEKQDR 486

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Oy 174 --TFVRSBETTKGAACLSVDPDNKAGLVKRYKIRKLDSSGF--YITSOTFNSJLOOLV 230
Db 487 ERTYSTLKTKTS-----ASINMLKPGYIVYFOIRAVTAAGYNTSPRLDVATILEE-- 537
Oy 231 AYSKHAODGLCHRLTIV-----CPTSKPOTQ 256
Db 538 -----ASGKMFPEATVSSSEQNPIIAVAVAGTIIIVFMVFGFIIGRRHCYGSKADQ 591
Oy 257 G-----LAKDAEIPRES-----LAEVYLGOGCGGCVWMMG-- 287
Db 552 GDEELYFHFKPFGYKYIDPEYEDENRRAHOFAKELDASCIIERTVIGAGEEGEVCSSGR 651
Oy 288 --TWNGTTRVAIKTLKPGTMSBEA--FLOEAOVMKKLREHKLVOUAAVSE--EPIYIVT 341
Db 652 LKLPGQDVAVAIKTLKVGYTEKQRDPICEASIMQPDHPNNVHLEGVUTRKEPWIIVI 711
Oy 342 EYMSGSLDLFLKGETGKYLRLPOLYDMAAQISGAAVYERNMYVHRDLPAANILVGENL 401
Db 712 EFMENGALDAFAFRKHDGQFTVI--QLVGMLRGIAAGKRYIADMKGYVHRDLAARILVNSNL 770
Oy 402 VCKVADFGIARLIBDNE--YTAROGAKFPIKATAPEALYGRFTIKSDVWSFGILLTEL 458
Db 771 VCKVSDFGISRIEDDPEAVYTT--TGSKIPIKRTALAEALOYKRFETASDVWSGIIWMEV 829
Oy 459 TTKGVRPYPGVAVREVLDOVERGYRMCPEPECESLIHLMCOGWRKEPEERPTFEYLOAF 518
Db 830 MSYGERPYWMDMSNOVUIKALIEGYRILPAPMDCPAGHQMLMDQMDQRAERPFEEQLVGI 889
Oy 519 LE 520
Db 890 LD 891

```

RESULT 11
 US-11-303-935-11
 * Sequence 11, Application US/11303935
 * Publication No. US20060099708A1
 * GENERAL INFORMATION:
 APPLICANT: Closesek, Thomas
 Ulrich, Axel
 Millauer, Birgit
 TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 AND TREATMENT OF MDX1
 SIGNAL TRANSDUCTION
 DISORDERS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/303,935
 FILING DATE: 19-Dec-2005
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/073,064
 FILING DATE: 12-Feb-2002
 APPLICATION NUMBER: US/08/438,265
 FILING DATE: MAY 9, 1995
 APPLICATION NUMBER: US/08/368,776
 FILING DATE: January 3, 1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>

```

1  ATTORNEY/AGENT INFORMATION:
2      NAME: Warburg, Richard J.
3      REGISTRATION NUMBER: 32,327
4      REFERENCE/DOCKET NUMBER: 208/007
5  TELECOMMUNICATION INFORMATION:
6      TELEPHONE: (213) 489-1600
7      TELEFAX: (213) 955-0440
8      TELEX: 67-3510
9  INFORMATION FOR SEQ ID NO: 11:
10     SEQUENCE CHARACTERISTICS:
11         LENGTH: 993 amino acids
12         TYPE: amino acid
13         STRANDEDNESS: single
14         TOPOLOGY: linear
15     MOLECULE TYPE: peptide
16     SEQUENCE DESCRIPTION: SEQ ID NO: 11:
17     SS-11-303-935-11

```

```

Query March 20.1% Score 569.5; DB 7; Length 993;
Match Local Similarity 32.6%; Pred. No. 3.4e-24;
Matches 151; Conservative 67; Mismatches 172; Indels 73; Gaps 14;

QY      84 GGVTFV-VALVDYRSRTETDLSFKKGERLQIVNNT- GDWMLAHSLSGTQGYIPSNYYA 141
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      471 GVIREVEIKYKXKQKQERTYSTLKTKTSASINNLKPGVVYFQJRAVTAAGY--GNYSB 528

QY      142 PSDSIQAEWYFGKITRRESERLLMANPRKGFVLRSEETTKGAYCLSVDPDNKAGLN 201
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      529 RLDAVTEEASATAVSSEQNPIVILAAVAVAGTILL-----VFVWFGFI----IG 574

QY      202 VKHYKIRLSDSG-----PYTSRTQFNSLQOLVAYYSKADGLCHRLTVV 247
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      575 RRRGCGSKADEGDEBELYFHKPFQTKYIIDET-YEDPNRAVHQPAAKELDASC----- 627

QY      248 CPTSKPQTQSLAKAMEIPRESRLRLVXLGGCGCFGEVWVG-----TWNCTTRVAIKTLKEG 303
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      628 -----IKIERVIGAGEFGEVCSGRKLKPGORDVAVAIKTLKVG 665

QY      304 TMSDEA--FLOEAOVMKLRHEKLVOLYAVVSE--EPITYIYEMSKGSLIDLKSETGKY 360
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      666 YTEKQRDPLCEASIMQGFDPHPNVVTHGVVTRGPWAVIEFPMENGLDALRLKRGDQF 725

QY      361 LRLPOLVDMAQIISGMAYVERMNVYHRDLRAANILVGENIVCKRAADFGIARLIEDNE-- 418
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      726 TVI-QVGLMRLGIAGKRYRLADMGVYHRDLAARNILVNSNLVCKISDGLSKVIEDDEPA 784

QY      419 -YTARQAKPEIKYTAPEALYGRFTIKSDVWSFGILLTELTKGRVVPYPGWNRREVLDQ 477
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      785 VYTT-TGGKIPVRYTAPPAIQRKFTSASDVWSYGIVMMEVWSYGERPFYDWSNODVIXA 843

QY      478 VERGYRMPCEPEPESLHDMCQCKRKEPERPRFEVYQAFLE 520
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      844 IEEGYRLPAPMDCPAGLHQLMLDCWQKRAERPFKEQIVGLID 886

RESULT 12
US-11-958-52
Sequence 52, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Siles-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 95410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 25431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13484 MOLECULES
FILE REFERENCE: MP102-027PILNOMNIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIORITY APPLICATION NUMBER: US/10/369,022

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? PRIOR FILING DATE: 2003-02-19
? PRIOR APPLICATION NUMBER: US 60/360,495
? PRIOR FILING DATE: 2002-02-28
? PRIOR APPLICATION NUMBER: US 60/370,121
? PRIOR FILING DATE: 2002-04-04
? PRIOR APPLICATION NUMBER: US 60/373,010
? PRIOR FILING DATE: 2002-04-16
? PRIOR APPLICATION NUMBER: US 60/373,908
? PRIOR FILING DATE: 2002-04-19
? PRIOR APPLICATION NUMBER: US 60/377,717
? PRIOR FILING DATE: 2002-05-03
? PRIOR APPLICATION NUMBER: US 60/379,949
? PRIOR FILING DATE: 2002-05-13
? PRIOR APPLICATION NUMBER: US 60/382,409
? PRIOR FILING DATE: 2002-05-21
? PRIOR APPLICATION NUMBER: US 60/385,280
? PRIOR FILING DATE: 2002-06-03
? PRIOR APPLICATION NUMBER: US 60/386,879
? PRIOR FILING DATE: 2002-06-06
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 64
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 52
? LENGTH: 1130
? TYPE: PRT
? ORGANISM: Homo sapiens
US-11-312-958-52

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:34 ; Search time 118.626 Seconds
(without alignments)
2085.165 Million cell updates/sec

Title: US-10-691-079-3
Perfect score: 2859
Sequence: 1 MSGNSKPKDASQRRSLP.....AFLEDTFTSTPEQYQDENTL 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2859	100.0	541	6	ABP57261 Mouse src
2	2859	100.0	541	8	ADY84077 Murine Src
3	2820.5	98.7	542	5	ABD97339 Novel hum
4	2820.5	98.7	542	8	ADY84075 Human Src
5	2778.5	97.2	536	2	AAR39706 Human pps
6	2778.5	97.2	536	5	ABG95123 Human v-s
7	2778.5	97.2	536	5	AAU78678 Human SH2
8	2778.5	97.2	536	6	ABP57260 Human src
9	2778.5	97.2	536	7	AD120072 Human c-s
10	2778.5	97.2	536	8	ADL22904 Human MP2
11	2778.5	97.2	536	8	ADQ88400 Human wll
12	2778.5	97.2	536	8	ADQ97772 Human can
13	2778.5	97.2	536	8	ADU04517 Protein c
14	2778.5	97.2	536	8	ADY84076 Human src
15	2778.5	97.2	536	9	ADV94834 Human wll
16	2778.5	97.2	536	9	AEA35914 Human src
17	2778.5	97.2	536	8	ADY84080 Human Src
18	2773.5	97.0	535	7	ADP45087 Human kin
19	2773.5	97.0	535	7	AE21154 Human non
20	2745.5	96.0	530	8	ADQ88402 Human mut
21	2745.5	96.0	530	8	ADV94836 Human mut
22	2645	92.5	533	3	AAy44447 Wild-type
23	2645	92.5	533	4	ABD84661 Amino aci

24	2645	92.5	533	9	ABE07192 Chicken c
25	2641	92.4	533	3	AAy44449 Mutant ch
26	2640	92.3	533	2	AAR39705 Chicken p
27	2639	92.3	533	3	AAy44451 Mutant ch
28	2463.5	86.2	523	9	ABE07190 Rous sarc
29	2389	83.6	565	4	ABG23778 Novel hum
30	2238	78.3	423	8	ADQ97769 Mouse can
31	2111	73.8	543	4	ABD84663 Amino aci
32	2111	73.8	543	4	ABG10302 Novel hum
33	2111	73.8	543	6	ADA00843 Human Src
34	2111	73.8	543	7	ADP45099 Human kin
35	2111	73.8	543	8	ADL22913 Human MP2
36	2111	73.8	543	8	ADQ19329 Human PRO
37	2111	73.8	543	8	ADQ19331 Human PRO
38	2111	73.8	543	8	ADQ26047 v-yes-1 y
39	2111	73.8	543	8	ADU06318 Novel bro
40	2111	73.8	543	9	ADW78761 Human Yam
41	2111	73.8	543	9	ADY19868 PRO polyP
42	2111	73.8	543	9	AEA33955 Human PRO
43	2111	73.8	543	9	AEA35915 Human Yes
44	2111	73.8	543	9	AE01122 Human c-y
45	2103	73.6	543	2	AAy24421 Human yes

ALIGNMENTS

RESULT 1	ABP57261	standard; protein; 541 AA.
ID	ABP57261	
XX	ABP57261;	
AC	ABP57261;	
XX	17-APR-2003 (first entry)	
DT	17-APR-2003 (first entry)	
XX	Mouse src-c protein SEQ ID NO:10.	
DE	Mouse src-c protein SEQ ID NO:10.	
XX		
XX	Mouse; src-c; tyrosine kinase; src-c inhibitor; cytosolic; osteopathic;	ABE07192 Chicken c
KW	antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;	AAy44449 Mutant ch
KW	antisense oligonucleotide; aberrant bone remodeling; breast cancer;	AAR39705 Chicken p
KW	hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;	AAy44451 Mutant ch
KW	ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;	ABE07190 Rous sarc
KW	Kaposi's sarcoma; infection; inflammation; tumour formation.	ABG23778 Novel hum
XX		ADQ97769 Mouse can
OS	Mus musculus.	ABD84663 Amino aci
XX		ABG10302 Novel hum
XX	WO200295053-A2.	ADA00843 Human Src
PN	28-NOV-2002.	ADP45099 Human kin
XX		ADL22913 Human MP2
XX	16-MAY-2002; 2002WO-US015684.	ADQ19329 Human PRO
PF	16-MAY-2001; 2001US-00860473.	ADQ19331 Human PRO
XX	(ISIS-) ISIS PHARM INC.	ADQ26047 v-yes-1 y
PA		ADU06318 Novel bro
XX	Bennett FC, Watt AT;	ADW78761 Human Yam
PI	WPI; 2003-120806/11.	ADY19868 PRO polyP
XX	N-PSDB; ABZ59389.	AEA33955 Human PRO
DR		AEA35915 Human Yes
XX		AE01122 Human c-y
XX		AAy24421 Human yes
PT	New antisense oligonucleotides targeted to nucleic acids encoding src-c,	
PT	useful for diagnosing, treating or preventing diseases associated with	
PT	the expression of src-c, e.g. cancer or inflammation, and in research	
PT	applications.	
XX	Example 13; Page 101-103; 137pp; English.	
PS		
XX	The present invention describes a compound (I) that is 8-50 nucleobases	
CC	in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,	
CC	coding region, intron region, stop codon, intron:exon	
CC	junction, exon:exon junction, or 5' mRNA variant of src-c, and which	
CC	specifically hybridises with and inhibits the expression of src-c. (1)	

CC have cytosolic, antiinflammatory, osteopathic and antibacterial
CC activities, and can be used in antisense therapy and in vaccines. The
CC antisense compound (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung
CC cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents mouse src-c, which is used in an example from the
CC present invention

XX
XX Sequence 541 AA;

Query Match 100.0%; Score 2859; DB 6; Length 541;
Best Local Similarity 100.0%; Pred. No. 7,2e-241;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDAQSRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAAFVPPAEP 60
DB 1 MGSNKSXPDAQSRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAAFVPPAEP 60
QY KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
DB KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
QY 121 VREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
DB 121 VREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
QY 181 LVRESSTTGAAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITSRTQFNSLQOLVAAYSK 240
DB 181 LVRESSTTGAAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITSRTQFNSLQOLVAAYSK 240
QY 241 HADGLCHRLTTCVPTSPKOTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTNGTTRV 300
DB 241 HADGLCHRLTTCVPTSPKOTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTNGTTRV 300
QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITEYNNKSLDLFLKG 360
DB 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITEYNNKSLDLFLKG 360
QY 361 ETGKYLRLPOLVMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRIE 420
DB 361 ETGKYLRLPOLVMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRIE 420
QY 421 DNEYTAROGAKFPPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVREVL 480
DB 421 DNEYTAROGAKFPPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVREVL 480
QY 481 DOVERGYRMPCEPCEESLHDLWCQCKRKEPERPTFEYLQAFLEDFYFSTEPQOYGEN 540
DB 481 DOVERGYRMPCEPCEESLHDLWCQCKRKEPERPTFEYLQAFLEDFYFSTEPQOYGEN 540
QY 541 L 541
DB 541 L 541

RESULT 2

ADY84077 standard; protein; 541 AA.

XX ADY84077;

DT 02-JUN-2005 (first entry)

XX Murine Src protein SEQ ID NO:3.

XX pharmaceutical; Alzheimers disease; neuroprotective; nootropic;

KW Src tyrosine kinase.

XX Mus sp.
XX EPI413887-A1.
XX 28-APR-2004.
XX 22-OCT-2002; 2002EP-00292608.
XX 22-OCT-2002; 2002EP-00292608.
XX (AVET) AVENTIS PHARMA SA.
XX Mercken L, Zambrano N, Ruoso T;
XX WPI, 2004-332834/31.
XX Identifying therapeutic compound for treating Alzheimer's disease,
XX PT involves providing Src protein and determining inhibitory effect of
XX PT compound on Src activity.

XX Claim 4; SEQ ID NO 3; 45pp; English.

CC The invention relates to a novel method for identifying (M1) a
CC therapeutic compound for the treatment of Alzheimer's disease, involving
CC providing a Src protein and determining the inhibitory effect of a
CC compound on the Src activity. The method optionally involves providing a
CC sequence which regulates Src expression and determining if a compound
CC inhibits the expression of Src protein. A compound of the invention has
CC neuroprotective and nootropic activity. The compound identified by the
CC method of the invention is useful for preparing a pharmaceutical for
CC treating Alzheimer's disease. The present sequence represents murine Src
CC protein.

XX
XX Sequence 541 AA;

Query Match 100.0%; Score 2859; DB 8; Length 541;
Best Local Similarity 100.0%; Pred. No. 7,2e-241;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNKSXPDAQSRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAAFVPPAEP 60
DB 1 MGSNKSXPDAQSRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAAFVPPAEP 60
QY 61 KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
DB 61 KLFGEFNSDPTVSPORAGALAGVTFVALYVESRTETDLSFKGERLQIVNTRKVD 120
QY 121 VREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
DB 121 VREGDWMHLAHSLSGTQGYIPSNVYAPSDSIQAEWYFGKITRRESERLLNENPRGTF 180
QY 181 LVRESSTTGAAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITSRTQFNSLQOLVAAYSK 240
DB 181 LVRESSTTGAAYCLSVSDPDNAKGLNVKIKIRKLDGSGFYITSRTQFNSLQOLVAAYSK 240
QY 241 HADGLCHRLTTCVPTSPKOTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTNGTTRV 300
DB 241 HADGLCHRLTTCVPTSPKOTQGLAKDAWEIPRESLRLEVLGQCGEGVMGTNGTTRV 300
QY 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITEYNNKSLDLFLKG 360
DB 301 AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVOLYAVVSEBPIYITEYNNKSLDLFLKG 360
QY 361 ETGKYLRLPOLVMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRIE 420
DB 361 ETGKYLRLPOLVMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRIE 420
QY 421 DNEYTAROGAKFPPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVREVL 480
DB 421 DNEYTAROGAKFPPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVREVL 480
QY 481 DOVERGYRMPCEPCEESLHDLWCQCKRKEPERPTFEYLQAFLEDFYFSTEPQOYGEN 540

Db 481 DQVGRGTRMPCPECPESLHDLMOQCMRKEPERPTEFYLAFLIEDYFTSTEPQYORGEN 540
QY 541 L 541
Db 541 L 541
RESULT 3
ABB97339
ID ABB97339 standard; protein; 542 AA.
AC ABB97339;
XX 27-JUN-2002 (first entry)
XX Novel human protein SEQ ID NO: 607.
XX Human; antihaemetic; vulnerary; antiinflammatory; immunomodulator;
XX antiinfertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
XX neuroprotective; antiparkinsonian; protein therapy; EST;
XX expressed sequence tag.
XX Homo sapiens.
XX MO200222660-A2.
XX 21-MAR-2002.
XX 10-SEP-2001; 2001WO-US026015.
XX 11-SEP-2000; 2000US-00659671.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-292408/33.
XX DR N-PSDB; ABN32525.
XX An isolated polynucleotide for treating diseases associated with its
XX encoded polypeptide such as cancer and multiple sclerosis.
XX Example 2; SEQ ID NO 607; 509pp; English.
XX The present invention provides the protein and coding sequences of 444
XX novel human proteins. These were isolated from expressed sequences tags
XX (ESTs). They can be used to stimulate cell growth, to regulate
XX haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
XX e.g. in burn treatment, to regulate the immune system e.g. to treat
XX multiple sclerosis, to regulate activin or inhibin e.g. to treat
XX infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
XX and cancer, to screen for drugs, to treat inflammatory conditions e.g.
XX rheumatoid arthritis, and to treat nervous system disorders e.g.
XX Parkinson's disease. The present sequence is a protein of the invention
XX SQ Sequence 542 AA;
Query Match 98.7%; Score 2820.5; DB 5; Length 542;
Best Local Similarity 98.7%; Pred. No. 1.7e-237;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 MGSNKSXPDKASQRRRSLEPSENVGA-GGAFPAQTPSPKASADGHRGSAALVPPAAE 59
DB 1 MGSNKSXPDKASQRRRSLEPSENVGA-GGAFPAQTPSPKASADGHRGSAALVPPAAE 60
QY 60 PKLFGGNSSDTVTSPPQAGALAGCVTTFVALYYESRTEETDLSFKGGERLQIVNTRKV 119
DB 61 PKLFGGNSSDTVTSPPQAGALAGCVTTFVALYYESRTEETDLSFKGGERLQIVNTRKV 120
QY 120 DVREGDWMLAHSLSGTQGYIPSNYVAPSDIOAEWYFGKITRRESRLLNENPRGT 179

Db 121 DVREGDWMLAHSLSGTQGYIPSNYVAPSDIOAEWYFGKITRRESRLLNENPRGT 180
QY 180 FLVRESSTTGAYCLSVDPDNAGLNVKHYKIRKLDSSGGYITSRQFNSLOOLVAYS 239
Db 181 FLVRESSTTGAYCLSVDPDNAGLNVKHYKIRKLDSSGGYITSRQFNSLOOLVAYS 240
QY 240 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVGLGGCGFGEVMGTWNGTTR 299
Db 241 KHADELCHRLTTVCPTSKPOTQGLAKDAWEIPRESLRLEVGLGGCGFGEVMGTWNGTTR 300
QY 300 VAIKTLKPGTMSPEAFLOEAQVMKQJNHEKLVOLYAVVSEPIYITEYNKGSLLDFLK 359
Db 301 VAIKTLKPGTMSPEAFLOEAQVMKQJNHEKLVOLYAVVSEPIYITEYNKGSLLDFLK 360
QY 360 GETGKYLRPLQVDMSQIASGNAVYERNNYVHRDLAANILVGENIVCKRADGLARLI 419
Db 361 GETGKYLRPLQVDMSQIASGNAVYERNNYVHRDLAANILVGENIVCKRADGLARLI 420
QY 420 EDNEYTAROGAKPFIKTAPPAALYGRFTIKSDVMSFGILLTELTKGRVVPYPCMVAREV 479
Db 421 EDNEYTAROGAKPFIKTAPPAALYGRFTIKSDVMSFGILLTELTKGRVVPYPCMVAREV 480
QY 480 LDQVGRGYRMPCEPCEPSLHDLMOQCMRKEPERPTEFYLAFLIEDYFTSTEPQYORGE 539
Db 481 LDQVGRGYRMPCEPCEPSLHDLMOQCMRKEPERPTEFYLAFLIEDYFTSTEPQYORGE 540
QY 540 NL 541
Db 541 NL 542
RESULT 4
ADY84075
ID ADY84075 standard; protein; 542 AA.
XX ADY84075;
AC 02-JUN-2005 (first entry)
XX Human Src protein isoform 1 SEQ ID NO:1.
XX pharmaceutical; Alzheimer's disease; neuroprotective; nootropic;
XX Src tyrosine kinase.
XX Homo sapiens.
XX EP1413887-A1.
XX 28-APR-2004.
XX 22-OCT-2002; 2002EP-00292608.
XX 22-OCT-2002; 2002EP-00292608.
XX (AVET) AVENTIS PHARMA SA.
XX Mercken L, Zambirano N, Russo T;
XX WPI; 2004-332834/31.
XX Identifying therapeutic compound for treating Alzheimer's disease,
XX PT involves providing Src protein and determining inhibitory effect of
XX compound on Src activity.
XX Claim 4; SEQ ID NO 1; 45pp; English.
XX The invention relates to a novel method for identifying (m1) a
XX therapeutic compound for the treatment of Alzheimer's disease, involving
XX providing a Src protein and determining the inhibitory effect of a
XX compound on the Src activity. The method optionally involves providing a
XX sequence which regulates Src expression and determining if a compound
XX inhibits the expression of Src protein. A compound of the invention has
XX neuroprotective and nootropic activity. The compound identified by the

CC method of the invention is useful for preparing a pharmaceutical for
CC treating Alzheimer's disease. The present sequence represents isoform 1
CC of human Src protein.

XX Sequence 542 AA:

Query Match 98.7%; Score 2820.5; DB 8; Length 542;
Best Local Similarity 98.7%; Pred. No. 1.7e-237;
Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKKPKDASGRRLSLEPSENVHGA-GGAPASQTPSKPASADGHRGSAAFVPPAAE 59
DB 1 MGSNKKPKDASGRRLSLEPSENVHGA-GGAPASQTPSKPASADGHRGSAAFVPPAAE 60
QY 60 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTRKY 119
DB 61 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTRKY 120
QY 120 DVREGDMMWLHSLSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 179
DB 121 DVREGDMMWLHSLSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 180
QY 180 FLVRESEETTKGAYCLSVSPFDNAKGLNVKRYKJ RKLDSGGFYITTSRTQFNSLQQLVAYYS 239
DB 181 FLVRESEETTKGAYCLSVSPFDNAKGLNVKRYKJ RKLDSGGFYITTSRTQFNSLQQLVAYYS 240
QY 240 KPADGLCHRLTTCPTSKPQTQGLADAWIEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 299
DB 241 KPADGLCHRLTTCPTSKPQTQGLADAWIEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 300
QY 300 VAIKTLKPGTMSPEALQEAQVWKCLRHEKLVOLYAVVSEEPYIYITEYMSKSLDPLK 359
DB 301 VAIKTLKPGTMSPEALQEAQVWKCLRHEKLVOLYAVVSEEPYIYITEYMSKSLDPLK 360
QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRLI 419
DB 361 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRLI 420
QY 420 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 479
DB 421 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 480
QY 480 LDQVERGYMPCPEPCPESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTEPQYQPGE 539
DB 481 LDQVERGYMPCPEPCPESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTEPQYQPGE 540
QY 540 NL 541
DB 541 NL 542

RESULT 5
AAR39706
ID AAR39706 standard; protein; 536 AA.

XX AAR39706;
XX
XX
XX 25-MAR-2003 (revised)
XX 23-DEC-1993 (first entry)
XX Human pp60 c-src protein.
XX DE
XX Endoheital; tyrosine kinase protein; pp60 c-src; 58.
XX OS Homo sapiens.
XX PN W09314193-A1.
XX PD 22-JUL-1993.
XX 05-JAN-1993; 93WO-US000445.
XX PF
XX 06-JAN-1992; 92US-00820011.
XX PR

XX (UYVA) UNIV YALE.
PA
XX Bell L, Madri JA, Warren SL, Luthringer DJ,
XX
XX WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX

PT Genetically engineered endothelial cells - which exhibit enhanced cell
PT migration, urokinase-type plasminogen activator activity, and reduced
PT mononuclear cell adhesion and fibronectin prodn.
PS Disclosure; Page 75-77; 91pp; English.

CC The DNA encoding a portion or (more preferably) the entire pp60 c-src
CC polypeptide (given in A046688) is used to transform endothelial cells.
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than non-
CC transformed counterparts; have an enhanced ability to inhibit the
CC formation of thrombi and/or dissolve thrombi once they have formed and
CC exhibit reduced mononuclear cell adhesion. They can also be used to
CC improve the success of surgical procedures such as coronary angioplasty,
CC heart bypass surgery, vessel graft and stent implantation. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX

XX Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 8e-234;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKKPKDASGRRLSLEPSENVHGA-GGAPASQTPSKPASADGHRGSAAFVPPAAE 59
DB 1 MGSNKKPKDASGRRLSLEPSENVHGA-GGAPASQTPSKPASADGHRGSAAFVPPAAE 60
QY 60 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTRKY 119
DB 61 PKLFGFNSDVTYSPQAGALAGVTTFFVALDYESTRTDLSFKKGERLQIVNNTRKY 117
QY 120 DVREGDMMWLHSLSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 179
DB 118 ---EGDMMWLHSLSTQGTGYIPSNVYAPSDSIQAEEMYPFKITRRSEERLLNAENPRGT 174
QY 180 FLVRESEETTKGAYCLSVSPFDNAKGLNVKRYKJ RKLDSGGFYITTSRTQFNSLQQLVAYYS 239
DB 175 FLVRESEETTKGAYCLSVSPFDNAKGLNVKRYKJ RKLDSGGFYITTSRTQFNSLQQLVAYYS 234
QY 240 KPADGLCHRLTTCPTSKPQTQGLADAWIEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 299
DB 235 KPADGLCHRLTTCPTSKPQTQGLADAWIEIPRESLRLEVKLGQCGFGEVMMGTWNGTTR 294
QY 300 VAIKTLKPGTMSPEALQEAQVWKCLRHEKLVOLYAVVSEEPYIYITEYMSKSLDPLK 359
DB 295 VAIKTLKPGTMSPEALQEAQVWKCLRHEKLVOLYAVVSEEPYIYITEYMSKSLDPLK 354
QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRLI 419
DB 355 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGRLRLI 414
QY 420 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 479
DB 415 EDNEYTARQAKPPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMVNRREV 474
QY 480 LDQVERGYMPCPEPCPESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTEPQYQPGE 539
DB 475 LDQVERGYMPCPEPCPESLHDLCCQMKRKEBERPTEFYLOAFLEDYFTSTEPQYQPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 6

ABG95123
ID ABG95123 standard; protein; 536 AA.
XX
AC ABG95123;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human v-src isoform.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW Proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX
EN MO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002MO-US006518.
XX
PR 01-MAR-2001; 2001US-0272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
XX
DR N-PSDB; ABS73324.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX
PS Disclosure; Page 310-312; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I); treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein
XX
XX Sequence 536 AA;
SQ
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 8e-234;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Db 61 PKLFGFNSSDVTYTSPPQAGLAGGVTTFVALYYESTERTDLSFKGGERLQIVNNT--- 117
Qy 120 DVREGDWMLAHSLSGTGTYIPSNVYAPSDSIQAEWYFGKITRRESERILLNENPRT 179
Db 118 ---EGDWMLAHSLSGTGTYIPSNVYAPSDSIQAEWYFGKITRRESERILLNENPRT 174
Qy 180 FLVRESSTTKGAYCLSYSDPNMAGLVNKHKIRKLDSGCFYTSRQFNSLQOLVAYYS 239
Db 175 FLVRESSTTKGAYCLSYSDPNMAGLVNKHKIRKLDSGCFYTSRQFNSLQOLVAYYS 234
Qy 240 KHADGLCHRLTTCPTSPKPTQGLADKAMEIPRESLRLEVVLGGCFGEVWMTNGTTR 299
Db 235 KHADGLCHRLTTCPTSPKPTQGLADKAMEIPRESLRLEVVLGGCFGEVWMTNGTTR 294
Qy 300 VAIKTLKPTWSPFAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIVTERYMKSGSLDLFLK 359
Db 295 VAIKTLKPTWSPFAFLQEAQVMKKLRHEKLVQLYAVVSEEPYIVTERYMKSGSLDLFLK 354
Qy 360 GETGKYLRLPOLVDMASQIASGMAVYERMYNVHRDLAAANTLVGENLVCKVADGLARLI 419
Db 355 GETGKYLRLPOLVDMASQIASGMAVYERMYNVHRDLAAANTLVGENLVCKVADGLARLI 414
Qy 420 EDNEYTAROGAKKPKIKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGVNVREV 479
Db 415 EDNEYTAROGAKKPKIKMTAPPAALYGRFTIKSDVMSFGILLTETTKGRVVPYPGVNVREV 474
Qy 480 LDQVERGYRMPCEPCESLHDLMCQCRKKEBERPTEFYLAQAFLEDFYSTEPQYQGB 539
Db 475 LDQVERGYRMPCEPCESLHDLMCQCRKKEBERPTEFYLAQAFLEDFYSTEPQYQGB 534
Qy 540 NL 541
Db 535 NL 536
RESULT 7
AAU78678
ID AAU78678 standard; protein; 536 AA.
AC AAU78678;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human SH2/SH3 domain containing protein. v-src.
XX
KW Protein profiling; c-src; SH2; SH3; antibody microarray;
KW protein microarray; DNA microarray; expression profiling; immunology;
KW protein analysis; proteome analysis; human; protein expression profiling.
XX
OS Homo sapiens.
XX
EN MO200214667-A2.
XX
PD 21-FEB-2002.
XX
PF 13-AUG-2001; 2001MO-US041709.
XX
PR 11-AUG-2000; 2000US-0224939P.
PR 12-APR-2001; 2001US-0283498P.
XX
PA (AGIL-) AGILIX CORP.
XX
PI Chait BT, Lattimer DR, Lizardi PM, Kershner ER, Morrow JS;
PI Roch ME, Matthesich WJ, McConnell KJ;
XX
DR WPI; 2002-304072/34.
XX
PT Detecting multiple analytes by separating a set of reporter signals
PT having common property from molecules lacking common property, altering
PT signal, detecting and distinguishing altered forms of signal from each
PT other.

PS Disclosure: Page 224; 341pp; English.

XX The invention relates to detecting (M1) multiple analytes involving
CC separating a set of reporter signals (RS), where each RS has a common
CC property, from molecules lacking the common property, altering the RS,
CC and detecting and distinguishing the altered forms of the RS from each
CC other. The method (M1) is useful for detecting multiple analytes M1 is
CC useful for detection of analytes and biomolecules, (such as proteins,
CC peptides and protein fragments), preferably for multiplex detection and
CC analysis of analytes and biomolecules. M1 is useful to detect a specific
CC analyte (in a specific sample or in multiple samples) or multiple
CC analytes (in a single sample or multiple samples), and to gather and
CC catalogue information about unknown analytes. M1 is useful as a detection
CC system in a number of fields, including antibody or protein microarrays,
CC DNA microarrays, expression profiling, comparative genomics, immunology,
CC diagnostic assay and quality control. M1 is useful as a detection and
CC analysis system for protein analysis, proteome analysis, proteomic,
CC protein expression profiling, de novo protein discovery, functional
CC genomics and protein detection. M1 increases the sensitivity and accuracy
CC of detection of analytes of interest, and allows a complex sample of
CC analytes to be quickly and easily catalogued in a reproducible manner. M1
CC is compatible with techniques involving cleavage, treatment or
CC fragmentation of a bulk sample in order to simplify the sample prior to
CC introduction into the first stage of a multistage detection system. M1 is
CC also compatible with any desired sample, including raw extracts and
CC fractionated samples. The present sequence is human c-erbB-2 whose SH3/SH2
CC domains are detected in a sample, using the method of the invention
XX

Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 5; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

DB 1 MGSNKKSPDASQRRSLSPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 59
1 MGSNKKSPDASQRRSLSPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 60
QY PKLFGFNSSDVTTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKV 119
60 PKLFGFNSSDVTTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKV 119
DB 61 PKLFGFNSSDVTTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKV 117
120 DVREGEWMLAHSLSTQGTGYPNSNYVAPSDIOAEEMYPFKITRRESERLILNAENRGT 179
DB 118 ---EGWMLAHSLSTQGTGYPNSNYVAPSDIOAEEMYPFKITRRESERLILNAENRGT 174
QY 180 FLVRESEETTKGAYCLSVSDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAYYS 239
175 FLVRESEETTKGAYCLSVSDFDNAGKLVNKHKIRKLDGSGFYITSRTOFNSLQOLVAYYS 234
DB 240 KAADGICHLITVCPFSKPTQGLADDAWEIPRESRLRLEKLGQGGCEGFWMGWNTTTR 239
235 KAADGICHLITVCPFSKPTQGLADDAWEIPRESRLRLEKLGQGGCEGFWMGWNTTTR 234
QY 300 VAIKTLKPGTSPPEAFQEAQVWKKLRHEGLVOLYAVVSEPIYIVTEYVWKKSLDLPLK 359
295 VAIKTLKPGTSPPEAFQEAQVWKKLRHEGLVOLYAVVSEPIYIVTEYVWKKSLDLPLK 354
DB 360 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 419
355 GETGKYLRLPOLVDMSAQIASGMAVYERMYVHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNEYIAROGAKPIKWTAPAEALYGRFTIKSDVWSGILLTTLTKGRIPYEGMNVREV 479
415 EDNEYIAROGAKPIKWTAPAEALYGRFTIKSDVWSGILLTTLTKGRIPYEGMNVREV 474
DB 480 LDQVERGYRMPCEPCEPSLHDLMOCKWRKEPERPFETYLQAFLEDFYFTSTEOYOPGE 539
475 LDQVERGYRMPCEPCEPSLHDLMOCKWRKEPERPFETYLQAFLEDFYFTSTEOYOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 8

ABP57260

ABP57260 standard; protein; 536 AA.

ABP57260;

17-APR-2003 (first entry)

Human src-c protein SEQ ID NO:3.

Human; src-c: tyrosine kinase; src-c inhibitor; cytosolic; osteopathic;

antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;

antisense oligonucleotide; aberrant bone remodeling; breast cancer;

hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;

ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;

Kaposi's sarcoma; infection; inflammation; tumour formation.

Homo sapiens.

16-MAY-2002; 2002MO-US015684.

18-MAY-2001; 2001US-00860473.

(ISIS-) ISIS PHARM INC.

Bennett FC, Watt AT;

WPI, 2003-120806/11.

N-PSDB; ABZ59382.

New antisense oligonucleotides targeted to nucleic acids encoding src-c,

useful for diagnosing, treating or preventing diseases associated with

the expression of src-c, e.g. cancer or inflammation, and in research

applications.

Example 13; Page 97-100; 137pp; English.

The present invention describes a compound (I) that is 8-50 nucleobases

in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,

coding region, intron region, exon region, stop codon, intron/exon

junction, exon/exon junction, or 5' mRNA variant of src-c, and which

specifically hybridizes with and inhibits the expression of src-c. (I)

have cytosolic, antiinflammatory, osteopathic and antibacterial

activities, and can be used in antisense therapy and in vaccines. The

antisense compounds (I) can be used for modulating the expression of src-

c and for treating diseases or conditions associated with expression of

src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,

particularly cancer, such as breast cancer, pancreatic cancer, lung

cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma

or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,

prophylaxis, e.g. to prevent or delay infection, inflammation or tumour

formation, as research reagents and kits, and in distinguishing between

functions of various members of a biological pathway. The present

sequence represents human src-c, which is used in an example from the

present invention

Sequence 536 AA:

Query Match 97.2%; Score 2778.5; DB 6; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

DB 1 MGSNKKSPDASQRRSLSPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 59

1 MGSNKKSPDASQRRSLSPSENVHGA-GGAPPASQTPSKPASADGHRGSAAFVPPAAE 60

QY PKLFGFNSSDVTTSPOKAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKV 119

```
Db 61 PKLFGFNSSDVTYSPQAGLAGVTFVALYDSESTETDLSFKGGERLQIVNNT--- 117
Qy 120 DVREGDWMLAHSLSSTGOTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 179
Db 118 ---EGDMMMLAHSLSSTGOTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
Qy 180 FLVRESSTTGAYCCLSVDFDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
Db 175 FLVRESSTTGAYCCLSVDFDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
Qy 240 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 299
Db 235 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 294
Qy 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 354
Qy 360 GETGKYLRPLPOLVDMASQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGRLRI 419
Db 355 GETGKYLRPLPOLVDMASQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGRLRI 414
Qy 420 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGRVPYPGMNVREV 479
Db 415 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGRVPYPGMNVREV 474
Qy 480 LDVERGYRMPCEPECESLHDLMCQCRKEPERPFEYLQAFLEDFYFSTEPYOYQGE 539
Db 475 LDVERGYRMPCEPECESLHDLMCQCRKEPERPFEYLQAFLEDFYFSTEPYOYQGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 9
ID ADI20072 standard; protein; 536 AA.
AC ADI20072;
DT 22-APR-2004 (first entry)
DE Human c-Src.
KW specific-binding agent; Src; Cytostatic; Cardiant; Src-positive tumor;
KM heart disease.
OS Homo sapiens.
XX MO2003057238-A1.
XX 17-JUL-2003.
XX 27-DEC-2002; 2002MO-US041564.
XX 28-DEC-2001; 2001US-0345888P.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Schmitt JM, Stork PJG,
XX PI MPI; 2003-587076/55.
XX DR N-PSDB; ADI20071.
XX
XX New specific-binding agent which specifically binds to Src when Src is
XX phosphorylated at serine-17 (Ser17) but does not detectably bind to Src
XX when Ser17 is not phosphorylated, useful for identifying abnormal cell
XX proliferation.
XX PS Disclosure; SEQ ID NO 2; 40pp; English.
XX
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CC The present invention relates to a specific-binding agent which
CC specifically binds to Src when Src is phosphorylated at serine at
CC position 17 (Ser17) but does not detectably bind to Src when Ser17 is not
CC phosphorylated. The specific-binding agent is useful as a diagnostic
CC agent. The agent and the methods may also be used for treating Src-
CC positive tumors or heart disease. The present sequence represents human c-
CC Src.
XX
XX Sequence 536 AA;
SQ
Qy Query Match 97.2%; Score 2778.5; DB 7; Length 536;
Db Best Local Similarity 97.6%; Pred. No. 8e-234;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
Qy 1 MGSNKSXPQDASQRRRLSEBSENVHGA-GGAFPASQTPSKPASADGHRGSPAAAVPPAAE 59
Db 1 MGSNKSXPQDASQRRRLSEBSENVHGA-GGAFPASQTPSKPASADGHRGSPAAAVPPAAE 60
Qy 60 PKLFGFNSSDVTYSPQAGLAGVTFVALYDSESTETDLSFKGGERLQIVNNTRKV 119
Db 61 PKLFGFNSSDVTYSPQAGLAGVTFVALYDSESTETDLSFKGGERLQIVNNT--- 117
Qy 120 DVREGDWMLAHSLSSTGOTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 179
Db 118 ---EGDMMMLAHSLSSTGOTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLLNENPRGT 174
Qy 180 FLVRESSTTGAYCCLSVDFDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
Db 175 FLVRESSTTGAYCCLSVDFDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
Qy 240 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 299
Db 235 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 294
Qy 240 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 299
Db 235 KHADGLCHRLTTYCPTSKPOTQGLAKDAMEIPRESLLEVLGCGCGEVMGTMNGTTR 294
Qy 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 354
Qy 360 GETGKYLRPLPOLVDMASQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGRLRI 419
Db 355 GETGKYLRPLPOLVDMASQIASGMAVYERMYVHRDLRANILVGENLVCKVADFGRLRI 414
Qy 420 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGRVPYPGMNVREV 479
Db 415 EDNEYTARQGAKEPIKWTAPBAALYGRFTIKSDVMSFGILLTELTTGRVPYPGMNVREV 474
Qy 480 LDVERGYRMPCEPECESLHDLMCQCRKEPERPFEYLQAFLEDFYFSTEPYOYQGE 539
Db 475 LDVERGYRMPCEPECESLHDLMCQCRKEPERPFEYLQAFLEDFYFSTEPYOYQGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 10
ADI22904
ID ADI22904 standard; protein; 536 AA.
AC ADI22904;
DT 20-MAY-2004 (first entry)
DE Human MP2153 polypeptide sequence SEQ ID NO: 24.
XX human; MP2153; p21; p53; cancer.
XX Homo sapiens.
XX MO2004015069-A2.
XX 19-FEB-2004.
XX
```

PF 06-AUG-2003; 2003WO-US024505.
 XX
 PR 07-AUG-2002; 2002US-0401701P.
 PR 16-SEP-2002; 2002US-0411017P.
 PR 30-DEC-2002; 2002US-0437107P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Francis-Iang H, Friedman L, Kidd T, Roche S, Belvin M;
 PI Ploman GD, Lickteig K, Zhang H, Amundsen CD;
 XX
 DR N-PSDB; ADL22887.
 XX
 WPI; 2004-180653/17.
 DR N-PSDB; ADL22887.
 XX
 PT Identifying a candidate p21 or p53 pathway modulating agent using an
 PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
 PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
 PT breast cancer.
 XX
 PS Example 3; Page 87-90; 110pp; English.

CC The present invention relates to a method of identifying a candidate p21
 CC or p53 pathway modulating agent. This comprises providing an assay system
 CC comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
 CC acid, contacting the assay system with a test agent, where in its
 CC presence the system provides a reference activity, and detecting a test
 CC agent-biased activity of the assay system, wherein a difference between
 CC the test agent-biased activity and the reference activity identifies the
 CC test agent as a candidate p21 or p53 pathway modulating agent. The
 CC methods and compositions of the present invention are useful for the
 CC diagnosis and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the p21 or p53 pathway, such as
 CC cancer, preferably colon or head and neck cancer. The present sequence is
 CC a human MP2153 protein sequence of the invention.
 XX
 XX Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAQSGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRPSAFAVPAAE 59
 DB 1 MGSNKSXPDAQSGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRPSAFAVPAAE 60
 QY 60 PKLFGGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 119
 DB 61 PKLFGGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 117
 QY 120 DVREGDMWLAHSLSTGQGYTPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGT 179
 DB 118 ---EGDMWLAHSLSTGQGYTPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGT 174
 QY 180 FLVRESETTKGAAYCLSVSPFDNAKGLNVHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 239
 DB 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 234
 QY 240 KAADGICHLUTYCPSPKSPOTQGLADANEIPRESIRLEVYKLCQGCGEGEYMGNTNCTTR 299
 DB 235 KAADGICHLUTYCPSPKSPOTQGLADANEIPRESIRLEVYKLCQGCGEGEYMGNTNCTTR 294
 QY 300 VAIKTLKPGTMSPEALQEAQWVKLRHEKLVOLYVVSSEPIYIVTEYNNKSLLDPLK 359
 DB 295 VAIKTLKPGTMSPEALQEAQWVKLRHEKLVOLYVVSSEPIYIVTEYNNKSLLDPLK 354
 QY 360 GETGKYLRLPOLVDMASQIASGMAVYERMYVVARDLRAANILVGENLVCKVADFGARLL 419
 DB 355 GETGKYLRLPOLVDMASQIASGMAVYERMYVVARDLRAANILVGENLVCKVADFGARLL 414
 QY 420 EBNETYARQAGKFPIMWTAPEALYGRFTIKSDVMSFGIILTELTKGRVPIYGMVNRREV 479
 DB 415 EBNETYARQAGKFPIMWTAPEALYGRFTIKSDVMSFGIILTELTKGRVPIYGMVNRREV 474

QY 480 LDQVERGYMPCBPCEPESLHDMCCMWKREPEREFTFEXLQAFLEDYFTSTEPQYQGE 539
 DB 475 LDQVERGYMPCBPCEPESLHDMCCMWKREPEREFTFEXLQAFLEDYFTSTEPQYQGE 534
 QY 540 NL 541
 DB 535 NL 536

RESULT 11

ADQ88400
 ID ADQ88400 standard; protein; 536 AA.

XX ADQ88400;

AC 07-OCT-2004 (first entry)

DE Human wild-type tyrosine kinase protein pp60.

KM Cellular oncogene Src; c-Src; tyrosine kinase protein pp60; cancer;

KW infection; inflammation; tumour; gene therapy; human.

XX Homo sapiens.

XX US6764833-B1.

XX 20-JUL-2004.

PF 24-NOV-1999; 99US-00444711.

PR 24-NOV-1999; 99US-00444711.

XX (UYSF-) UNITV SOUTH FLORIDA.

XX Yeatman TJ, Irby RB;

DR WPI; 2004-532511/51.

XX N-PSDB; ADQ88399.

PT New isolated c-Src tyrosine kinase polynucleotide, useful for treating
 PT diseases associated or caused by mutant Src, cancer, or for preventing
 PT infection, inflammation, or tumor formation.

PS Disclosure; SEQ ID NO 2; 29pp; English.

XX CC The invention relates to novel mutant cellular oncogene Src (c-Src) which
 CC codes for mutant tyrosine kinase protein pp60. c-Src sequences are useful
 CC for treating diseases which are associated or caused by mutant Src. They
 CC are useful for treating cancer, to delay or prevent infection,
 CC inflammation or tumor formation. The invention is also useful in gene
 CC therapy. The present sequence is human wild-type tyrosine kinase protein
 CC pp60.
 XX

Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234; Indels 7; Gaps 2;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAQSGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRPSAFAVPAAE 59
 DB 1 MGSNKSXPDAQSGRRSLSPSENVHGA-GGAPPASQTPSPKPSADGHRPSAFAVPAAE 60
 QY 60 PKLFGGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 119
 DB 61 PKLFGGFNSSDVTYSPQAGALAGVTTVALYDYSRTETDLSFKKGERLQIVNNTKRY 117
 QY 120 DVREGDMWLAHSLSTGQGYTPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGT 179
 DB 118 ---EGDMWLAHSLSTGQGYTPSNVYAPSDSIQAEEMWFGKTRRESERLLNAENPRGT 174
 QY 180 FLVRESETTKGAAYCLSVSPFDNAKGLNVHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 239
 DB 175 FLVRESETTKGAAYCLSVSPFDNAKGLNVHYKIRKLDGSGFYITSRTOFNSLQOLVAAYS 234

Db 175 FLVRESEFTTGAYCLSVDFDNAGKLVNKHKIRKLDSDGGFYITSRTOFNSLQQLVAYYS 234
QY 240 KHADGLCHRLTTCPTSKPTQTQGLAKDAWEIPRESLLEVKLGCGCGEYVMGTWNGTTR 299
Db 235 KHADGLCHRLTTCPTSKPTQTQGLAKDAWEIPRESLLEVKLGCGCGEYVMGTWNGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPYIYTEMNKGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPYIYTEMNKGSLDPLK 354
QY 360 GETGKYLRPLQVDMASQIASGMAVYVERMYVHRDLAANILVGENLVCKVADFGLARLI 419
Db 355 GETGKYLRPLQVDMASQIASGMAVYVERMYVHRDLAANILVGENLVCKVADFGLARLI 414
QY 420 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 479
Db 415 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 474
QY 480 LDQVERGYRMPCEPECSLHDLMCQCRKEPEERPFTEYLQAFLEDEYFTSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPECSLHDLMCQCRKEPEERPFTEYLQAFLEDEYFTSTEPQYQGE 534
QY 540 NL 541
QY 535 NL 536
Db

RESULT 12

ADQ97772
ID ADQ97772 standard; protein; 536 AA.

XX AC ADQ97772;

XX DT 07-OCT-2004 (first entry)

XX DE Human cancer associated sequence HP10-043, SEQ ID 749.

XX KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.

XX OS Homo sapiens.

XX PN WO2004060304-A2.

XX PD 22-JUL-2004.

XX PF 22-DEC-2003; 2003WO-US041389.

XX PR 27-DEC-2002; 2002US-00330773.

XX PA (SAGR-) SAGRES DISCOVERY INC.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2004-543781/52.

XX PT New isolated cancer associated nucleic acids comprising at least 10

XX PT contiguous nucleotides; useful for diagnosing, preventing and/or treating

XX PT cancers such as leukemia and lymphoma.

XX PS Claim 1, SEQ ID NO 749; 199pp; English.

XX CC The present invention relates to cancer associated sequences (ADQ97025-

XX CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or

XX CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic formate directly from WIFO at

XX CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPXASORRRLBPSENVHGA-GGAFPASOTPSKXPASADGHRGSPAAPPAE 59
Db 1 MGSNKSXPXASORRRLBPSENVHGA-GGAFPASOTPSKXPASADGHRGSPAAPPAE 60
QY 60 PKLFGFNSSDYVTSPOBAGLAGVTFVALYDESRTETDLSFKKGBERLOIVNNTKRV 119
Db 61 PKLFGFNSSDYVTSPOBAGLAGVTFVALYDESRTETDLSFKKGBERLOIVNNTKRV 117
QY 120 DVREGDWMLAHSISTGOTGYIPSNYVAPSDSIQAEEMVFGKITRSEBRLLNENRGT 179
Db 118 ---EGDWMLAHSISTGOTGYIPSNYVAPSDSIQAEEMVFGKITRSEBRLLNENRGT 174
QY 180 FLVRESEFTTGAYCLSVDFDNAGKLVNKHKIRKLDSDGGFYITSRTOFNSLQQLVAYYS 239
Db 175 FLVRESEFTTGAYCLSVDFDNAGKLVNKHKIRKLDSDGGFYITSRTOFNSLQQLVAYYS 234
QY 240 KHADGLCHRLTTCPTSKPTQTQGLAKDAWEIPRESLLEVKLGCGCGEYVMGTWNGTTR 299
Db 235 KHADGLCHRLTTCPTSKPTQTQGLAKDAWEIPRESLLEVKLGCGCGEYVMGTWNGTTR 294
QY 300 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPYIYTEMNKGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFLOEAQVMKCLRHEKLVOLYAVVSEEPYIYTEMNKGSLDPLK 354
QY 360 GETGKYLRPLQVDMASQIASGMAVYVERMYVHRDLAANILVGENLVCKVADFGLARLI 419
Db 355 GETGKYLRPLQVDMASQIASGMAVYVERMYVHRDLAANILVGENLVCKVADFGLARLI 414
QY 420 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 479
Db 415 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVYPGMVNRV 474
QY 480 LDQVERGYRMPCEPECSLHDLMCQCRKEPEERPFTEYLQAFLEDEYFTSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPECSLHDLMCQCRKEPEERPFTEYLQAFLEDEYFTSTEPQYQGE 534
QY 540 NL 541
QY 535 NL 536
Db

RESULT 13

ADU04517
ID ADU04517 standard; peptide; 536 AA.

XX AC ADU04517;

XX DT 13-JAN-2005 (first entry)

XX DE Protein tyrosine Kinase Src.

XX KW Protein tyrosine kinase; Src; proto-oncogene; phosphorylation;

XX KW protein structure; enzyme; EC_2.7.1.112.

XX OS unidentified.

XX FT Key Location/Qualifiers

FT Modified-site 216 /note= "Tyr phosphorylation site"

FT Modified-site 419 /note= "Tyr phosphorylation site"

FT Modified-site 530 /note= "Tyr phosphorylation site"

XX PN WO2004092703-A2.

XX PD 28-OCT-2004.

XX PF 09-APR-2004; 2004WO-US010834.

XX PR 11-APR-2003; 2003US-0462083P.

XX PR 11-APR-2003; 2003US-0462472P.

PR 25-JUL-2003; 2003US-0490057P.
 PR 08-MAR-2004; 2004US-055131P.
 PR 19-MAR-2004; 2004US-0554701P.
 PR 08-APR-2004; 2004US-00821231.
 XX
 PA (PURDUE RES FOUND.
 XX

PI Zhang D, Amotz B, Xie Y, Davison VJ, Mrozek M, Ortiz C;
 XX
 DR WPI; 2004-784629/77.
 XX

PT Obtaining structural characteristic information for separation and
 PT detection of e.g. proteins comprises irradiating a region formed by
 PT evaporating specimen-containing solvent in a droplet on planar solvo-
 PT phobic sample support.
 XX
 XX
 PS Example C; Page 25; 91pp; English.
 XX

CC The present sequence is that of proto-oncogene protein tyrosine kinase
 CC Src (p60-src, c-src). The invention relates to the combined use of solid
 CC substrates, micro-deposition techniques, spectral imaging methods, and
 CC data processing to facilitate the concentration and separate detection of
 CC biological molecules including proteins, peptides, polysaccharides,
 CC glycans and nucleotides, in a liquid mixture, using spectral analysis
 CC such as normal Raman spectroscopy, infrared spectroscopy and matrix-
 CC assisted laser desorption/ionisation (MALDI) time-of-flight mass
 CC spectrometry. The methods were demonstrated in examples from the high
 CC invention using peptide fragments of Src. These demonstrated the high
 CC level of analyte discrimination that can be achieved and that the method
 CC can be used to detect and quantify Tyr phosphorylation in tryptic digests
 CC of physiologically important proteins.
 XX

SQ Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 59
 DB 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 60
 QY 60 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTEITDLSFKKGERLQIVNNT--- 117
 QY 120 DVREGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIOAEEMWFGKTRRSEERLLNAENPRGT 179
 DB 118 ---EGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIOAEEMWFGKTRRSEERLLNAENPRGT 174
 QY 180 FLVRESEETTKGAYCISVSPFDNAKGLNVGKIKRLDSGGFYITTSRTQNSLQOLVAYYS 239
 DB 175 FLVRESEETTKGAYCISVSPFDNAKGLNVGKIKRLDSGGFYITTSRTQNSLQOLVAYYS 234
 QY 240 KPADGCHRLTTYCPTSPKPTQGLADAMEIPRESRLRYKLGQGGEGEWMGMNTGTR 229
 DB 235 KPADGCHRLTTYCPTSPKPTQGLADAMEIPRESRLRYKLGQGGEGEWMGMNTGTR 234
 QY 300 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEEPYIYIVTEYNNKSLDLFLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEEPYIYIVTEYNNKSLDLFLK 354
 QY 360 GETGKYLRLPOLVDMGAQIASGMAVYERMYVHARDLPAANILVGENLVCKVADFGLARLI 419
 DB 355 GETGKYLRLPOLVDMGAQIASGMAVYERMYVHARDLPAANILVGENLVCKVADFGLARLI 414
 QY 420 ENEEYVARAGAKRPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMNREV 419
 DB 415 ENEEYVARAGAKRPIKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVPYGMNREV 414
 QY 480 LDQVERGYRMPCEPPECESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGE 539
 DB 475 LDQVERGYRMPCEPPECESLHDLCCMKRKEPERPTFEYLQAFLEDYFTSTEPQYOPGE 534

QY 540 NL 541
 DB 535 NL 536

RESULT 14
 ID ADY84076 standard; protein; 536 AA.
 XX
 AC ADY84076;
 XX
 DT 02-JUN-2005 (first entry)
 XX

DE Human Src protein isoform 2 SEQ ID NO:2.

XX pharmaceutical; Alzheimers disease; neuroprotective; nootropic;
 KW Src tyrosine kinase.
 XX

OS Homo sapiens.
 XX

PN EP1413887-A1.
 XX

PD 28-APR-2004.
 XX

PF 22-OCT-2002; 2002EP-00292608.
 XX

PR 22-OCT-2002; 2002EP-00292608.
 XX

PA (AVENTIS PHARMA SA.
 XX

PI Mercken L, Zambirano N, Russo T;
 XX

DR WPI; 2004-332834/31.
 XX

PT Identifying therapeutic compound for treating Alzheimer's disease,
 PT involves providing Src protein and determining inhibitory effect of
 PT compound on Src activity.
 XX

PS Claim 4; SEQ ID NO 2; 45pp; English.
 XX

CC The invention relates to a novel method for identifying (M1) a
 CC therapeutic compound for the treatment of Alzheimer's disease, involving
 CC providing a Src protein and determining the inhibitory effect of a
 CC compound on the Src activity. The method optionally involves providing a
 CC sequence which regulates Src expression and determining if a compound
 CC inhibits the expression of Src protein. A compound of the invention has
 CC neuroprotective and nootropic activity. The compound identified by the
 CC method of the invention is useful for preparing a pharmaceutical for
 CC treating Alzheimer's disease. The present sequence represents isoform 2
 CC of human Src protein.
 XX

SQ Sequence 536 AA;

Query Match 97.2%; Score 2778.5; DB 8; Length 536;
 Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 59
 DB 1 MGSNKKPKPDASQRRRLSPSENVHGA-GGAPASQTPSPKPSADGHRGSAAFVPPAAE 60
 QY 60 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTEITDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYTSPOKAGALAGVTTFVALYDYESRTEITDLSFKKGERLQIVNNT--- 117
 QY 120 DVREGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIOAEEMWFGKTRRSEERLLNAENPRGT 179
 DB 118 ---EGDWMHLAHSLSGTQGTGYPNSNYVAPSDSIOAEEMWFGKTRRSEERLLNAENPRGT 174
 QY 180 FLVRESEETTKGAYCISVSPFDNAKGLNVGKIKRLDSGGFYITTSRTQNSLQOLVAYYS 239
 DB 175 FLVRESEETTKGAYCISVSPFDNAKGLNVGKIKRLDSGGFYITTSRTQNSLQOLVAYYS 234

QY 240 KHADELCHRLTTCVPTSKPOTQGLAKDAMEIPRESLRELVKLGCCGCEGVMMGTNGTTR 299
 DB 235 KHADELCHRLTTCVPTSKPOTQGLAKDAMEIPRESLRELVKLGCCGCEGVMMGTNGTTR 294
 QY 300 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEPIYIYTEYNNKSLDPLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEPIYIYTEYNNKSLDPLK 354
 QY 360 GETGKYLRPLQVDMASQIASGMAVVERMYVHRDLPAANTLVGENLVCKVADFGIARLI 419
 DB 355 GETGKYLRPLQVDMASQIASGMAVVERMYVHRDLPAANTLVGENLVCKVADFGIARLI 414
 QY 420 EDNEYTRAGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 479
 DB 415 EDNEYTRAGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 474
 QY 480 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFSTEPQYQGE 539
 DB 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFSTEPQYQGE 534
 QY 540 NL 541
 DB 535 NL 536

RESULT 15
 ADV94834
 ID ADV94834 standard; protein; 536 AA.
 XX
 AC ADV94834;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Human wild type c-Src protein.
 XX
 KM Cytostatic; gene therapy; mutagenesis; tumor; sarcoma; neuroblastoma;
 KM breast carcinoma; c-Src; tyrosine kinase inhibitor; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN US2004261142-A1.
 XX
 PD 23-DEC-2004.
 XX
 PF 09-JUL-2004; 2004US-00887588.
 XX
 PR 24-NOV-1999; 99US-00444711.
 XX
 PA (YEAT/) YEATMAN T J.
 PA (IRBY/) IRBY R B.
 PI Yeatman TJ, Irby RB;
 XX
 DR MPI: 2005-038810/04.
 DR N-PSDB; ADV94833.
 XX
 PT New truncated c-Src polypeptide, useful for treating and/or preventing
 PT clinical conditions associated with or caused by Src mutation, e.g.
 PT tumors.
 XX
 PS Disclosure; SEQ ID NO 2; 26pp; English.
 XX
 CC The invention relates to a truncated c-Src polypeptide comprising a
 CC sequence of 530 amino acids given in the specification. The polypeptide,
 CC composition and method are useful for treating and/or preventing clinical
 CC conditions associated with or caused by Src mutation e.g. tumors
 CC (sarcoma, neuroblastoma, breast carcinoma). This sequence corresponds to
 CC the wild type c-Src protein.
 XX
 SQ Sequence 536 AA;
 Query Match 97.2%; Score 2778.5; DB 9; Length 536;

Best Local Similarity 97.6%; Pred. No. 8e-234;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
 QY 1 MGSNKSFKPKASQRRRLBPSENVHGA-GGAFPASQTPSKPASADGHRGPAFAVPPAAE 59
 DB 1 MGSNKSFKPKASQRRRLBPSENVHGA-GGAFPASQTPSKPASADGHRGPAFAVPPAAE 60
 QY 60 PKLFGGNSSDTVTSPPRAGLAGVTFVALYVESRTETDLSFKGGERLIQVNNVT-- 117
 DB 61 PKLFGGNSSDTVTSPPRAGLAGVTFVALYVESRTETDLSFKGGERLIQVNNVT-- 117
 QY 120 DVREBDMWLAHSLSTQGTGYIPSNYVAPSDSIQAEWYFGKITRSEERLLNENPRGT 179
 DB 118 ---BGDMWLAHSLSTQGTGYIPSNYVAPSDSIQAEWYFGKITRSEERLLNENPRGT 174
 QY 180 FLVRESSTTGAVCYLSVDFDNAGKLVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
 DB 175 FLVRESSTTGAVCYLSVDFDNAGKLVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
 QY 240 KHADELCHRLTTCVPTSKPOTQGLAKDAMEIPRESLRELVKLGCCGCEGVMMGTNGTTR 299
 DB 235 KHADELCHRLTTCVPTSKPOTQGLAKDAMEIPRESLRELVKLGCCGCEGVMMGTNGTTR 294
 QY 300 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEPIYIYTEYNNKSLDPLK 359
 DB 295 VAIKTLKPGTMSPEAFLOEAQVMKQLRHEKLVOLYAVVSEPIYIYTEYNNKSLDPLK 354
 QY 360 GETGKYLRPLQVDMASQIASGMAVVERMYVHRDLPAANTLVGENLVCKVADFGIARLI 419
 DB 355 GETGKYLRPLQVDMASQIASGMAVVERMYVHRDLPAANTLVGENLVCKVADFGIARLI 414
 QY 420 EDNEYTRAGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 479
 DB 415 EDNEYTRAGAKPPIKMTAPPAALYGRFTIKSDVMSFGILLTETTTGGRVYPGMVNRV 474
 QY 480 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFSTEPQYQGE 539
 DB 475 LDQVERGYRMPCEPCEPSLHDLMCQCRKEPERPTEFYLOAFLEDFYFSTEPQYQGE 534
 QY 540 NL 541
 DB 535 NL 536

Search completed: June 5, 2006, 17:07:39
 Job time : 121.626 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:08:03 ; Search time 21.7202 Seconds

(without alignments)

2396.538 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSQPKDASQRRSLRLEP.....AFLEDYFTSTPEQYQGENL 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2859	100.0	541	1 A43610	protein-tyrosine k
2	2820.5	98.7	542	1 TVHUSC	protein-tyrosine k
3	2643	92.4	533	1 TVCHS	protein-tyrosine k
4	2603	91.0	587	1 TVFVPR	protein-tyrosine k
5	2596	90.8	568	1 TVFVSI	protein-tyrosine k
6	2581	90.3	357	1 TVFVS2	protein-tyrosine k
7	2498	87.4	526	1 TVFV60	protein-tyrosine k
8	2479	86.7	526	1 S20808	protein-tyrosine k
9	2473	86.5	526	1 OKFYR	protein-tyrosine k
10	2465	86.3	526	1 S15582	protein-tyrosine k
11	2463	86.1	526	1 TVFVR	protein-tyrosine k
12	2448	85.6	526	1 S26420	protein-tyrosine k
13	2444.5	85.5	532	1 B34104	protein-tyrosine k
14	2442.5	85.4	532	1 A34104	protein-tyrosine k
15	2431	85.0	545	1 S52313	protein-tyrosine k
16	2428	84.9	546	2 S52314	protein-tyrosine k
17	2399.5	83.9	523	1 TVFVMT	protein-tyrosine k
18	2122	74.2	537	1 A45501	protein-tyrosine k
19	2111	73.8	543	1 TVHUVS	protein-tyrosine k
20	2108	73.7	541	2 S31645	protein-tyrosine k
21	2103	73.6	541	1 TVCHXS	protein-tyrosine k
22	2052	71.8	544	2 S15193	protein-tyrosine k
23	2032	71.1	528	1 TVFVGS	protein-tyrosine k
24	1965.5	68.7	534	1 A44991	protein-tyrosine k
25	1947	68.1	537	2 S15192	protein-tyrosine k
26	1942.5	67.9	534	1 S33568	protein-tyrosine k
27	1929.5	67.5	536	2 S33569	protein-tyrosine k
28	1928	67.4	537	1 TVHUSY	protein-tyrosine k
29	1913	66.9	542	2 A49114	protein-tyrosine k

30	1910.5	66.8	539	2 B49114	protein-tyrosine k
31	1904	66.6	537	1 A43806	protein-tyrosine k
32	1847.5	64.6	529	1 TVHUR	protein-tyrosine k
33	1829.5	64.0	517	2 A43807	protein-tyrosine k
34	1793.5	62.7	517	2 S24547	protein-tyrosine k
35	1589	55.6	663	1 TVMVVR	protein-tyrosine k
36	1581.5	55.3	509	1 TVHAST	protein-tyrosine k
37	1568	54.8	392	2 S04205	protein-tyrosine k
38	1526	53.4	503	1 JQ1321	protein-tyrosine k
39	1523	53.3	503	1 TVMSHC	protein-tyrosine k
40	1515.5	53.0	505	1 TVHUC	protein-tyrosine k
41	1488	52.0	507	1 A39939	protein-tyrosine k
42	1462.5	51.2	512	1 TVHULY	protein-tyrosine k
43	1455	50.9	509	1 OKHUK	protein-tyrosine k
44	1453.5	50.8	512	1 S56160	protein-tyrosine k
45	1447.5	50.6	509	1 I48845	protein-tyrosine k

ALIGNMENTS

RESULT 1

A43610 protein-tyrosine kinase (BC 2.7.1.112) src, neuronal [similarity] - mouse

N:Alternate names: Rouse sarcoma oncogene

C:Species: Mus musculus (house mouse)

C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004

C:Accession: A43610

R:Martinez, R.; Mathey-Prevot, B.; Bernards, A.; Baltimore, D.

Science 237, 411-415, 1987

A:Title: Neuronal pp60(c-src) contains a six-amino acid insertion relative to its non-ne

A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610

A:Molecule type: mRNA

A:Residues: 1-541 <MAR>

A:Cross-references: UNIPROT:P05480; UNIPARC:UP10000161D19; GB:M17031; NID:9201056; PIDN::

C:Comment: The neuronal c-src has an 6 residue insertion of RLVMVR within the amino-term

C:Genetics:

A:Gene: Src

A:Cross-references: MGI:98397

A:Map position: 2:91.0

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipidprotein; myristylation; pho

F:90-145/Domain: SH3 homology <SH3>

F:156-253/Domain: SH2 homology <SH2>

F:273-531/Domain: protein kinase homology <KIN>

F:281-289/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:303/Active site: Lys #status predicted

F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 2859; DB 1; Length 541;

Best Local Similarity 100.0%; Pred. No. 2, 4e-136;

Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSQPKDASQRRSLRLEPSENVHAGGAFPPASQTPSKPASADGHRGPAATFPAAEP	60
DB	1	MGSNKSQPKDASQRRSLRLEPSENVHAGGAFPPASQTPSKPASADGHRGPAATFPAAEP	60
QY	61	KLKRGFNSSDTVTSPQAGALAGGVTFVALYDSESTETDLSFKKGERLQIVNTRKVD	120
DB	61	KLKRGFNSSDTVTSPQAGALAGGVTFVALYDSESTETDLSFKKGERLQIVNTRKVD	120
QY	121	VREGDWMLAHSLSGTQGTYPISNVVAPSDSIQAEWYFGKITRRESRLLNAMPRTGF	180
DB	121	VREGDWMLAHSLSGTQGTYPISNVVAPSDSIQAEWYFGKITRRESRLLNAMPRTGF	180
QY	181	LVNSETTKGAYCISVDFPNAGLVNKHKKIRKLDSCGFTYTSRTQFNSLQQLVAYYSK	240
DB	181	LVNSETTKGAYCISVDFPNAGLVNKHKKIRKLDSCGFTYTSRTQFNSLQQLVAYYSK	240
QY	241	HAGGLCHRLTTPVPTSPKQVGLAKDAWEI PRESLREVLKGGCGFGVMMGTNGTTRV	300
DB	241	HAGGLCHRLTTPVPTSPKQVGLAKDAWEI PRESLREVLKGGCGFGVMMGTNGTTRV	300

Db 241 HADGLCHRLTTVCPTSPKQTOGLAKDAMEIPRESRLRLVKGCGFGEVMMGTWNGTTRV 300
QY 301 AITLTKPGTMSPEAFLOEAQVWKLRHKKIYOLYAVVSESPYIVTEYMKSGSLDPLKG 360
Db 301 AITLTKPGTMSPEAFLOEAQVWKLRHKKIYOLYAVVSESPYIVTEYMKSGSLDPLKG 360
QY 361 ETGKTYLRLPOLVDMSAQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
Db 361 ETGKTYLRLPOLVDMSAQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
QY 421 DNEITYAROGAKFPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVL 480
Db 421 DNEITYAROGAKFPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVL 480
QY 481 DQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
Db 481 DQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
QY 541 L 541
Db 541 L 541

RESULT 2

TVHUSC

protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004

C/Accession: A26891; A61083; B61083; A23287; A28833; B34704

R/Tanaka, A.; Glibbs, C.P.; Archut, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.

MoJ. Cell. Biol. 7, 1978-1983, 1987

A/Title: DNA sequence encoding the amino-terminal region of the human c-src protein: img

A/Reference number: A26891; PMID:87257903; PMID:3299057

A/Accession: A26891

A/Molecule type: mRNA

A/Residues: 1-117/124-191 <TAN>

A/Cross-references: UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M16

R/Pyper, J.M.; Bolen, J.B.

J. Neurosci. Res. 24, 89-96, 1989

A/Title: Neuron-specific splicing of C-src RNA in human brain.

A/Reference number: A61083; PMID:9040822; PMID:2681803

A/Accession: A61083

A/Molecule type: mRNA

A/Residues: 98-145 <PY>

A/Cross-references: UNIPARC:UPI000017257A

A/Accession: B61083

A/Molecule type: mRNA

A/Residues: 98-117/124-145 <PY2>

A/Cross-references: UNIPARC:UPI000017257A

R/Anderson, S.K.; Glibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.

MoJ. Cell. Biol. 5, 1122-1129, 1985

A/Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of

A/Reference number: A23287; PMID:85213483; PMID:2582238

A/Accession: A23287

A/Molecule type: mRNA

A/Residues: 192-542 <AND>

A/Cross-references: UNIPARC:UPI000016B068; GB:X02647; NID:G36588; PIND:CA26485.1; PID:G

R/Parer, R.C.; Maron, G.; Lebo, R.V.; Varmus, H.E.; Bishop, J.M.

MoJ. Cell. Biol. 5, 831-838, 1985

A/Title: Isolation of duplicated human c-src genes located on chromosomes 1 and 20.

A/Reference number: A28832; PMID:85187981; PMID:2581127

A/Accession: A28832

A/Molecule type: mRNA

A/Residues: 382-542 <PAR>

A/Cross-references: UNIPARC:UPI000017257D

R/Pyper, J.M.; Bolen, J.B.

MoJ. Cell. Biol. 10, 2035-2040, 1990

A/Title: Identification of a novel neuronal C-src exon expressed in human brain.

A/Reference number: A34704; PMID:90220588; PMID:1691439

A/Accession: B34704

A/Molecule type: mRNA

A/Residues: 118-123 <PY3>

A/Cross-references: UNIPARC:UPI000017257E

C/Genetics:
A:Gene: GDB:SRC
A/Cross-references: GDB:120750; OMIM:190090
A:Map position: 20q11.2-20q11.2
A/Insertions: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1
C/Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F:1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <MA2>
F:1-117/124-542/Product: protein-tyrosine kinase src, short form #status predicted <MA2>
F:91-146/Domain: SH3 homology <SH3>
F:157-254/Domain: SH2 homology <SH2>
F:274-532/Domain: protein kinase homology <KIN>
F:282-390/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/4/Active site: Lys #status predicted
F:425/536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 98.7%; Score 2820.5; DB 1; Length 542;

Best Local Similarity 98.7%; Pred. No. 2e-134; 3; Indels 1; Gaps 1;

Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKSXPXDAQGRRLSPSENVHGA-GGAPASQTPSKPKASADGHRGSAFVPPAAE 59
Db 1 MGSNKSXPXDAQGRRLSPSENVHGA-GGAPASQTPSKPKASADGHRGSAFVPPAAE 60
QY 60 PKLFGFNSDDTYTSQORAGALAGYTTVALYDYSRRTDLSFKKGERLOIVNNTRKY 119
Db 61 PKLFGFNSDDTYTSQORAGALAGYTTVALYDYSRRTDLSFKKGERLOIVNNTRKY 120
QY 120 DVEGGMWLAHSLSTQGTGYIPSNVYAPSPDSIQAEEMYGKTIRESERLLNAENPRGT 179
Db 121 DVEGGMWLAHSLSTQGTGYIPSNVYAPSPDSIQAEEMYGKTIRESERLLNAENPRGT 180
QY 180 FLVRESEETTKGAYCLSVSPDNAGKLVNHYKIRKLDGCFYITSRTQFNSLQOLVAYYS 239
Db 181 FLVRESEETTKGAYCLSVSPDNAGKLVNHYKIRKLDGCFYITSRTQFNSLQOLVAYYS 240
QY 240 KHADGCHRLTTVCPTSPKQTOGLAKDAMEIPRESRLRLVKGCGFGEVMMGTWNGTTR 299
Db 241 KHADGCHRLTTVCPTSPKQTOGLAKDAMEIPRESRLRLVKGCGFGEVMMGTWNGTTR 300
QY 300 VAITKLPKGTMSPEAFLOEAQVWKLRHKKIYOLYAVVSESPYIVTEYMKSGSLDPLK 359
Db 301 VAITKLPKGTMSPEAFLOEAQVWKLRHKKIYOLYAVVSESPYIVTEYMKSGSLDPLK 360
QY 360 GETGKTYLRLPOLVDMSAQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 419
Db 361 GETGKTYLRLPOLVDMSAQIASGMAVVERMNVYHRDLRAANILVGENLVCKVADFGIARLI 420
QY 420 EDNEYTAROGAKFPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVL 479
Db 421 EDNEYTAROGAKFPFKMTAPBALYGRFTIKSDVMSFGILLTELTKGRVPYPGMNVREVL 480
QY 480 LDQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 539
Db 481 LDQVERGYRMPCCPECPESLHDLMOCCMKRKEPERFTPEYLOAFLEDYFTSTEPQYOPGE 540
QY 540 NL 541
Db 541 NL 542

RESULT 3
TVHUSC
protein-tyrosine kinase (EC 2.7.1.112) src - chicken
N/Alternate names: kinase-related transforming protein src
C/Species: Gallus gallus (chicken)
C/Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C/Accession: A00630; 150217; A41256; C35650; A32432
R/Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983

A>Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A/Reference number: A00630; MUID:83155664; PMID:6299580
A/Accession: A00630
A/Molecule type: DNA
A/Residues: 1-500; 'R', 502-533 <TAK>
A/Cross-references: UNIPROT:P00523; UNIPROT:Q09093; UNIPARC:UPI000017257F; GB:J00844; NT
R:Takeya, T.; Hanafusa, H.
Cell 34, 319, 1983
A/Reference number: A90838
A/Contents: annotation; extractum, correct translation of residue 526
R:Takeya, T.; Hanafusa, H.
J. Virol. 44, 12-18, 1982
A>Title: DNA sequence of the viral and cellular src gene of chickens: II comparison of t
A/Reference number: I50217; MUID:83059861; PMID:6292480
A/Accession: I50217
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <TA2>
A/Cross-references: UNIPARC:UPI000011887; GB:J00908; NID:g211690; PIDN:AA48732.1; PID:
A/Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr an
R:Dora, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
Mol. Cell. Biol. 11, 4165-4176, 1991
A>Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and pc
A/Reference number: A41256; MUID:91304409; PMID:1712905
A/Accession: A41256
A/Molecule type: mRNA
A/Residues: 484-533 <DOR1>
A/Cross-references: UNIPARC:UPI0000171468; GB:S43579; NID:g167964; PIDN:AA19353.1; PID:
A/Note: the authors translated the codon CAG for residue 527 as Glu
R:Dora, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A>Title: An alternative non-cytosine protein kinase product of the c-src gene in chicken
A/Reference number: A35650; MUID:90318371; PMID:2115117
A/Accession: C35650
A/Molecule type: mRNA
A/Residues: 1-182; 'DPCIPPLSCLC' <DOR2>
A/Cross-references: UNIPARC:UPI000008P0344; GB:M57290; NID:g212703; PIDN:AA49078.1; PID:
A/Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle
R:Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Waller, J.L.; Shalloway, D.
Cell 57, 763-774, 1989
A>Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites ph
A/Reference number: A32432; MUID:8924341; PMID:2470512
A/Accession: A32432
A/Molecule type: protein
A/Residues: 2-88 <SHB>
A/Cross-references: UNIPARC:UPI0000172580
A/Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C/Genetics:
A/Gene: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12/48/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:17/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:34/46/Binding site: phosphate (Thr) (covalent) #status experimental
F:72/Binding site: phosphate (Ser) (covalent) #status experimental
F:25/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 92.4%; Score 2643; DB 1; Length 533;
Best Local Similarity 93.0%; Pred. No. 1.5e-125;
Matches 503; Conservative 12; Mismatches 18; Indels 8; Gaps 2;
Qy 1 MGSNKSXPXKASQRRRLSPSENVHAGAFPASQTSKPSASDGHGSPSAFVPPAEP 60
Db 1 MGSNKSXPXKASQRRRLSPSENVHAGAFPASQTSKPSASDGHGSPSAFVPPAEP 58
Qy 61 KLFSGFNSSDPTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120
Db 59 KLFSGFNSSDPTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120

Query Match 91.0%; Score 2603; DB 1; Length 587;
Best Local Similarity 93.1%; Pred. No. 1.7e-123;
Matches 496; Conservative 12; Mismatches 17; Indels 8; Gaps 2;
Qy 1 MGSNKSXPXKASQRRRLSPSENVHAGAFPASQTSKPSASDGHGSPSAFVPPAEP 60
Db 1 MGSNKSXPXKASQRRRLSPSENVHAGAFPASQTSKPSASDGHGSPSAFVPPAEP 58
Qy 61 KLFSGFNSSDPTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 120
Db 59 KLFSGFNSSDPTVTSPOAGALAGVTTFFVALLYDRESRTETDLSPKGERLQIVNTRKVD 114

RESULT 4
TVFVPR
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus PR2257
C/Species: avian sarcoma virus PR2257
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C/Accession: A30174
R:Geryk, J.; Dezelic, P.; Barnier, J.V.; Svoboda, J.; Nehyba, J.; Karakoz, I.; Rynditch,
J. Virol. 63, 481-492, 1989
A>Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom
A/Reference number: A30174; MUID:89094972; PMID:2463376
A/Accession: A30174
A/Molecule type: DNA
A/Residues: 1-587 <GER>
A/Cross-references: UNIPROT:P15054; UNIPARC:UPI0000135F23; GB:M21526; NID:g210264; PIDN:
A/Gene: src
C/Genetics:
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F:88-137/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:12/48/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status pred
F:25/Active site: Lys #status predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Qy	121	VRESDMMWLAHSJLSTGOTGYIPSNVYA	PSNSIOAEEMYGKTRARESELLMANP	PGTF
Db	115	--BGDMWLAHSJLTGOTGYIPSNVYAP	SDSIOAEEMYGKTRARESELLMANPEN	PGTF
Qy	181	LVARESETTKGAYCLSVSDFDNAKGLN	VKRYKLRKJLDSGGFYTSRQNSLQOL	VAAYSK
Db	173	LVARESETTKGAYCLSVSDFDNAGKGLN	VKHRYKLRKJLDSGGFYTSRQNSLQOL	VAYYSK
Qy	241	HADGLCHRLTTVCPTSKPOTQGLAND	AMEIPRESLRLEVKLGQCGCFGEVM	GTNGTTRV
Db	233	HADGLCHRLTWCPTSKPOTQGLAND	AMEIPRESLRLEVKLGQCGCFGEVM	GTNGTTRV
Qy	301	AITKLKPGTMSPEALFOEAOVMKKLR	PHCKLQOLYAVVSEEPYYIYTEKMN	GSLLDPLK
Db	293	AITKLKPGTMSPEALFOEAOVMKKLR	HEKLVQLYAVVSEEPYYIYTEKMS	KSLLDPLK
Qy	361	ETGKYLRLLPOLVMSAOIASGMAVY	ERNMYVRDRDRAANILVGEVLCK	EVADFGIARLIE
Db	353	EMGKYLRLLPOLVMAAOIASGMAVY	ERNMYVRDRDRAANILVGEVLCK	EVADFGIARLIE
Qy	421	DNEYTARQAKPEIKTATPEALYGR	FTIKSDVMSFGILLTELTTKGR	VPYGMVNEEVL
Db	413	DNEYTARQAKPEIKTATPEALYGR	FTIKSDVMSFGILLTELTTKGR	VPYGMVNEEVL
Qy	481	DOVERGRNPPCEPECESLHDLMCQ	WRKEPERPTFEYLQAFLEDYTT	STEP 533
Db	473	DOVERGRNPPCEPECESLHDLMCQ	WRDPERPTFEYLQAFLEDYTT	STEP 525

RESULT 5

protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
 C:Species: avian sarcoma virus S1
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
 C:Accession: A25375
 R:Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
 Mol. Cell. Biol. 6, 2420-2428, 1986
 A:Title: Activation of the cellular src gene by transducing retrovirus.
 A:Reference number: A25375; MUID:87064539; PMID:3097513
 A:Accession: A25375
 A:Molecule type: DNA
 A:Residues: 1-568 <IKK>
 A:Cross-references: UNIPROT:P14084, UNIPARC:UPI0000135F25
 C:Genetics:
 A:Gene: src
 C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F:88-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:25/Active site: lys #status predicted
 F:416/binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

	Score	DB 1	Length
Query Match	90.8%	2536	568
Best Local Similarly	92.7%	Pred. No. 3.7e-173	
Matches 494; Conservative	14;	Mismatches 17;	Indels 8; Gaps 2;

QY		1	MGSNKSXPKAKASQRRRSLEPSENHAGACAFASQTPSPKAPADGHRGSAAFPVPAARP	60
Db		1	MGSSSKSRKSDSQRRRSLPEPDSTH-HGGFASQTPTNTTAPADTRTSRSGVTATPP	58
QY		61	KLFGGPNSSDPIVTSPOBAGALAGVTTFAALVDYSRTETDISFKKGELQIVNNRKTD	120
Db		59	KLFGGFNTSDPIVTSPOBAGALAGGVTTFAALVDYSRIETDISFKKGELQIVNNR----	114
QY		121	VREGDWMLAHLSLTGQTGYIPSNVYAPSDSIQAEEYYFFPKITRRESERILLNAENRGTF	180
Db		115	--EGDWMLAHLSLTGQTGYIPSNVYAPSDSIQAEMYFPKITRRBSERILLNPENRGTF	172
QY		181	LVRSEETTKGAYCLVSDFDNAAKGLNVKKIKRLDGSGFYITSRTQFNLSLOOLVAAYSK	240

Db	173	LVRESEITTKGAYCCLSVSPDNARGLANVGHYKIRKLDSSGFYITTSRTQPSBLSQJLVAYYRK	232
Qy	241	HADGJCHRLJTVVCPTSKPOTQGLADAMEIPRESIRLEVKLGQSGFGEVWMTGNTTREV	300
Db	233	HADGJCHRLJTVVCPTSKPOTQGLADAMEIPRESIRLEVKLGQSGFGEVWMTGNTTREV	292
Qy	301	AIKTLKPCPTMSPEAFLOAQWKKLRHKLVOLVAVVSEEPYIYTEVWNNKSLDLELKG	360
Db	293	AIKTLKPCPTMSPEAFLOAQWKKLRHKLVOLVAVVSEEPYIYTEVWNNKSLDLELKG	352
Qy	361	ETGKXLRPLPOLVDSMAQJASGMAYYERNWVYHRDLRAANILVGENLVCKADFGJLARLIE	420
Db	353	EMGKTLRLPLPOLVDSMAQJASGMAYYERNWVYHRDLRAANILVGENLVCKADFGJLARLIE	412
Qy	421	DNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGJLLTBLTTKGRVPYGMVNRREVJ	480
Db	413	DNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGJLLTBLTTKGRVPYGMVNRREVJ	472
Qy	481	DOVERGVMPCPPECPESLHLMQCMKKEPERPTEFYLOAFLELDYFSTEB	533
Db	473	DOVERGVMPCPPECPESLHLMQCMKKEPERPTEFYLOAFLELDYFSTEB	525

RESULT 6

1VFV52
 Protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
 C:Species: avian sarcoma virus S2
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #ext_change 05-Oct-2004
 C:Accession: B25375
 R:Ikawa, S.; Heginio-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
 Mol. Cell. Biol. 6, 2420-2428, 1986
 A:Title: Activation of the cellular src gene by transducing retrovirus.
 A:Reference number: A25375; MUID:87064539; PMID:3097513
 A:Accession: B25375
 A:Molecule type: DNA
 A:Residues: 1-557 <IK>
 A:Cis08-References: UNIPROT:P14085; UNIPARC:UPI0000135F26
 C:Genetics:
 A:Gene: src
 C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onco
 C:18-137/Domain: SH3 homology <SH3>
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:25/Active site: Lys #status predicted
 F:145/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:145/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	90.3%	Score 2581;	DB 1;	Length 557;
Best Local Similarity	88.7%	Pred. No. 2.1e-12;		
Matches 495; Conservative	16;	Mismatches 21;	Indels 26;	Gaps 3.

Qy	1	MGSNKSRKDA	QRRRLSE	BNVH	KAGCA	FPA	SQTP	SKAS	ADG	HGBA	ATV	PAAP	60												
Db	1	MGSSKSRKDP	QRRRLSE	PPD	STH--	HGF	PAS	QTPN	KKA	ADP	TH	TPRS	FG	YATEP	58										
Qy																									
Db																									
Qy	61	KLFGFN	SDTV	IS	PO	GAL	AGV	TT	FV	AL	Y	YES	K	ET	TD	LS	PK	GER	LO	I	VN	TR	KV	120	
Db	59	KLFGFN	SDTV	IS	PO	GAL	AGV	TT	FV	AL	Y	YES	K	ET	TD	LS	PK	GER	LO	I	VN	TR	KV	114	
Qy	121	V	R	B	D	M	M	L	A	S	T	G	C	G	T	P	S	N	V	A	P	S	D	S	180
Db	115	--	B	D	M	M	L	A	S	T	G	C	G	T	P	S	N	V	A	P	S	D	S	172	
Qy	181	L	V	R	E	S	E	T	T	K	A	C	L	S	V	D	P	N	A	K	L	V	N	K	240
Db	173	L	V	R	E	S	E	T	T	K	A	C	L	S	V	D	P	N	A	K	L	V	N	K	232
Qy	241	H	A	D	G	L	C	H	R	L	T	T	V	C	P	T	S	P	R	O	G	L	A	K	300
Db	233	H	A	D	G	L	C	H	R	L	T	T	V	C	P	T	S	P	R	O	G	L	A	K	292

F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.7%; Score 2479; DB 2; Length 526;

Best Local Similarity 90.6%; Pred. No. 2.5e-117;

Matches 475; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

```
QY 1 MGSNKSXPQASQRRSLSEPSENVHAGAGAFPAQSOTPSKPASADGHRGSAAFVPPAEP 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPQASQRRSLSEPSDTH--HGFPASQTPDETAAPDAHNPBSRGTVATEP 58
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KLFEGNSDPTVTSPPRAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTKVD 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 KLFMGNTSDPTVTSPPRAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNT- 114
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VREGDWLHLSLSTGGTGYIPSNVYAPSDSIQAEEMVFGKITRSESRLLLNENPRGT 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 --EGDWLHLSLSTGGTGYIPSNVYAPSDSIQAEEMVFGKITRSESRLLLNENPRGT 172
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LVRESSTTGAYCLSDPDNAKGLNVKHYKIRKLDGSGFYTSRTOFNSLQDLVAYYSK 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 LVKSESTAKAYCLSDPDNAKGPVVKYKICLYSGGFYTSRTOFNSLQDLVAYYSK 232
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 300
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 292
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AITLKPGMTSPBAFLQEAQVMMKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDFLKG 360
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 AITLKPGMTSPBAFLQEAQVMMKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDFLKG 352
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 ETGKYRLPOLVDMASQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 420
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 EMGKYRLPOLVDMAAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 412
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYEGMVREVL 480
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYEGMVREVL 472
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPFEYLOAFL 524
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPFEYLOAFL 516
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 9

OKFEVYR

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)
N/Alternate names: kinase-related transforming protein src
C/Species: Rous sarcoma virus

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C/Accession: S09609

R/Bodor, J.; Poljak, E.; Pichrtova, J.; Geryk, J.; Svoboda, J.
Nucleic Acids Res. 17, 8869, 1989

A/Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.
A/Reference number: S09609; PMID:90067864; PMID:2587228

A/Accession: S09609
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-526 <BOD>

A/Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:961706; PIDN
C/Genetics:

A/Genes: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F:148-245/Domain: SH2 homology <SH2>

F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:295/Active site: Lys #status predicted
F:116/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.5%; Score 2473; DB 1; Length 526;
Best Local Similarity 90.5%; Pred. No. 5e-117;

Matches 474; Conservative 13; Mismatches 29; Indels 8; Gaps 2;

```
QY 1 MGSNKSXPQASQRRSLSEPSENVHAGAGAFPAQSOTPSKPASADGHRGSAAFVPPAEP 60
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSNKSXPQASQRRSLSEPSDTH--HGFPASQTPDETAAPDAHNPBSRGTVATEP 58
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KLFEGNSDPTVTSPPRAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNTKVD 120
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 KLFMGNTSDPTVTSPPRAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNNT- 114
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VREGDWLHLSLSTGGTGYIPSNVYAPSDSIQAEEMVFGKITRSESRLLLNENPRGT 180
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 --EGDWLHLSLSTGGTGYIPSNVYAPSDSIQAEEMVFGKITRSESRLLLNENPRGT 172
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LVRESSTTGAYCLSDPDNAKGLNVKHYKIRKLDGSGFYTSRTOFNSLQDLVAYYSK 240
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 LVKSESTAKAYCLSDPDNAKGPVVKYKICLYSGGFYTSRTOFNSLQDLVAYYSK 232
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 300
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 HADGLCHRLTTCPTSKPOTQGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 292
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AITLKPGMTSPBAFLQEAQVMMKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDFLKG 360
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 AITLKPGMTSPBAFLQEAQVMMKLRHEKLVOLYAVSEEPYIVTEYNNKSGSLDFLKG 352
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 ETGKYRLPOLVDMASQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 420
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 EMGKYRLPOLVDMAAQISGMAYVERMYVHRDLRAANILVGENLVCKVADGLARLIE 412
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYEGMVREVL 480
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 DNEYTARQAKAPFIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPYEGMVREVL 472
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPFEYLOAFL 524
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPBERPFEYLOAFL 516
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 10

S15582

protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)

C/Species: Rous sarcoma virus
A/Variety: strain Prague A

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004
C/Accession: S15582; S09665

R/Liu, Z.; Hackett, P.B.
Nucleic Acids Res. 17, 3986, 1989

A/Title: Sequence variation of the Rous sarcoma virus PTA src gene.
A/Reference number: S15582; PMID:89282411; PMID:2543959

A/Accession: S15582
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Residues: 1-526 <LIU>

A/Cross-references: UNIPROT:Q64994; UNIPROT:Q92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP
A/Experimental source: strain Prague A

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
A/Note: only a list of differences from sequence S09665 is given; however, the list is tr

R./Fincham, V.J.; Wyke, J.A.
J. Virol. 58, 694-699, 1986

A/Title: Localization of temperature-sensitive transformation mutations and back mutator
A/Reference number: S09665; PMID:86200422; PMID:3009882

A/Accession: S09665
A/Status: nucleic acid sequence not shown

A/Molecule type: DNA
A/Residues: 231-241, 'TH', '244-287', 'G', '289-463', 'P', '465-501', 'N', '503-526 <FIN>

A/Cross-references: UNIPARC:UPI00001755F1
C/Genetics:

A/Genes: src
C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F:98-137/Domain: SH2 homology <SH2>
F:148-245/Domain: SH2 homology <SH2>

F:265-523/Domain: protein kinase homology <KIN>
 F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:295/Active site: lys #status predicted
 F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 86.3%; Score 2466; DB 2; Length 526;
 Best Local Similarity 90.3%; Pred. No. 1,1e-116;
 Matches 473; Conservative 13; Mismatches 30; Indels 8; Gaps 2;

```

QY 1 MGSNKSFKPKASQRRRLSEENVHAGAFPPASQTSKPAADGHRGSPAAFPAAEP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSNKSFKPKASQRRRLSEENVHAGAFPPASQTSKPAADGHRGSPAAFPAAEP 58
QY 61 KLGGFNSSDPTVNSPQAGALAGGVTTFVALYDYESRETDLSFKKERLQIVNNTKVD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 59 KLFWGFNTSDTVNSPQAGALAGGVTTFVALYDYESRETDLSFKKERLQIVNNTKVD 114
QY 121 VREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESRLLLNAENPGTF 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 --EGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESRLLLNAENPGTF 172
QY 181 LVRESETTKAYCISVDFPNAGKLVNKHKKIRLDSGFFYITSRTOFNSIQQLVAYYSK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 LVKSEETTKAYCISVDFPNAGKLVNKHKKIRLDSGFFYITSRTOFNSIQQLVAYYSK 232
QY 241 HAAGLCHRLTTCVPTSPQOTGLAKDAWETPRESLREVLGQCCFGEVWMTGNTTRV 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 233 HAAGLCHRLANVCPTSPQOTGLAKDAWETPRESLREVLGQCCFGEVWMTGNTTRV 292
QY 301 AITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLVAVVSEEPYIVTETYNKGSLLDFLKG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 293 AITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLVAVVSEEPYIVTETYNKGSLLDFLKG 352
QY 361 ETGKYRLPOLVMSAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 353 EMGKYRLPOLVMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 412
QY 421 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKGRVPPGVNREVL 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 413 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKGRVPPGVNREVL 472
QY 481 DVERGYRMPCEPCEPSLHDLMOQCWRKPEERPTREYLAQFL 524
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 473 DVERGYRMPCEPCEPSLHDLMOQCWRKPEERPTREYLAQFL 516

```

RESULT 11

TVFVR
 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)

C/Species: Rous sarcoma virus
 C/Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
 C/Accession: A00632
 R/Schwarz, D.; Tizard, R.; Gilbert, W.
 submitted to the Nucleic Acid Sequence Database, September 1982
 A/Reference number: A00632
 A/Accession: A00632
 A/Molecule type: genomic RNA
 A/Residues: 1-526 <SCH>
 A/Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63
 A/Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and R/Well, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
 Nature 291, 675-677, 1981
 A/Title: Homologous tyrosine phosphorylation sites in transformation-specific gene products
 A/Reference number: A38019; MUID:81220979; PMID:6264320
 A/Contents: annotation; phosphorylation site
 C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; 1lipoprotein; myristylation; and
 F:148-245/Domain: SH2 homology <SH2>
 F:265-523/Domain: protein kinase homology <KIN>

F:273-281/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:295/Active site: lys #status predicted
 F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experim

Query Match 86.1%; Score 2463; DB 1; Length 526;
 Best Local Similarity 90.1%; Pred. No. 1,1e-116;
 Matches 472; Conservative 13; Mismatches 31; Indels 8; Gaps 2;

```

QY 1 MGSNKSFKPKASQRRRLSEENVHAGAFPPASQTSKPAADGHRGSPAAFPAAEP 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSNKSFKPKASQRRRLSEENVHAGAFPPASQTSKPAADGHRGSPAAFPAAEP 58
QY 61 KLGGFNSSDPTVNSPQAGALAGGVTTFVALYDYESRETDLSFKKERLQIVNNTKVD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 59 KLFWGFNTSDTVNSPQAGALAGGVTTFVALYDYESRETDLSFKKERLQIVNNTKVD 114
QY 121 VREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESRLLLNAENPGTF 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 --EGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRRESRLLLNAENPGTF 172
QY 181 LVRESETTKAYCISVDFPNAGKLVNKHKKIRLDSGFFYITSRTOFNSIQQLVAYYSK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 LVKSEETTKAYCISVDFPNAGKLVNKHKKIRLDSGFFYITSRTOFNSIQQLVAYYSK 232
QY 241 HAAGLCHRLTTCVPTSPQOTGLAKDAWETPRESLREVLGQCCFGEVWMTGNTTRV 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 233 HAAGLCHRLANVCPTSPQOTGLAKDAWETPRESLREVLGQCCFGEVWMTGNTTRV 292
QY 301 AITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLVAVVSEEPYIVTETYNKGSLLDFLKG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 293 AITLKPGTMSPEAFLOEAQVMKKLRHEKLVQLVAVVSEEPYIVTETYNKGSLLDFLKG 352
QY 361 ETGKYRLPOLVMSAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 353 EMGKYRLPOLVMAAQIASGMAYVERMYVHRDLRAANILVGENLVCKVADFGIARLIE 412
QY 421 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKGRVPPGVNREVL 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 413 DNEYTARQAGKFPKWTAPAPALYGRFTIKSDWVSFEILLTELTKGRVPPGVNREVL 472
QY 481 DVERGYRMPCEPCEPSLHDLMOQCWRKPEERPTREYLAQFL 524
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 473 DVERGYRMPCEPCEPSLHDLMOQCWRKPEERPTREYLAQFL 516

```

RESULT 12

S26420
 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C/Species: Rous sarcoma virus
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
 C/Accession: S26420; S20676
 R/Kashuba, V.I.; Rynditch, A.V.; Doscalova, V.; Hlozaneck, I.; Zubak, S.V.; Kavanan, V.M.
 submitted to the EMBL Data Library, September 1992
 A/Description: Molecular Cloning and DNA sequence analysis of duck-adapted variant of Rous sarcoma virus
 A/Reference number: S26417
 A/Accession: S26420
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-526 <KAS>
 A/Cross-references: UNIPROT:Q07461; UNIPARC:UPI000010512B; EMBL:X68524; NID:961903; PIDN
 R/Kashuba, V.I.; Serge, Z.V.; Rynditch, A.V.; Kavanan, V.M.; Hlozaneck, I.
 submitted to the EMBL Data Library, March 1990
 A/Reference number: S20676
 A/Accession: S20676
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-526 <KAS>
 A/Cross-references: UNIPARC:UPI000010512B; EMBL:X51861; NID:961896; PIDN:CAA36154.1; PID
 C/Genetics:
 A/Gene: src
 C/Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
 C/Keywords: ATP; autophosphorylation; blocked amino end; 1lipoprotein; myristylation; phos

A:Residues: 1-532 <STE>
A:Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:004822; NID:g21
R:Steele, R.E.; Choon, R.; Rai, B.B.A.; Winkler, S.T.; Unger, T.F.
Oncogene 7, 2345-2350, 1992
A>Title: Structural organization of a src gene from xenopus laevis.
A:Reference number: 151564; MUID:93064714; PMID:11437158
A:Accession: 151564
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-113 <ST2>
A:Cross-references: UNIPARC:UPI00000FD97A; GB:M33646; NID:g214808; PIDN:AAA4963.1; PID:
C:Genetics:
A:Insertions: 80/1
C:Superfamily: protein kinase homology; SH2 homology; SH3 homology
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F:87-136/Domain: SH3 homology <SH3>
F:147-244/Domain: SH2 homology <SH2>
F:264-522/Domain: protein kinase homology <KIN>
F:272-280/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:294/Active site: Lys #status predicted
F:415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 85.44; Score 2442.5; DB 1; Length 532;
Best Local Similarity 85.54; Pred. No. 1,7e-115;
Matches 467; Conservative 27; Mismatches 33; Indels 19; Gaps 4;

QY 1 MGSNKSXPXASQRRSLSEPNVHAGAFPAASQTPSKASDGHGSPSAF-----VP 55
DB 1 MGATSKSPREGRSRSLDIVEGSHQPTSLASQTNNK--SLDSHRPAPQFGNCDLT 58
QY 56 PAAPKPLFGFNSSDTYSPOKAGALAGVTTFPALYDYSRTETDLSFKKGERLQIVNN 115
DB 59 P-----FGINPSDITTSPOKTPAGVTFPALYDYSRTETDLSFKKGERLQIVNN 112
QY 116 TRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGKITRRESERLLAEN 175
DB 113 T-----EGDMLKRLSSSGQTGYIPSNVAPSDSIQAEWYFGKITRRESERLLEEN 166
QY 176 PRGTFVLRSEETTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLOLV 235
DB 167 PRGTFVLRSEETTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGFYITSRTOFNSLOLV 226
QY 236 AYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVLCQGCGEYVMGTNN 295
DB 227 AYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEVLCQGCGEYVMGTNN 286
QY 296 GTTRVVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYITEVMNKGSL 355
DB 287 GTTRVVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSEEPYIYITEVMNKGSL 346
QY 356 DFLKGETGKYLRLPOLVDMASQIASGMAVVERMYVARDLRANILVGENLVCKVADFG 415
DB 347 DFLKGETGKYLRLPOLVDMASQIASGMAVVERMYVARDLRANILVGENLVCKVADFG 406
QY 416 ARLIDNEYTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGIILTELTTRGRVPYGMV 475
DB 407 ARLIDNEYTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGIILTELTTRGRVPYGMV 466
QY 476 NREVLDOVERGYMPCPECPESLHDLMOCKMKREPERPTFEYLQFLDYFTSTPEY 535
DB 467 NREVLDOVERGYMPCPECPESLHDLMOCKMKREPERPTFEYLQFLDYFTSTPEY 526
QY 536 QPGENTL 541
DB 527 QPGDNL 532

RESULT 15
S52313
protein-tyrosine kinase (BC 2.7.1.112) src - Rous sarcoma virus
C:Species: Rous sarcoma virus
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004

C:Accession: S52313
R:Tokoyan, A.; Yatsula, B.; Shurman, M.; Molinova, E.; Kaverina, I.; Musackina, E.; Leeb
submitted to the EMBL Data Library, January 1995
A:Description: Two new isoforms of v-src oncogene isolated from low and high metastatic R
A:Reference number: S52313
A:Accession: S52313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <TIT>
A:Cross-references: UNIPROT:Q86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:9663083; PIDN
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology,
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F:108-157/Domain: SH3 homology <SH3>
F:168-265/Domain: SH2 homology <SH2>
F:285-543/Domain: protein kinase homology <KIN>
F:293-301/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:315/Active site: Lys #status predicted
F:436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.04; Score 2431; DB 2; Length 545;
Best Local Similarity 86.84; Pred. No. 6.6e-115;
Matches 472; Conservative 15; Mismatches 29; Indels 28; Gaps 4;

QY 1 MGSNKSXPXASQRRSLSEPNVHAGAFPAASQTPSK-----PAS----- 42
DB 1 MGSNKSXPXASQRRSLSEPNVHAGAFPAASQTPSK-----PAS----- 58
QY 43 --ADGHRPSAAFPVPAAPKPLFGFNSSDTYSPOKAGALAGVTTFPALYDYSRTET 100
DB 59 AARDTRHTPSPRSFGTYANERKLFQDPFTSDTYSPOKAGALAGVTTFPALYDYSRTET 118
QY 101 DLSFKGERLQIVNNTRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGK 160
DB 119 DLSFKGERLQIVNNTRKVDVREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEWYFGK 172
QY 161 ITRRESERLLMNPNGTFLVRESSETTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGF 220
DB 173 ITRRESERLLMNPNGTFLVRESSETTKGAYCLSVSDPDNAKGLNVKHKIRKLDGSGF 232
QY 221 YITSRTQFNSLOLVAVYYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEV 280
DB 233 YITSRTQFNSLOLVAVYYSKADGICHRLLTYCPTSKPOTQGLADAMEIPRESLRLEV 292
QY 281 LGGCGFGEYVMGTNNGTTRVVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSE 340
DB 293 LGGCGFGEYVMGTNNGTTRVVAIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQLYAVVSE 352
QY 341 PIYIYITEVMNKGSLDPLKGETGKYLRLPOLVDMASQIASGMAVVERMYVARDLRAN 400
DB 353 PIYIYITEVMNKGSLDPLKGETGKYLRLPOLVDMASQIASGMAVVERMYVARDLRAN 412
QY 401 LVGENLVCKVADFGIARLIDNEYTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGIIL 460
DB 413 LVGENLVCKVADFGIARLIDNEYTAROGAKFPIKMTAPEALYGRFTIKSDVMSFGIIL 472
QY 461 TELTTGRVVPYGMVNVREVLDOVERGYMPCPECPESLHDLMOCKMKREPERPTFEYL 520
DB 473 TELTTGRVVPYGMVNVREVLDOVERGYMPCPECPESLHDLMOCKMKREPERPTFEYL 532
QY 521 QAFU 524
DB 533 QAFU 536

Search completed: June 5, 2006, 17:16:39
Job time : 23.7202 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:01:48 ; Search time 155.049 Seconds

(without alignments)
3227.587 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSXPKXASQRRSLRP.....AFLEDFYTSRTPQYQPENL 541

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2854	99.8	540	1 SRC_MOUSE	P05480 mus musculus
2	2854	99.8	541	2 Q2M414_MOUSE	Q2M414 mus musculus
3	2837.5	99.2	542	2 Q9J310_RAT	Q9J310 ratius norv
4	2820.5	98.7	542	2 Q76P87_HUMAN	Q76P87 homo sapien
5	2812	98.4	535	2 Q80XU2_MOUSE	Q80XU2 mus musculus
6	2795	97.8	535	2 Q3UXD6_MOUSE	Q3UXD6 mus musculus
7	2773.5	97.0	535	1 SRC_HUMAN	P12931 homo sapien
8	2772.5	97.0	535	1 SRC_RAT	Q9WUD9 ratius norv
9	2707.5	94.7	523	2 Q45QJ2_RAT	Q45QJ2 ratius norv
10	2643	92.4	532	1 SRC_CHICK	P00523 gallus galli
11	2598	90.9	566	1 SRC_AVIS2	P15054 avian sarco
12	2591	90.6	567	1 SRC_AVIS	P14084 avian sarco
13	2590	90.6	587	2 Q64817_GRETR	Q64817 avian sarco
14	2576	90.1	536	1 SRC_AVIS1	P14085 avian sarco
15	2510	87.8	525	1 SRC_RSUSA	P00524 avian sarco
16	2510	87.8	525	1 SRC_RSUSA	P00524 avian sarco
17	2479	86.7	526	2 Q60567_GRETR	Q60567 rous sarcom
18	2468	86.3	537	1 SRC_RSUSA	P25020 rous sarcom
19	2468	86.3	537	2 Q7ZX73_XENLA	Q7ZX73 xenopus lae
20	2467	86.3	526	2 Q64994_GRETR	Q64994 rous sarcom
21	2465.5	86.2	532	2 Q5MA59_XENTR	Q5MA59 xenopus tro
22	2465	86.2	526	2 Q93080_GRETR	Q93080 rous sarcom
23	2463.5	86.2	523	2 Q85477_GRETR	Q85477 rous sarcom
24	2463.5	86.2	535	2 Q92957_RSUSA	Q92957 rous sarcom
25	2463	86.1	526	2 Q92806_GRETR	Q92806 rous sarcom
26	2462	86.1	525	1 SRC_RSUSA	P63185 rous sarcom
27	2458	86.0	525	1 SRC_RSUSA	P00526 rous sarcom
28	2452	85.8	526	2 Q64993_RSUSA	Q64993 rous sarcom
29	2448	85.6	526	2 Q07461_GRETR	Q07461 rous sarcom
30	2443.5	85.5	532	2 Q2TAR1_XENLA	Q2TAR1 xenopus lae
31	2439.5	85.3	531	1 SRC2_XENLA	P13116 xenopus lae

32	2434.5	85.2	531	1 SRC1_XENLA	P13115 xenopus lae
33	2431	85.0	545	2 Q86352_GRETR	Q86352 rous sarcom
34	2428	84.9	546	2 Q86353_GRETR	Q86353 rous sarcom
35	2394.5	83.8	522	1 SRC_RSUSA	P31693 rous sarcom
36	2311.5	80.8	534	2 Q6EWH0_BRARE	Q6EWH0 brachydantio
37	2182	76.3	527	2 Q91952_XIPXI	Q91952 xiphophorus
38	2124	74.3	537	2 Q6PF70_XENLA	Q6PF70 xenopus lae
39	2120	74.2	537	2 Q640S9_XENTR	Q640S9 xenopus tro
40	2114	73.9	537	2 Q498G3_XENLA	Q498G3 xenopus lae
41	2113	73.9	536	1 YES_XENLA	P10936 xenopus lae
42	2113	73.9	541	2 Q8C762_MOUSE	Q8C762 mus musculus
43	2113	73.9	541	2 Q99PW1_RAT	Q99PW1 ratius norv
44	2108	73.7	541	2 Q3TJ17_MOUSE	Q3TJ17 mus musculus
45	2106.5	73.7	542	1 YES_HUMAN	P07947 homo sapien

ALIGNMENTS

RESULT 1
SRC_MOUSE STANDARD; PRT; 540 AA.
ID SRC_MOUSE
AC P05480;
DT 01-NOV-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 2.
DT 07-MAR-2006, entry version 65.
DE Neuronal proto-oncogene tyrosine-protein kinase Src (BC 2.7.1.112)
DE (p60-Src) (c-Src) (pp60c-src).
GN Name=Src;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MENA].
RC STRAIN=BALB/c;
RX MEDLINE=87263406; PubMed=2440106;
RA Martinez R., Machev-Prevot B., Bernards A., Baltimore D.;
RT "Neuronal pp60c-src contains a six-amino acid insertion relative to
its non-neuronal counterpart.";
RL Science 237:411-415(1987).
RN [2]
RP INTERACTION WITH DDEF1/ASAP1.
RX MEDLINE=99038209; PubMed=9819391;
RA Brown M.T., Andrade J., Radhakrishna H., Donaldson J.G., Cooper J.A.,
Randazzo P.A.;
RT "ASAP1, a phospholipid-dependent arf GTPase-activating protein that
associates with and is phosphorylated by Src.";
RL Mol. Cell. Biol. 18:7038-7051(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
tyrosine phosphate.
CC -1- INTERACTION: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC -1- SUBUNIT: Interacts with DDEF1/ASAP1 via its SH3 domain.
CC -1- PTM: Phosphorylated on Tyr-534 by c-Src kinase (CSK). The
phosphorylated form is termed pp60c-src. The phosphorylated tail
interacts with the SH2 domain thereby repressing kinase activity
(by similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.

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EMBL; M17031; AAA40135.1; -; mRNA.
DR PIR; A43610; A43610.
DR HSSP; P12931; 1A09.
DR SMR; P05480; 85-540.
DR IntAct; P05480; -;
DR Ensembl; ENSMUSG0000027646; Mus musculus.

DR	MG1; MG1.98397; Src.		
DR	GO; GO:0005515; F:protein binding; IPI.		
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IMP.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IDA.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR000980; SH2.		
DR	InterPro; IPR001452; SH3.		
DR	InterPro; IPR001243; Tyr_kinase.		
DR	InterPro; IPR008266; Tyr_kinase_AS.		
DR	Pfam; PF07714; Kinase_Tyr/1.		
DR	Pfam; PF00017; SH2; 1.		
DR	Pfam; PF00018; SH3_1; 1.		
DR	PRINTS; PRO0401; SH2DOMAIN.		
DR	PRINTS; PRO0452; SH3DOMAIN.		
DR	PRINTS; PRO0109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	ProDom; PD000093; SH2; 1.		
DR	ProDom; PD000066; SH3; 1.		
DR	SMART; SMO0252; SH2; 1.		
DR	SMART; SMO0326; SH3; 1.		
DR	SMART; SMO0219; TyKc; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS50001; SH2; 1.		
DR	PROSITE; PS50002; SH3; 1.		
KV	ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;		
KV	phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;		
KM	tyrosine-protein kinase.		
FT	INT MET	0	
FT	CHAIN	1	540
FT			By similarity.
FT			Neuronal proto-oncogene tyrosine-protein kinase Src.
FT			/FTId=PRO_000088142.
FT	DOMAIN	82	149
FT	DOMAIN	155	252
FT	DOMAIN	274	527
FT	NP BIND	280	288
FT	ACT SITE	393	393
FT	BINDING	302	302
FT	MOD_RRS	423	423
FT			phosphotyrosine (by autocatalysis) (By similarity).
FT	MOD_RRS	534	534
FT	LIPID	1	1
FT	SEQUENCE	540 AA;	60487 MM;
Q			N-myristoyl glycine (By similarity).
Q			44ABA0EB55D752AA CRC64;

Query Match	99.84%	Score 2854	DB 1	Length 540
Best Local Similarity	100.0%	Pred. No. 2.5e-160		
Matches 540	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	2	GSNKKPKDASQRRSLLEPSENVHAGAGAFPASQTPSPKASADGHRGSAAFVPPAAEPK	61	
Db	1	GSNKKPKDASQRRSLLEPSENVHAGAGAFPASQTPSPKAPADGHRGSAAFVPPAAEPK	60	
QY	62	LFQGFNSSDVTSPQAGALAGVTFVALYDYBSRTETDLSFKKGERLQIVNTRKVDY	121	
Db	61	LFQGFNSSDVTSPQAGALAGVTFVALYDYBSRTETDLSFKKGERLQIVNTRKVDY	120	
QY	122	REGQWMLAHSISTQGTGYIPSNVYAPSPSIQAEERYFEKTIIRREBERLLNAENRGTFLL	181	
Db	121	REGQWMLAHSISTQGTGYIPSNVYAPSPSIQAEERYFEKTIIRREBERLLNAENRGTFLL	180	
QY	182	VRESEETTKGAYCLSVDPDNKAGLVNKKYIKRKLDGSGFYTTSRQFNSLOOLVAYYSKH	241	
Db	181	VRESEETTKGAYCLSVDPDNKAGLVNKKYIKRKLDGSGFYTTSRQFNSLOOLVAYYSKH	240	
QY	242	ADGLCHRLITVCPSPKPTQGLADAMEIPRESIRLEVLKLGCGCGEYVMGTWGTTFVA	301	
Db	241	ADGLCHRLITVCPSPKPTQGLADAMEIPRESIRLEVLKLGCGCGEYVMGTWGTTFVA	300	
QY	302	IKTILKPGTMSAEALQEOAQVWKKLRHEKLVOLYAVVSEEPYIYVTEYNKKSLLDFLKEG	361	
Db	301	IKTILKPGTMSAEALQEOAQVWKKLRHEKLVOLYAVVSEEPYIYVTEYNKKSLLDFLKEG	360	

QY	362	TGKTLRLPOLVDM	SAQISGAAYVERNNYVRHDL	PAANILVGENLVCKRADGFLARLIE	421
QY	361	TGKTLRLPOLVDM <td>SAQISGAAYVERNNYVRHDL<th>PAANILVGENLVCKRADGFLARLIE</th><td>420</td></td>	SAQISGAAYVERNNYVRHDL <th>PAANILVGENLVCKRADGFLARLIE</th> <td>420</td>	PAANILVGENLVCKRADGFLARLIE	420
QY	422	NEYTAROGAKPPIKWT	APALYGRFTLKS	DVMSFGILLTELTTKGRVVP	PGWVNRVEDL 481
QY	421	NEYTAROGAKPPIKWT	APALYGRFTLKS	DVMSFGILLTELTTKGRVVP	PGWVNRVEDL 480
QY	482	QVERGYRMPCEPCE	SHDLMQCMRKEPBERPTE	YLQAFLEDTSTSEPOYOGENTL	541
QY	481	QVERGYRMPCEPCE	SHDLMQCMRKEPBERPTE	YLQAFLEDTSTSEPOYOGENTL	540
RESULT 2					
Q2M414	MOUSE	PRELIMINARY	PRT	541 AA.	
ID	Q2M414	MOUSE	PRELIMINARY	PRT	541 AA.
AC	Q2M414				
DT	21-FEB-2006				
DT	21-FEB-2006				
DT	21-FEB-2006				
DT	21-FEB-2006				
DE	Src				
GN	Name=Src				
OS	Mus musculus (Mouse)				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
CC	Muroidea; Muridae; Murinae; Mus.				
CC	NCBI_TaxID=10090;				
CC	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=CAST/EJ; TISSUE=Brain;				
RA	Farber C.R., Correa P.M., Medrano J.F.;				
RT	"Characterization of quantitative trait loci influencing growth and				
RL	adiposity using congenic mouse strains."				
RL	Submitted (Jan-2005) to the EMBL/Genbank/DBJ databases.				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NoDerivs License				
CC	-----				
DR	EMBL; AY902331; AAX90616.1; -; Genomic DNA.				
DR	SEQUENCE 541 AA; 60645 MW; 0534AF027783BCF CRC64;				
DR	-----				
QY	Query Match				
QY	Best Local Similarity 99.8%; Score 2854; DB 2; Length 541;				
QY	Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0				
QY	1	MGSNKSRPKDASQRRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAFVPPAAEP	60		
QY	1	MGSNKSRPKDASQRRRLSPSENVHAGAGAPASQTPSKPASADGHRGSAFVPPAAEP	60		
QY	61	KLPGFNSDPVTSPOPAGALAGVTFVVALYDVSFRFETLSFKKGRLOLVNTRKVD	120		
QY	121	VRESDWMLAHSLSGQGTGYPISNVAPSDSIOAEWYRGKITRRESERLLNAENPRGT	180		
QY	121	VRESDWMLAHSLSGQGTGYPISNVAPSDSIOAEWYRGKITRRESERLLNAENPRGT	180		
QY	181	LVRESFTTGAYCLSVSDFDNAKGLNVGHYIKRKIDSGGFYITSRTQFNSLQOLVAAYSK	240		
QY	181	LVRESFTTGAYCLSVSDFDNAKGLNVGHYIKRKIDSGGFYITSRTQFNSLQOLVAAYSK	240		
QY	241	HADGLCHRLTTCVCTSPKPTQGLAKDAEIPRESRLREVKLGQCGFGEVMMGTNGTTRV	300		
QY	241	HADGLCHRLTTCVCTSPKPTQGLAKDAEIPRESRLREVKLGQCGFGEVMMGTNGTTRV	300		
QY	301	AIKTLKGTMSPEAFLOEAOVMKKLRHKLVLQVLAVSEEPYIYTEVNNKSLDLFLKG	360		
QY	301	AIKTLKGTMSPEAFLOEAOVMKKLRHKLVLQVLAVSEEPYIYTEVNNKSLDLFLKG	360		
QY	361	ETGKTLRLPOLVDM	SAQISGAAYVERNNYVRHDL	PAANILVGENLVCKRADGFLARLIE	420
QY	361	ETGKTLRLPOLVDM	SAQISGAAYVERNNYVRHDL	PAANILVGENLVCKRADGFLARLIE	420

QY 421 DNEYTAROGAKPPIKWTAPAPALYGRFTIKSDVWSFGILLTETLTGKRVPPGVNREV 480
DB 421 DNEYTAROGAKPPIKWTAPAPALYGRFTIKSDVWSFGILLTETLTGKRVPPGVNREV 480
QY 481 DQVERGYRMPCEPCESLHDLMCQCRKEPERPTEYLQAFLEDFSTSTEPQYQGEN 540
DB 481 DQVERGYRMPCEPCESLHDLMCQCRKEPERPTEYLQAFLEDFSTSTEPQYQGEN 540
QY 541 L 541
DB 541 L 541
RESULT 3
Q9J10_RAT PRELIMINARY; PRT; 542 AA.
AC Q9J10; Integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 01-OCT-2000, entry version 1.
DE Neuronal C-SRC tyrosine-specific protein kinase.
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_NUCLEOTIDE SEQUENCE.
RP MEDLINE=21148003; PubMed=1124956; DOI=10.1016/S0028-3908(00)00185-4;
RX Linden A., Storevik M., Lakso M., Haapaalo A., Lee D., Winklin J.M.,
RA Sei Y., Caestre E., Wong G.;
RT "Increased expression of neuronal Src and tyrosine phosphorylation of
NMDA receptors in rat brain after systemic treatment with MK-801.";
RL Neuropharmacology 40:469-481(2001).
[2]_NUCLEOTIDE SEQUENCE.
RP Linden A.-M., Storevik M., Lakso M., Wong G., Caestre E.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AF157016; AAF80335.1; -; mRNA.
CC HSSP; P12931; 1043.
DR Ensemble; ENSRNOG0000009495; Rattus norvegicus.
DR RCD; 620795; Src.
DR GO; GO:0016301; F:kinase activity; TAS.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Chr_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000065; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00329; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.
KM KINASE.
SQ SEQUENCE 542 AA; 60727 MM; 6AC21D6DD66B039 CRC64;
Query Match 99.2%; Score 2837.5; DB 2; Length 542;
Best Local Similarity 99.3%; Pred. No. 3.1e-179;
Matches 538; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 MGSVKSXPYKASQRRRLSESENVHAGGAPAPASQTSKSPASAGCHGSPSAFPFPAAE 59
DB 1 MGSVKSXPYKASQRRRLSESENVHAGGAPAPASQTSKSPASAGCHGSPSAFPFPAAE 60
QY PKLFGFNSSDPTVTSPPRAGLAGVTFVALDYESTETEDLSFKKGERLQIVNTRKV 119
DB 61 PKLFGFNSSDPTVTSPPRAGLAGVTFVALDYESTETEDLSFKKGERLQIVNTRKV 120
QY 120 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRSEBRLLINENPRT 179
DB 121 DVREGDWMLAHSLSGTQGYI PSNYVAPSDSIQAEWYFGKITRSEBRLLINENPRT 180
QY 180 FLVRESSTTGAYCLSYSDPNAGKLVKIKIKLDSGGFYITSRQFNSLQQLVAYYS 239
DB 181 FLVRESSTTGAYCLSYSDPNAGKLVKIKIKLDSGGFYITSRQFNSLQQLVAYYS 240
QY 240 KHADELCHRLTTCVPTSKPOTQGLAKDAWEIPRESLRELVLAGGCGEVMGTMGTTR 299
DB 241 KHADELCHRLTTCVPTSKPOTQGLAKDAWEIPRESLRELVLAGGCGEVMGTMGTTR 300
QY 300 VAIKTLKPGTMSPEAFLOEAVMKLRHEKLVQLVAVSEPIYIVTEYNNKGLLDFLK 359
DB 301 VAIKTLKPGTMSPEAFLOEAVMKLRHEKLVQLVAVSEPIYIVTEYNNKGLLDFLK 360
QY 360 GETGKYRLPOLVMSAQISGMAVERMAYVHDLPAANILVGENLYCKVADGLARLI 419
DB 361 GETGKYRLPOLVMSAQISGMAVERMAYVHDLPAANILVGENLYCKVADGLARLI 420
QY 420 EDNEYTAROGAKPPIKWTAPAPALYGRFTIKSDVWSFGILLTETLTGKRVPPGVNREV 479
DB 421 EDNEYTAROGAKPPIKWTAPAPALYGRFTIKSDVWSFGILLTETLTGKRVPPGVNREV 480
QY 480 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPTEYLQAFLEDFSTSTEPQYQGE 539
DB 481 LDQVERGYRMPCEPCESLHDLMCQCRKEPERPTEYLQAFLEDFSTSTEPQYQGE 540
QY 540 NL 541
DB 541 NL 542
RESULT 4
Q76P87_HUMAN PRELIMINARY; PRT; 542 AA.
ID Q76P87; Integrated into UniProtKB/TrEMBL.
AC Q76P87;
DT 05-JUL-2004, sequence version 1.
DT 05-JUL-2004, entry version 12.
DE 07-FEB-2006, entry version 12.
GN OTHUMP00000030931.
GN Name=SRC; ORFNames=RP5-823N20.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_NUCLEOTIDE SEQUENCE.
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL Wallis J.;
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC EMBL; AL133293; CAC10573.1; -; genomic DNA.
DR HSSP; P12931; 1A09.

DR SMR; Q76P87; 87-542.
 DR Ensembl; ENSG00000197122; Homo sapiens.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000093; Prot_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SQUINCE 542 AA; 60589 MW; C12D30FB8DC5FF6B CRC64;

Query Match 98.7%; Score 2820.5; DB 2; Length 542;
 Best Local Similarity 98.7%; Pred. No. 4.1e-178;

Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGSNKSFPKQASQRRSLSPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 59
 DB 1 MGSNKSFPKQASQRRSLSPSENVHGA-GGAFPASQTPSKPASADGHRGSAAFVPPAAE 60
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 DB 61 PKLFGGNSDVTYTPORALAGCVTFVALDYESTRTEDLSFKKGEKQIVNTRKY 120
 QY 120 DVAEGMWLAHSLSTGQTGYIPSNVYVPSDIOAEEMYPFKITRRESERILLNAENRGT 179
 DB 121 DVAEGMWLAHSLSTGQTGYIPSNVYVPSDIOAEEMYPFKITRRESERILLNAENRGT 180
 QY 180 FLVRESSETTGAYCLSVSDFDNAGKLVNKHKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 239
 DB 181 FLVRESSETTGAYCLSVSDFDNAGKLVNKHKIRKLDGSGFYITSTRTOFNSLQOLVAYYS 240
 QY 240 KAADGLCHRLTYTCPTSKPTOTGLADAMEIPRESLRLEVKCGCGCGEYVMGTNGTTR 239
 DB 241 KAADGLCHRLTYTCPTSKPTOTGLADAMEIPRESLRLEVKCGCGEYVMGTNGTTR 300
 QY 300 VALKTLKPGMSBEAFLOEAOVMKCLRHEKLVOLYAVVSEPTIYIVEMNKKSLIDELK 359
 DB 301 VALKTLKPGMSBEAFLOEAOVMKCLRHEKLVOLYAVVSEPTIYIVEMNKKSLIDELK 360
 QY 360 GETGKTLRLPOLVDMSQIASGMAVYRMNYYHRDLAANIIVGENLVCKVADFGIARLI 419
 DB 361 GETGKTLRLPOLVDMSQIASGMAVYRMNYYHRDLAANIIVGENLVCKVADFGIARLI 420
 QY 420 EDNEYTARQCAKPIPKTAPBAALYGRFTTKSDVMSGILLTELTTKGRVPYGMVNRREV 479
 DB 421 EDNEYTARQCAKPIPKTAPBAALYGRFTTKSDVMSGILLTELTTKGRVPYGMVNRREV 480
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 DB 481 LDQVERGYRMPCEPCESLHDLCCOCMKREPERPFVEYLOAFLNEYFTSTEPQVQGE 540
 QY 540 NL 541
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DB 541 NL 542
 RESULT 5
 ID Q80XU2_MOUSE PRELIMINARY; PRT; 535 AA.
 AC Q80XU2;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Rous sarcoma oncogene, isoform 2.
 OS Name=Src;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=salivary gland;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusla K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulvaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
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 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Skalska D.E.,
 RA Schenker A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=salivary gland;
 RG NIH MGC Project;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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 CC
 EMBL; BC039953; AAH39953.1; -; mRNA.
 DR HSSP; P12931; 1043.
 DR SMR; Q80XU2; 86-535.
 DR Ensembl; ENSMUSG00000027646; Mus musculus.
 DR MGI; MGI:98397; Src.
 DR GO; GO:0005515; F-protein binding; IPI.
 DR GO; GO:0004713; F-protein serine/threonine kinase activity; RCA.
 DR GO; GO:0004713; F-protein-tyrosine kinase activity; IMP.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
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 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000093; Prot_kinase; 1.
 DR ProDom; PD000066; SH3; 1.

RA Nagashima T., Nimata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius U.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid Y., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempke C.A., Setton M., Shindala K.,
RA Sultana R., Takemaidy Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vezardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yamaigawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sasaki K., Sasaki D., Shibata K., Shingawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y. ;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." ;
RL Nature 420:563-573(2002).
[5]
RP NOCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=21085660; PubMed=1121781; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi T., Fukuda S.,
RA Saito K., Iizawa M., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Satoh T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaent T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo I., Nikido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sasaki K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein W.J., Bull C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Guertelich S., Hill D., Hofmann M., Hume D., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama M., Mazzarelli J., Mombaers P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y. ;
RT "Functional annotation of a full-length mouse cDNA collection." ;
RL Nature 409:685-690(2001).
[6]
RP NOCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes." ;
RL Genome Res. 10:1617-1630(2000).
[7]
RP NOCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Katsunaka T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiyagi K.,
RA Fujitake S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watanaki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y. ;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer." ;
RL Genome Res. 10:1757-1771(2000).
[8]
RP NOCLECTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Areakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida Y., Imamura K., Imocani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shitaki T., Tagami Y., Tagami Y., Waki K., Wataniki A.,
RA Yamamatsu M., Hayashizaki Y. ;

Query Match	Similarity	Score	DB 2	Length	535
Best Local	98.2%	0	Match No. 2e-176		
Matches	531	Conservative	0	Mismatches	4
				Indels	6
				Gaps	1
CC	Submitted (MAR-2004)	to the EMBL/GenBank/DBJ databases.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NonDerivs License				
CC	-----				
DR	EMBL: AK146056; BAE26865.1; -; mRNA.				
DR	MGI: 98397; Src.				
DR	GO: 0005515; F:protein binding, IPI.				
DR	GO: 0004674; F:protein serine/threonine kinase activity; RCA.				
DR	GO: 0004713; F:protein-tyrosine kinase activity; IMP.				
DR	GO: 0006466; P:protein amino acid phosphorylation; IDA.				
DR	InterPro: IPR00719; Prot kinase.				
DR	InterPro: IPR02290; Ser_Thr_kinase.				
DR	InterPro: IPR00980; SH2.				
DR	InterPro: IPR01452; SH3.				
DR	InterPro: IPR01245; Tyr_kinase.				
DR	InterPro: IPR008266; Tyr_kinase_AS.				
DR	Pfam: PF00714; Pkinase_Tyr. 1.				
DR	Pfam: PF00017; SH2; 1.				
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DR	PRINTS: PR00401; SH2DOMAIN.				
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DR	PRINTS: PR00109; TYRKINASE.				
DR	ProDom: PD000001; Prot_kinase; 1.				
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DR	SMART: SM00326; SH3; 1.				
DR	SMART: SM00219; TyrcK; 1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.				
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QY	301	AIKTLKPGTMSPEAFLOEAQVMKKLRHEKLVQVLAAYVSEEDPIYITEYMNKGSLLDFLKG	360		
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QY	421	DNEYTAAGAKAFPIKMTAPAEALIGRFITKSDWSFGILLTELTTKGVVPIPGMWNREVL	480		
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QY	481	DQVRGVRMPCCPCEPSILDMQCRKKEEERPTFEYLAQFLADYPTSTEPQYQPEEN	540		

Db 475 DQYERGRMCPPECPSLMDMCMQCRKREPERETFEYLOAFEDFTSTEPYQFGEN 534
 QY 541 L 541
 Db 535 L 535

RESULT 7
 SRC HUMAN STANDARD; PRT; 535 AA.
 ID MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 AC Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 DT 01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 2.
 DT 07-MAR-2006, entry version 75.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-Src) (p60c-src).
 GN Name=SRC; Synonyms=SRC1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffam D.V., Griffiths C., Griffiths M.N.D., Gilliland R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jeronch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leveasleho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Pratchinham S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B.,
 RA Swan R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Beek S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Kizywiniski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.T.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 1-184 (ISOFORM 1).
 RX MEDLINE=87257903; PubMed=3299057;
 RA Tanaka A., Gibbs C.P., Arthur R.R., Anderson S.K., Kung H.-J.,
 RA Fujita D.J.;
 RT "DNA sequence encoding the amino-terminal region of the human c-src
 RT protein: implications of sequence divergence among src-type kinase
 RT oncogenes.";
 RL Mol. Cell. Biol. 7:1978-1983(1987).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 185-535 (ISOFORM 1).
 RX MEDLINE=85213483; PubMed=2582238;
 RA Anderson S.K., Gibbs C.P., Tanaka A., Kung H.-J., Fujita D.J.;
 RT "Human cellular src gene: nucleotide sequence and derived amino acid
 RT sequence of the region coding for the carboxy-terminal two-thirds of
 RT p60c-src.";
 RL Mol. Cell. Biol. 5:1122-1129(1985).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 97-138 (ISOFORM 2).
 RX MEDLINE=90040822; PubMed=2681803;
 RA Pyper J.M., Bolen J.B.;
 RT "Neuron-specific splicing of C-SRC RNA in human brain.";
 RL J. Neurosci. Res. 24:89-96(1989).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 375-535 (ISOFORM 1).
 RX MEDLINE=85187981; PubMed=2581127;
 RA Parker R.C., Mardon G., Lebo R.V., Varnus H.E., Bishop J.M.;
 RT "Isolation of duplicated human c-src genes located on chromosomes 1
 RT and 20.";
 RL Mol. Cell. Biol. 5:831-838(1985).
 RN [7]
 RP ALTERNATIVE SPLICING.
 RX PubMed=1691439;
 RA Pyper J.M., Bolen J.B.;
 RT "Identification of a novel neuronal C-SRC exon expressed in human
 RT brain.";
 RL Mol. Cell. Biol. 10:2035-2040(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 85-535.
 RX MEDLINE=97177105; PubMed=9024657; DOI=10.1038/385595a0;
 RA Xu W., Harrison S.C., Eck M.J.;
 RT "Three-dimensional structure of the tyrosine kinase c-Src.";
 RL Nature 385:595-602(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 144-248.
 RX MEDLINE=97317069; PubMed=9174343; DOI=10.1021/b1970019n;
 RA Charlifson P.S., Shevchuk L.M., Rocque W., Hummel C.W., Jordan S.R.,
 RA Mohr C., Pacofsky G.J., Peel M.R., Rodriguez M., Sternbach D.D.,
 RA Consler T.G.;
 RT "Peptide ligands of p60(c-src) SH2 domains: a thermodynamic and
 RT structural study.";
 RL Biochemistry 36:6283-6293(1997).
 RN [10]
 RP STRUCTURE BY NMR OF 203-248.
 RX MEDLINE=95161382; PubMed=7532003;
 RA Xu R.X., Word J.M., Davis D.G., Rink M.J., Willard D.H. Jr.,
 RA Gampe R.T. Jr.;
 RT "Solution structure of the human p60c-src SH2 domain complexed with a
 RT phosphorylated tyrosine pentapeptide.";
 RL Biochemistry 34:2107-2121(1995).
 CC -1- CATALYTIC ACTIVITY. ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- INTERACTION:
 CC G9VNF1:Cent3 (xeno); NDExp=3; InAct=EBI-621482, EBI-621463;
 CC G9Y6R3:IKBK; NDExp=1; InAct=EBI-621482, EBI-81279;
 CC O60749:Kdrbel (xeno); NDExp=1; InAct=EBI-621482, EBI-519077;
 CC -1- ALTERNATIVE PRODUCTS:
 CC Evnt=Alternative splicing; Named isoforms=2;
 CC Name=1;

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CC      Isoleu=PI2931-1; Sequence=Displayed;
CC      Name=2;
CC      -1- P1M: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
CC      phosphorylated form is termed pp60c-src. The phosphorylated tail
CC      interacts with the SH2 domain thereby repressing kinase activity.
CC      -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 SH2 domain.
CC      -1- SIMILARITY: Contains 1 SH3 domain.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivative License
CC
DR      EMBL: A133293; CAC34523.1; -; Genomic_DNA.
DR      EMBL: BC011566; AAH11566.1; -; mRNA.
DR      EMBL: BC051270; AAH51270.2; -; mRNA.
DR      EMBL: M03218; AAA60584.1; -; Genomic_DNA.
DR      EMBL: M16237; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M16243; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M16244; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M16245; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03212; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03213; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03214; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03215; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03216; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M03217; AAA60584.1; JOINED; Genomic_DNA.
DR      EMBL: M02647; CAA26485.1; -; Genomic_DNA.
DR      EMBL: M03995; CAA26485.1; JOINED; Genomic_DNA.
DR      EMBL: M03996; CAA26485.1; JOINED; Genomic_DNA.
DR      EMBL: M03997; CAA26485.1; JOINED; Genomic_DNA.
DR      EMBL: M03998; CAA26485.1; JOINED; Genomic_DNA.
DR      EMBL: M03999; CAA26485.1; JOINED; Genomic_DNA.
DR      EMBL: X04000; CAA26485.1; JOINED; Genomic_DNA.
DR      PIR: A26891; TVHUSC.
DR      PDB: 1A07; X-ray; A/B=143-248.
DR      PDB: 1A08; X-ray; A/B=143-248.
DR      PDB: 1A09; X-ray; A/B=143-248.
DR      PDB: 1A1A; X-ray; A/B=143-248.
DR      PDB: 1A1B; X-ray; A/B=143-248.
DR      PDB: 1A1C; X-ray; A/B=143-248.
DR      PDB: 1A1E; X-ray; A/B=143-248.
DR      PDB: 1FMK; X-ray; A/B=143-248.
DR      PDB: 1HCS; NMR; B=143-248.
DR      PDB: 1HCT; NMR; B=143-248.
DR      PDB: 1KSW; X-ray; A=85-535.
DR      PDB: 1O41; X-ray; A=144-251.
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DR      PDB: 1O44; X-ray; A=144-251.
DR      PDB: 1O45; X-ray; A=144-251.
DR      PDB: 1O46; X-ray; A=144-251.
DR      PDB: 1O47; X-ray; A=144-251.
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DR      PDB: 1O49; X-ray; A=144-251.
DR      PDB: 1O4A; X-ray; A=144-251.
DR      PDB: 1O4B; X-ray; A=144-251.
DR      PDB: 1O4C; X-ray; A=144-251.
DR      PDB: 1O4D; X-ray; A=144-251.
DR      PDB: 1O4E; X-ray; A=144-251.
DR      PDB: 1O4F; X-ray; A=144-251.
DR      PDB: 1O4G; X-ray; A=144-251.
DR      PDB: 1O4H; X-ray; A=144-251.

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 Best Local Similarity 97.6%; Pred. No. 5,2e-175;
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QY 2 GSNKSKPKDASQRRSLSEPVNTGHA-GGAFPAISQTPSPKASADGHRGSPAAVPPAAEP 60
 DB 1 GSNKSKPKDASQRRSLSEPVNTGHA-GGAFPAISQTPSPKASADGHRGSPAAVPPAAEP 60

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DB      61 KLFGEFNSDDVTYSPOAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNNT----- 116
QY      121 VREGDWMLHLSLSTGOTGYIIPSNYVAPSPDSIQAEEMYPFGKITRREBRLLNANENRGT 180
DB      117 --EGDWMLHLSLSTGOTGYIIPSNYVAPSPDSIQAEEMYPFGKITRREBRLLNANENRGT 174
QY      181 LVRESEFTGAYCLSYSDFDNAKGLNVKHKYKRLKDSGGFYTISRQFNSLOOLVAYYSK 240
DB      175 LVRESEFTGAYCLSYSDFDNAKGLNVKHKYKRLKDSGGFYTISRQFNSLOOLVAYYSK 234
QY      241 HADGLCHRLTTCPTSPKPTOGGLAKDAWEIPRESLRLRYLGGCGCEYVMGTWNGTTRV 300
DB      235 HADGLCHRLTTCPTSPKPTOGGLAKDAWEIPRESLRLRYLGGCGCEYVMGTWNGTTRV 294
QY      301 AITTLKPGTMSPEAFIQEAQVMKLRHEKLVOLYAVVSEBPITYTETYNKSGSLDPLKG 360
DB      295 AITTLKPGTMSPEAFIQEAQVMKLRHEKLVOLYAVVSEBPITYTETYNKSGSLDPLKG 354
QY      361 EFGKYRLRLPOLVMSAQISGMAVYVERMYVHRDLAAANILVGENLVCKVADPGLARLIE 420
DB      415 DNEYTARQAGAKPKIKTAPBALYGRFTIKSDVMSFGILLTTLTKGRVPPGMVREYL 474
QY      481 DOVERGYRMPCEPECESLHDLMOCCWRKEPBERPFVEYLQAFLEYPFSTEPQYQYGEN 540
DB      475 DOVERGYRMPCEPECESLHDLMOCCWRKEPBERPFVEYLQAFLEYPFSTEPQYQYGEN 534
QY      541 L 541
DB      535 L 535

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RESULT 8

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SRC_RAT STANDARD, PRT, 535 AA.
ID_ID SRC_RAT
AC 09WUD09;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2000, sequence version 2.
DT 07-MAR-2006, entry version 46.
DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
DE (c-Src) (pp60c-src).
GN Name=Src;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBT_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RA Stockand J.D., Al-Khalili O., Spier B.J., Eaton D.C.;
RT "Rattus norvegicus proto-oncogene encoding tyrosine-protein kinase
RT pp60-c-src."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- P1M: Phosphorylated on Tyr-529 by c-Src kinase (CSK). The
CC phosphorylated form is termed pp60c-src. The phosphorylated tail
CC interacts with the SH2 domain thereby repressing kinase activity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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DR EMBL: AF130457; AAD24180.1; -, mRNA.
DR HSP: P12931.1A09.
DR ENR: Q9WUD9; 86-535.
DR Ensembl: ENSRNOG0000009495; Rattus norvegicus.
DR RGD: 620795; Src.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR009880; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
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DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; Tyrc; 1.
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DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KM Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KM Tyrosine-protein kinase.
PT INIT MET 0 By similarity.
PT CHAIN 1 535 Proto-oncogene tyrosine-protein kinase
Src.
FT DOMAIN 83 144 /Ftrid=PRO_000088143.
FT DOMAIN 150 247 SH2.
FT DOMAIN 269 522 SH3.
FT NP BIND 275 283 Protein kinase.
FT ACT SITE 388 388 ATP (By similarity).
FT BINDING 297 297 Proton acceptor (By similarity).
FT MOD_RES 419 419 ATP (By similarity).
FT MOD_RES 419 419 Phosphochreonine (by autocatalysis) (By
similarity).
FT MOD_RES 529 529 Phosphotyrosine (by CSK) (By similarity).
FT LIPID 1 1 N-myristoyl glycine (By similarity).
SQ SEQUENCE 535 AA; 53947 MW; AD083DD2357890BC CRC64;

Query Match 97.0%; Score 2772.5; DB 1; Length 535;
Best Local Similarity 97.6%; Pred. No. 6.1e-175;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 2 GSNKSKPKDASORRRSLSPSENNVAGAGAPASQTPSKPASADGHRGSAFVPP-AAEP 60
DB 1 GSNKSKPKDASORRRSLSPSENNVAGAGAPASQTPSKPASADGHRGSAFVPPAAEP 60
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DB 61 KLFGEFNSSDTVTSPQRAAGALAGVTTFVALVDYESTRTDLSFKKGERLQIVNTRKVD 120
QY 61 KLFGEFNSSDTVTSPQRAAGALAGVTTFVALVDYESTRTDLSFKKGERLQIVNTRKVD 120
DB 61 KLFGEFNSSDTVTSPQRAAGALAGVTTFVALVDYESTRTDLSFKKGERLQIVNTRKVD 120
QY 121 VRGSDWMLASLSLSTGQGYIPSNVAPSDSIQAEEWFGKTRRESRLILNANPRTGF 180
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QY 117 - -RGDWMLASLSLSTGQGYIPSNVAPSDSIQAEEWFGKTRRESRLILNANPRTGF 174
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QY 181 LVRESEETTKGAYCLSVDPNNAKLANVHYKIRKLDGSGFYTSRTQFNSLQQLVAAYSK 240
DB 181 LVRESEETTKGAYCLSVDPNNAKLANVHYKIRKLDGSGFYTSRTQFNSLQQLVAAYSK 240
QY 175 LVRESEETTKGAYCLSVDPNNAKLANVHYKIRKLDGSGFYTSRTQFNSLQQLVAAYSK 234
DB 175 LVRESEETTKGAYCLSVDPNNAKLANVHYKIRKLDGSGFYTSRTQFNSLQQLVAAYSK 234
QY 241 HADGLCHRLTTCVCTSPQTOGLAKDAWEIPRESRLAEVKLGCCFCGEVWMTNGTTRV 300
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QY 235 HADGLCHRLTTCVCTSPQTOGLAKDAWEIPRESRLAEVKLGCCFCGEVWMTNGTTRV 294
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QY 301 AIKTLKGTSPFAFLQEAQVMKKLRHEKLVQLVAVSEBPIYVTEVMNKGSLDLFLKG 360
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DB 295 AIKTLKGTSPFAFLQEAQVMKKLRHEKLVQLVAVSEBPIYVTEVMNKGSLDLFLKG 354
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QY 421 DNEYTAQAKFPFKWTAPEAALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVL 480
DB 415 DNEYTAQAKFPFKWTAPEAALYGRFTIKSDVMSFGILLTELTTKGRVPPYGVNREVL 474
QY 481 DVEYGRYMPCEPESPELHDMQCWRKSEBERPFEYLAQFLADYFTSTEPQYQGEN 540
DB 475 DVEYGRYMPCEPESPELHDMQCWRKSEBERPFEYLAQFLADYFTSTEPQYQGEN 534
QY 541 L 541
DB 535 L 535

RESULT 9
ID Q450J2_RAT PRELIMINARY; PRT; 523 AA.
AC Q450J2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Tyrosine protein kinase c-src (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHR, and WKY.
RA Jackson E.K., Zhu C.;
RT "Genetic Similarity Between Spontaneously Hypertensive Rats and
RT Wistar-Kyoto Rats in the Coding Regions of Signal Transduction
RT Proteins."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DB EMBL: DQ120510; AA223849.1; -, mRNA.
DB EMBL: DQ120509; AA223848.1; -, mRNA.
DB GO: GO:0005524; F:ATP binding; IEA.
DB GO: GO:0000166; F:nucleotide binding; IEA.
DB GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DB GO: GO:0016740; F:transferase activity; IEA.
DB GO: GO:0007242; P:intracellular signaling cascade; IEA.
DB GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DB InterPro: IPR000719; Prot_kinase.
DB InterPro: IPR002290; Ser_Thr_kinase.
DB InterPro: IPR009880; SH2.
DB InterPro: IPR001452; SH3.
DB InterPro: IPR001245; Tyr_kinase.
DB InterPro: IPR008266; Tyr_kinase_AS.
DB Pfam: PF07714; Pkinase_Tyr; 1.
DB Pfam: PF00017; SH2; 1.
DB Pfam: PF00018; SH3; 1.
DB PRINTS: PR00401; SH2DOMAIN.
DB PRINTS: PR00452; SH3DOMAIN.
DB PRINTS: PR00109; TYRKINASE.
DB ProDom: PD000001; Prot_kinase; 1.
DB ProDom: PD000093; SH2; 1.
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DB SMART: SM00252; SH2; 1.
DB SMART: SM00326; SH3; 1.
DB SMART: SM00219; Tyrc; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
 KW Tyrosine-protein kinase.
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 FT NON TER 1
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QY 7 KPDAAGRRRLSLPSENVHAGAFAPASQTPSKASADGHRGPAAVVP-AAEPKLFQ 65
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 DB 61 FNSSDVTSPORAGALAGVTFVALVDYESTRTEDSPFKGGERLQIVNTRKVDVREGD 114
 QY 126 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLVRES 185
 DB 115 WMLAHSLSGTQTYIPSNVYAPSDSIQAEEMVFGKTRRESERLLNAENPRGTFLVRES 174
 QY 186 ETTKGAICYLVSVPDNAGKLVNHYKTRKLDGSGFYITSTQPSLQQLVAYISKADGL 245
 DB 175 ETTKGAICYLVSVPDNAGKLVNHYKTRKLDGSGFYITSTQPSLQQLVAYISKADGL 234
 QY 246 CHRLTVCPSTKSPOTQGLADAMEIPRESRLLEVYKLGQGFGEVGMGTNGTRVAIKTL 305
 DB 235 CHRLTVCPSTKSPOTQGLADAMEIPRESRLLEVYKLGQGFGEVGMGTNGTRVAIKTL 294
 QY 306 KPQTSPEAFLOEAQVWKLRHEKLVQLYAVSEEPYIYTEYNNKSLDPLKGETGY 365
 DB 295 KPQTSPEAFLOEAQVWKLRHEKLVQLYAVSEEPYIYTEYNNKSLDPLKGETGY 354
 QY 366 LRLPOLVDSNAQJASGMAIYERMYVNRDILRAANILVGENLVCKVADFGILRIEDNEYT 425
 DB 355 LRLPOLVDSNAQJASGMAIYERMYVNRDILRAANILVGENLVCKVADFGILRIEDNEYT 414
 QY 426 ARQGAEPFKMTAPEALYGRFTIKSDVSGFILLTELTKGRVYRGVNRREVLDQVER 485
 DB 415 ARQGAEPFKMTAPEALYGRFTIKSDVSGFILLTELTKGRVYRGVNRREVLDQVER 474
 QY 486 GYRMPCEPCEPSLHDMCQCMRKEPERPTFEYLQAFLEDFYFTSTEPQ 534
 DB 475 GYRMPCEPCEPSLHDMCQCMRKEPERPTFEYLQAFLEDFYFTSTEPQ 523

RESULT 10
 SRC CHICK STANDARD; PRT; 532 AA.
 AC P00523; Q90992; Q91343; Q91345; Q92013; Q98915;
 DT 21-JUL-1986; Integrated into UniProtKB/Swiss-Prot.
 DT 15-JUL-1999; sequence version 3.
 DT 07-MAR-2006; entry version 78.
 DE Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src)
 DE (c-Src) (pp60c-src).
 GN Name=SRC;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=8315564; PubMed=6299580; DOI=10.1016/0092-8674(83)90073-9;
 RA Takeya T., Hanafusa H.;
 RT "Structure and sequence of the cellular gene homologous to the RSV src
 RT gene and the mechanism for generating the transforming virus.";

RL Cell 32:881-890(1983).
 RN [2]
 RP ERRATUM, AND SEQUENCE REVISION TO 525.
 RA Takeya T., Hanafusa H.;
 RL Cell 34:319-319(1983).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE=90318371; PubMed=2115117;
 RA Dorai T., Wang L.-H.;
 RT "An alternative non-tyrosine protein kinase product of the c-src gene
 RT in chicken skeletal muscle.";
 RL Mol. Cell. Biol. 10:4068-4079(1990).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PHOSPHORYLATION SITES TYR-415 AND
 RP TYR-435.
 RX MEDLINE=97008971; PubMed=8856081;
 RA Weijland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
 RA Superti-Furga G.;
 RT "The purification and characterization of the catalytic domain of Src
 RT expressed in Schistosoma haematophyllum. Comparison of unphosphorylated
 RT and tyrosine phosphorylated species.";
 RL Eur. J. Biochem. 240:756-764(1996).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 1-6.
 RX MEDLINE=83059861; PubMed=6292480;
 RA Takeya T., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. II.
 RT Comparison of the src genes of two strains of Avian sarcoma virus and
 RT of the cellular homolog.";
 RL J. Virol. 44:12-18(1982).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 1-18 AND 484-533 (ISOFORM 1).
 RX MEDLINE=91304409; PubMed=1712905;
 RA Dorai T., Levy J.B., Kang L., Brugge J.S., Wang L.-H.;
 RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
 RT exon and possible mechanism for the genesis of the 3' end of v-src.";
 RL Mol. Cell. Biol. 11:4165-4176(1991).
 RN [7]
 RP ATP-BINDING SITE.
 RX MEDLINE=84270751; PubMed=6431300;
 RA Kampe M.P., Taylor S.S., Setton B.M.;
 RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
 RT dependent protein kinase have homologous ATP-binding sites.";
 RL Nature 310:589-592(1984).
 RN [8]
 RP PHOSPHORYLATION.
 RX MEDLINE=86028181; PubMed=2996780; DOI=10.1016/0092-8674(85)90281-8;
 RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
 RA Hunter T.;
 RT "protein kinase C phosphorylates pp60src at a novel site.";
 RL Cell 42:849-857(1985).
 RN [9]
 RP PHOSPHORYLATION SITE TYR-415.
 RX MEDLINE=82082387; PubMed=6273838;
 RA Smart J.E., Oppermann H., Cernilofsky A.P., Purchio A.F.,
 RA Erikson R.L., Bishop J.M.;
 RT "Characterization of sites for tyrosine phosphorylation in the
 RT transforming protein of Rous sarcoma virus (pp60v-src) and its normal
 RT cellular homolog (pp60c-src)."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).
 RN [10]
 RP PHOSPHORYLATION SITE TYR-526.
 RX MEDLINE=86151652; PubMed=2420005;
 RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
 RT "Tyrosine 527 is phosphorylated in pp60c-src: implications for regulation.";
 RL Science 231:1431-1434(1986).
 RN [11]
 RP PHOSPHORYLATION SITES THR-33; THR-45 AND SER-71.
 RX MEDLINE=89249341; PubMed=2470512; DOI=10.1016/0092-8674(89)90791-5;
 RA Shenoy S., Choi J.K., Bagrodia S., Copeland T.D., Maller J.L.,
 RA Shalloway D.;
 RT "Purified maturation promoting factor phosphorylates pp60c-src at the

RT sites phosphorylated during fibroblast mitosis.";
RL Cell 57:763-774(1989).
RN (12)
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.
RX MEDLINE=98070614; PubMed=9405157; DOI=10.1006/jmb.1997.1426;
RA Williams J.C., Weijland A., Gonfloni S., Thompson A.,
RA Courtenidge S.A., Superti-Furga G., Wierenga R.K.;
RT "The 2.35 Å crystal structure of the inactivated form of chicken Src:
a dynamic molecule with multiple regulatory interactions.";
RL J. Mol. Biol. 274:757-775(1997).
RN (13)
RP STRUCTURE BY NMR OF 80-139.
RX MEDLINE=93279385; PubMed=8504863; DOI=10.1016/0014-5793(93)81538-B;
RA Yu H., Rosen M.R., Schneider S.L.;
RT "H and 15N assignments and secondary structure of the Src SH3
domain.";
RL FEBS Lett. 324:87-92(1993).
CC -1- FUNCTION: Unknown.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
tyrosine phosphate.
CC -1- ENZYME REGULATION: Becomes activated when its major tyrosine
phosphorylation site is not phosphorylated. It can also be
activated by point mutations as well as by truncations at the C-
terminal end or by other mutations.
CC -1- SUBUNIT: p60c-src forms a complex with polyoma virus middle T
antigen.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=1;
CC IsoId=P00523-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P00523-2; Sequence=VSP_011844, VSP_011845;
CC Note=Membrane-bound;
CC -1- TISSUE SPECIFICITY: Expressed to high levels, and with a high
degree of kinase activity, in certain fully differentiated cells
such as neurons, platelets and macrophages. Isoform 1 is widely
expressed. Isoform 2 is expressed only in the muscle.
CC -1- PTM: Phosphorylated on Tyr-526 by c-Src kinase (CSK). The
phosphorylated form is termed p60c-src. The phosphorylated tail
interacts with the SH2 domain thereby repressing kinase activity
(By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: V00402; CA23696.1; -; Genomic DNA.
DR EMBL: J00908; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL: M57290; AAA49078.1; -; mRNA.
DR EMBL: S43604; AAD13831.1; -; mRNA.
DR EMBL: S43616; AAD13835.1; -; mRNA.
DR EMBL: S43587; AAD13830.1; -; mRNA.
DR EMBL: S43609; AAD13832.1; -; mRNA.
DR EMBL: S43614; AAD13834.1; -; mRNA.
DR EMBL: S43579; AAB19353.2; -; mRNA.
DR PIR: A00630; TVCHS.
DR PDB: 1P1W; X-ray; A=144-246.
DR PDB: 1P2F; X-ray; A=144-246.
DR PDB: 1NLO; NMR; C=80-139.
DR PDB: 1NLP; NMR; C=80-139.
DR PDB: 1P13; X-ray; A/B=144-245.
DR PDB: 1PRL; NMR; C=76-139.
DR PDB: 1PRM; NMR; C=76-139.
DR PDB: 1RLP; NMR; C=76-139.
DR PDB: 1RLQ; NMR; C=76-139.
DR PDB: 1SRJ; NMR; @=76-139.
DR PDB: 1SRM; NMR; @=76-139.
DR PDB: 2PTK; X-ray; @=-.
DR Ensembl: ENSGALG00000003855; Gallus gallus.
DR LinkDb: P00523; -.

DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser_Chr_kinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00714; Pkinase_Tyr; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3_1; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000066; SH3; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW 3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW Myristate; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT INIT_MET 0 By similarity.
FT CHAIN 1 532 Proto-oncogene tyrosine-protein kinase
Src.
FT FT /FtId=PRO_0000086144.
FT DOMAIN 80 141 SH3.
FT DOMAIN 147 244 SH2.
FT NP_BIND 266 519 Protein kinase.
FT NP_BIND 272 280 ATP (By similarity).
FT ACT_SITE 385 385 Proton acceptor (By similarity).

Query Match 92.4%; Score 2643; DB 1; Length 532;
Best Local Similarity 93.1%; Pred. No. 2.3e-166;
Matches 503; Conservative 12; Mismatches 17; Indels 8; Gaps 2;

QY 2 GSNKSPKASQRRSLSEPSNVHAGAPASQSPKSPASADGHRGSAFVPPAEPK 61
1 GSSKSKRQDSQRRLSEPPSTH--HGFPASQTPKNTAPDTHRTSRSEFGVATPEK 58
62 LFGFNSSDVTSPQRAAGALAGVTTTVALYDYESRTETDLSFKKERLQIVNTRKDV 121
59 LFGFNTSDVTSPQRAAGALAGVTTTVALYDYESRTETDLSFKKERLQIVNNT----- 113
122 REGGWLALHSLSTGQGYISNYVAPSDSIQAEWYFGKTRRSERLLNAENPRGTEL 181
114 -EGGWLALHSLTQQTGYISNYVAPSDSIQAEWYFGKTRRSERLLNAENPRGTEL 172
182 VRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRQFNSLQOLVAAYYSKH 241
173 VRESEETTKGAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSTRQFNSLQOLVAAYYSKH 232
242 ADGCHRLTIVVCPTSPQTOGLADAWEPRESRLLEVKLGQCGFGEVWGTNNGTTRVA 301
233 ADGCHRLTIVVCPTSPQTOGLADAWEPRESRLLEVKLGQCGFGEVWGTNNGTTRVA 292
302 IKTIKPGTMSPEARLQEAQVKKLRHKKLVQLVAVVSEEPYIYTEYNNKSLDPLKGE 361
293 IKTIKPGTMSPEARLQEAQVKKLRHKKLVQLVAVVSEEPYIYTEYNNKSLDPLKGE 352
362 TKGTLRLPOLVDMSAOLASGAYVERANVYRDRAANILVGENLVCCVADFGRLATED 421
353 MGTLRLLPOLVDMSAOLASGAYVERANVYRDRAANILVGENLVCCVADFGRLATED 412
422 NEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPGVMNREYLD 481
413 NEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVPGVMNREYLD 472
482 QVERGYMPCEPPECSLHDLMLCCMKRKEPERFTPEYLQAFLEDYFTSTEPQVQGENL 541

Db 473 OVERGYRMPCEPESLHDMOCCKWKOPBEERPTFEYLQAFLEDTSTSTPEQPCENL 532

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RESULT 11
SRC_AVIS2 STANDARD; PRT; 586 AA.
AC p15054;
DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-ANG-2005, sequence version 2.
DT 07-MAR-2006, entry version 64.
DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain PR2257).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxID=11879;
[1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=89094972; PubMed=2463376;
RA Geryk J., Dezelee P., Barnter J.V., Svoboda J., Nehyba J., Karakoz I.,
RA Rynditch A.V., Yatsula B.A., Calothy G.;
RT "Transduction of the cellular src gene and 3' adjacent sequences in
RT avian sarcoma virus PR2257."
RL J. Virol. 63:481-492(1989).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calothy G.,
RA Dezelee P.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- PTM: The phosphorylated form is termed pp60v-src.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
CC EMBL, W21526; AAA42583.1; -; Genomic_RNA.
CC EMBL, X51863; CA436156.1; -; Genomic_RNA.
CC PIR, A30174; TVFVPR.
CC HSSP, P00523; 2PTK.
CC SMR, P15054; 83-524.
DR InterPro, IPR000719; Prot_kinase.
DR InterPro, IPR002290; Ser_thr_kinase.
DR InterPro, IPR000980; SH2.
DR InterPro, IPR001452; SH3.
DR InterPro, IPR001245; Tyr_kinase.
DR InterPro, IPR008266; Tyr_kinase_AS.
DR Pfam, PF07714; Kinase_Tyr; 1.
DR Pfam, PF00017; SH2; 1.
DR Pfam, PF00018; SH3; 1.
DR PRINTS, PR00401; SH2DOMAIN.
DR PRINTS, PR00452; SH3DOMAIN.
DR PRINTS, PR00109; TYRKINASE.
DR ProDom, PD000001; Prot_kinase; 1.
DR ProDom, PD000093; SH2; 1.
DR ProDom, PD000066; SH3; 1.
DR SMART, SM00252; SH2; 1.
DR SMART, SM00326; SH3; 1.
DR SMART, SM00219; TyrKc; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE, PS00001; SH2; 1.

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DR PROSITE, PS00002; SH3; 1.
KM ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KM Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferrase;
KM Tyrosine-protein kinase.
FT INIT_MET 0
FT CHAIN 1 586
FT By similarity.
FT Tyrosine-protein kinase transforming
FT protein Src.
FT /Pfam=PRO_0000088148.
FT SH2.
FT DOMAIN 80 141
FT 147 244
FT 266 519
FT 272 280
FT 385 385
FT ACT_SITE 294 294
FT BINDING 294 294
FT MOD_RES 415 415
FT Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT N-myristoyl glycine (by hoec) (By
FT similarity).
FT LIPID 1 1
FT SEQUENCE 586 AA; 65670 MW; 76520EP485B5CD02 CRC64;
SQ
Query Match 90.9%; Score 2598; DB 1; Length 586;
Best Local Similarity 93.0%; Pred. No. 2,5e-163;
Matches 495; Conservative 12; Mismatches 17; Indels 8; Gaps 2;
QY 2 GSNKSPKXASQRRRLSEENVHAGAFAPASQTPSKASADGHRGPAAPVPAAPK 61
DB 1 GSKSKPKDPSQRRRLSEPPDSTH--HGCFPASPQTKRAADPTHTPSRSPTVATEK 58
QY 62 LFGFNSDPTVTSPPORAGLAGVTFVALYDESFTETDLSFKKERLQIVNTRKDV 121
DB 59 LFGFPTSTVTSPPORAGLAGVTFVALYDESFTETDLSFKKERLQIVNTRKDV 113
QY 122 REGDMLASLSGQGGYPSNVVAPSDISOAEWFGKITRESRLILNENPGTEFL 181
DB 114 -EGDMLASLSGQGGYPSNVVAPSDISOAEWFGKITRESRLILNENPGTEFL 172
QY 182 VRESSTKAYCISVDFPNAGKLVKHKIKLDSGFIYSRTQFNSLQQLVAYYSKH 241
DB 173 VRESSTKAYCISVDFPNAGKLVKHKIKLDSGFIYSRTQFNSLQQLVAYYSKH 232
QY 242 ADGLCHRLTTCPTSPKQTOGLAKDAMEIPRESLRLEVKLGQCGFGEVMGTGTRVA 301
DB 233 ADGLCHRLTTCPTSPKQTOGLAKDAMEIPRESLRLEVKLGQCGFGEVMGTGTRVA 292
QY 302 ITLKPGTSPAPFLOEAVMKRLRHEKLVQYAVVSESPITYVYNNKSLDPLKGB 361
DB 293 ITLKPGTSPAPFLOEAVMKRLRHEKLVQYAVVSESPITYVYNNKSLDPLKGB 352
QY 362 TGYRLRLPOLVMSAQIAGMAVERMYVHDLRAANILVGENLVCKYADFGALRIED 421
DB 353 MGYRLRLPOLVMSAQIAGMAVERMYVHDLRAANILVGENLVCKYADFGALRIED 412
QY 422 NEXYAROGAKFPIKWTAPAAALYGRFTIKSDVMSFGILLTELTKGRVYPGVNREVID 481
DB 413 NEXYAROGAKFPIKWTAPAAALYGRFTIKSDVMSFGILLTELTKGRVYPGVNREVID 472
QY 482 OVERGYRMPCEPESLHDMOCCKWKOPBEERPTFEYLQAFLEDTSTSTPEQPCENL 533
DB 473 OVERGYRMPCEPESLHDMOCCKWKOPBEERPTFEYLQAFLEDTSTSTPEQPCENL 524

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RESULT 12
SRC_AVIS2 STANDARD; PRT; 567 AA.
AC p14084;
DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT 30-ANG-2005, sequence version 2.
DT 07-MAR-2006, entry version 60.
DE Tyrosine-protein kinase transforming protein Src (EC 2.7.1.112) (p60-
DE Src) (v-Src) (pp60v-src).
GN Name=v-Src;
OS Avian sarcoma virus (strain S1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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Alpharetrovirus; unclassified Alpharetrovirus.
 NCBI_TaxID=11881;
 [1]
 NUCLEOTIDE SEQUENCE.
 MEDLINE=87064539; PubMed=3097513;
 Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.,
 "Activation of the cellular src gene by transducing retrovirus.";
 Mol. Cell. Biol. 6:2420-2428(1986).
 -1- FUNCTION: This phosphoprotein, required for both the initiation
 and the maintenance of neoplastic transformation, is a protein
 kinase that catalyzes the phosphorylation of tyrosine residues in
 vitro.
 -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 tyrosine phosphate.
 -1- PFM: The phosphorylated form is termed pp60v-src.
 -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 subfamily.
 -1- SIMILARITY: Contains 1 SH2 domain.

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 PIR: A25375; TVPVS1.
 DR HSSP; P00523; 2PTK.
 DR SMR; P14084; 83-524.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001452; SH2.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF07714; SH2_Tyr_1.
 DR Pfam; PF00017; SH2_1.
 DR Pfam; PF00018; SH3_1; 1.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRINTS; PRO0452; SH3DOMAIN.
 DR PRINTS; PRO0109; TYRKINASE.
 DR ProDom; PD000001; Prot_Kinase.
 DR ProDom; PD000093; SH2_1.
 DR ProDom; PD000066; SH3_1.
 DR SMART; SM00252; SH2_1.
 DR SMART; SM00326; SH3_1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50013; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2_1.
 DR PROSITE; PS50002; SH3_1.
 DR ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-Binding;
 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; Transferase;
 TYROSINE-protein kinase.
 KW Tyrosine-protein kinase.
 FT INIT_MET 0
 FT CHAIN 1 567
 FT By similarity.
 FT Tyrosine-protein kinase transforming
 FT protein Src.
 FT /FTID=PRO_000008150.
 FT SH3.
 FT DOMAIN 147 141
 FT SH2.
 FT DOMAIN 147 244
 FT SH2.
 FT DOMAIN 266 519
 FT Protein kinase.
 FT ACT_SITE 272 280
 FT ATP (By similarity).
 FT ACCT_SITE 385 385
 FT Proton acceptor (By similarity).
 FT BINDING 294 294
 FT ATP (By similarity).
 FT MOD_RES 415 415
 FT Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT N-myristoyl glycine (by host).
 FT LIPID 1 1
 FT SEQUENCE 567 AA; 63501 MW; EA4FCC38195A098D CRC64;
 Query Match 90.6%; Score 2591; DB 1; Length 567;
 Best Local Similarity 92.7%; Pred. No. 6,8e-163;
 Matches 493; Conservative 14; Mismatches 17; Indels 8; Gaps 2;
 2 GSNKSKPDASQRRRSLEPSNVHGAGAFPAASQTPSPASADGHRGSAFVPPAPK 61

DR DB GSSSKRPDPQGRRRSLSEPDSTH--HGCFPASQTNPNTKAADPTNTPRSFCTVATEPK 58
1 CSSKSPKPDPSGRARRSLSEPDSTH--HGCFPASQTNPNTKAADPTNTPRSFCTVATEPK 58

DY QY LFGFNSSDVTYSPPRAGALACGVTTFVALYYESRTETDLSPKKERLQIYNNTKADV 121
|||
DB 59 LFGFNSTDVTYSPPRAGLAGGVTTFFVALYYESRTETDLSPKKERLQIYNNT 113
|||

DY QY REGDWLAHSJLTGGTGYIPSNYYVAPOSIOAEEMVFGITPRESERLLMANPBGFTL 161
|||
DB 114 -EGDWMLAHSJLTGGTGYIPSNYYVAPSDSIQAEBWFKITRESERLLANPENPGFTL 172
|||

DY QY VRESETTKGAYCLSYSDFDNAKNGLVKHKIRKLDSGCVYTISRTOFNSLOQLVAAYSKH 241
173 VRESITTKGAYCLSYSDFDNAGNLVKHKIRKLDSGCVYTISRTOFNSLOQLVAAYSKH 222
|||

DY QY ADGLCHRLTTCVPTSKPOTOGIAKDAMEIPRESLRLEVLGGCCFGEVMWGTNGTTRVA 301
223 ADGLCHRLTNVCPTSKPOTOGIAKDAMEIPRESLRLEVLLGGCCFGEVMWGTNGTTRVA 292
|||

DY QY IKTLKPGTMSPPAFIQEAOVMKKLHEKLVOLYAVASEEPITYVEYMNKGSLLDPLKGE 361
293 IKTLKPGTMSPPAFIQEAOVMKKLHEKLVRYLYAVASEEPITYIVYMKSGLLDPLKGE 352
|||

DY QY TGKYTRLPOLVYMSAOIASGMAYVERMYVHBDLRANILVGENLVCKVADFGLARLID 421
362 TGKYTRLPOLVYMSAOIASGMAYVERMYVHBDLRANILVGENLVCKVADFGLARLID 421
363 MGYTRLPOLVYMAOIASGMAYVERMYVHBDLRANILVGENLVCKVADFGLARLID 412
|||

DY QY NEYTAROGAKFPDKWTAPEDPALYGRFTIKSDVSFGILLTELTTKGRPVPYGVNREVLD 481
413 NEYTAROGAKFPDKWTAPEDPALYGRFTIKSDVSFGILLTELTTKGRPVPYGVNREVLD 472
|||

DY QY OVERGIRMPCEPCESLHDLMCOCRKRPERRPTFEYLQAFLEDYFTSTEP 533
473 OVERGIRMPCEPCESLHDLMCOCRKRDPEERPTEYLQAFLEDYFTSTEP 524
|||

RESULT 13
Q64817_9RET R PRELIMINARY; PRT; 587 AA.
ID AC Q64817;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Protein-tyrosine kinase.
GN Name=src;
OS Avian sarcoma virus.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus; unclassified Alpharetrovirus.
OX NCBI_TaxId=11876;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PR2257/16;
RX MEDLINE=95016532; PubMed=7931166;
RA Yatsula B.A., Geryk J., Svoboda J., Rynditch A.V., Calochy G.,
RA Dezelle P.;
RT "Evolution and origin of virus PR2257, a recent c-src transducing
RT virus".
RU J. Gen. Virol. 75:2777-2781(1994).
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DR DR HMBL_L21974; AAC37877.1; -; Genomic_DNA.
DR DR HSBP_P00523; 2PTRK.
DR DR SMK_Q64817; 84-525.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006466; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Kinase; Tyrosine-protein kinase.
 KW SEQUENCE 587 AA; 65779 MW; BAAC3F5A44234F02 CRC64;
 Query Match 90.6%; Score 2590; DB 2; Length 587;
 Best Local Similarity 92.7%; Pred. No. 8.4e-163;
 Matches 494; Conservative 12; Mismatches 19; Indels 8; Gaps 2;

QY 1 MGSKSKPKDASQRRRLSEPNVHGAGAFPAQSPKSPADSGHGRPSAFAVPAAP 60
 DB 1 MGSSKSKPKDPSQRRSLRPPDSTH--HGEPFASQTNKRAADPTHTPSRSTYATEP 58
 QY KLFEGFNSDVTVPQAGALAGVTFVALYDSESTETDLSFKGERLQIVNTRKVD 120
 DB KLFEGFNTSDVTVPQAGALAGVTFVALYDSESTETDLSFKGERLQIVNTRKVD 114
 QY 121 VRGSDWLAHSLSTGCGYIPSNYVAPSDSIQAEWYFGKITRRESRLILNENPRTG 180
 DB 115 --EGDWLAHSLSTGCGYIPSNYVAPSDSIQAEWYFGKITRRESRLILNENPRTG 172
 QY 181 LVASEETTKAYCGLSYDPFNAGLNVKHYKIRKLDGGGYITSRQFNLSLOOLVAYYSK 240
 DB 173 LVASEETTKAYCGLSYDPFNAGLNVKHYKIRKLDGGGYITSRQFNLSLOOLVAYYSK 232
 QY 241 HADGCLRLTVCTSPKPTQGLAKDAWEIPRESLRLEVLGCGCFGEVWMTNGTTRV 300
 DB 233 HADGCLRLTVCTSPKPTQGLAKDAWEIPRESLRLEVLGCGCFGEVWMTNGTTRV 292
 QY 301 AITTLKPGTMSPAFLOEAQVKKLRHEKVLQYAVVSEPTITVETYNKGLLDPLKG 360
 DB 293 AITTLKPGTMSPAFLOEAQVKKLRHEKVLQYAVVSEPTITVETYNKGLLDPLKG 352
 QY 361 ETGKYRLPOLVMSAQISGMAYVERMNVVHDLRAANTLVGENLVCKVADPGLRLIE 420
 DB 353 ETGKYRLPOLVMSAQISGMAYVERMNVVHDLRAANTLVGENLVCKVADPGLRLIE 412
 QY 421 DNEYTARQAKFPKIKTAPAPALYGRFTIKSDVMSFGILLTTLTKGRVYPGVNVREVL 480
 DB 413 DNEYTARQAKFPKIKTAPAPALYGRFTIKSDVMSFGILLTTLTKGRVYPGVNVREVL 472
 QY 481 DQVERGYRNPCEPCESLHDLCCCKRKEPERPFEYIQAFLDYFTSTEP 533
 DB 473 DQVERGYRNPCEPCESLHDLCCCKRKEPERPFEYIQAFLDYFTSTEP 525

RESULT 14
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 AC P14085;
 DT 01-JUN-1990, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 60.
 DE Tyrosine-protein kinase transforming protein Src (BC 2.7.1.112) (p60-Src) (v-Src) (pp60v-src).
 GN Name=v-Src;
 OS Avian sarcoma virus (strain S2).

CC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 CC Alpharetrovirus; unclassified Alpharetrovirus.
 CC NCBI_TaxID=11882;
 RN [1]
 RX NCLECTIDE SEQUENCE.
 RX MEDLINE=87064539; Pubmed=3097513;
 RA Ikawa S., Hagino-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.;
 RT "Activation of the cellular src gene by transducing retrovirus.";
 RL Mol. Cell. Biol. 6:2420-2428(1986).
 CC -1- FUNCTION: This phosphoprotein, required for both the initiation
 CC and the maintenance of neoplastic transformation, is a protein
 CC kinase that catalyzes the phosphorylation of tyrosine residues in
 CC vitro.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -1- PTM: The phosphorylated form is termed p60v-src.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----

DR PIR; B25375; TVFV82.
 DR HSSP; P00523; 2PTK.
 DR SWP; P14085; 83-532.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
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 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
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 KW Oncogene; Phosphorylation; SH2 domain; SH3 domain; transferase;
 KW Tyrosine-protein kinase.
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 FT DOMAIN 80 141
 FT DOMAIN 147 244
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 FT LIPID 1 1
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 SO SEQUENCE 556 AA; 62452 MW; 0F7A904CA3FEA9CC CRC64;

Query Match 90.1%; Score 2576; DB 1; Length 556;
 Best Local Similarity 88.7%; Pred. No. 6.5e-162;
 Matches 494; Conservative 16; Mismatches 21; Indels 26; Gaps 3;

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QY 529 -----TSTEPQYQGEN 540
DB 533 GPRGETASNKQERGED 549

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RA Feng S., Chen J.K., Yu H., Simon J.A., Schreiber S.L.;
RT "Two binding orientations for peptides to the Src SH3 domain:
RL development of a general model for SH3-ligand interactions.";
CC Science 266:1241-1247(1994).
CC -1- FUNCTION: This phosphoprotein, required for both the initiation
CC and the maintenance of neoplastic transformation, is a protein
CC kinase that catalyzes the phosphorylation of tyrosine residues in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- PTM: The phosphorylated form is termed pp60v-src.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC subfamily.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DB EMBL, K00928; AAA42565.1; -, Genomic_RNA.
DB PDB, 1QWE; NMR, A=80-139.
DB PDB, 1QWE; NMR, A=80-139.
DB SMR, P00525; 83-515.
DB LinkHub, P00525; -.
DB InterPro, IPR000719; Prot_kinase.
DB InterPro, IPR002290; Ser_Thr_kinase.
DB InterPro, IPR000980; SH2.
DB InterPro, IPR001452; SH3.
DB InterPro, IPR001245; Tyr_kinase.
DB InterPro, IPR008266; Tyr_kinase_AS.
DB Pfam, PR07714; Kinase_Tyr; 1.
DB Pfam, PF00017; SH2; 1.
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DB PRINTS, PR00401; SH2DOMAIN.
DB PRINTS, PR00452; SH3DOMAIN.
DB PRINTS, PR00109; TYRKINASE.
DB ProDom, PD000001; Prot_kinase; 1.
DB ProDom, PD000093; SH2; 1.
DB ProDom, PD000066; SH3; 1.
DB SMART, SM00252; SH2; 1.
DB SMART, SM00326; SH3; 1.
DB SMART, SM00219; TyrcK; 1.
DB PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DB PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
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DB PROSITE, PS50002; SH3; 1.
DB 3D-structure, ATP-binding; Kinase; Lipoprotein; Myristate;
DB Nucleotide-binding; Oncogene; Phosphorylation; SH2 domain; SH3 domain;
DB Transferase; Tyrosine-protein kinase.
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DB CHAIN 1 525
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FT 0 protein Src.
FT 0 /Ftrid=PRO_0000088147.
FT 0 SH3.
FT 0 SH2.
FT 0 Protein kinase.
FT 0 ATP (By similarity).
FT 0 Proton acceptor (By similarity).
FT 0 ATP (By similarity).
FT 0 Phosphotyrosine (by autocatalysis).
FT 0 N-myristoyl glycine (by host) (By
FT 0 similarity).
FT STRAND 85 87
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Query Match 87.8%; Score 2510; DB 1; Length 525;
Best Local Similarity 91.8%; Pred. No. 1,46-157;
Matches 480; Conservative 14; Mismatches 21; Indels 8; Gaps 2;

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Db 62 LFGGFNSDVTVTSFORAGALAGVTTFFVALYDYESRTETDLSFKKGERLQIVNTRKDV 121
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Db 482 QVERGTRMPCPECPESLHDLMLCCMKRKEPERPTFEYLOAFL 524
   473 RVERGYRMPCPECPESLHDLMLCCMKRKEPERPTFEYLOAFL 515
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Search completed: June 5, 2006, 17:15:29
Job time : 158.049 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:15:49 ; Search time 31.0766 Seconds

(Without alignments)
1523.786 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859
Sequence: 1 MSNKSXPKKASQRRSLR.....APLEDTSTREPOYQENL 541Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/1aa/5.COMB.pep:*
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- 7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2778.5	97.2	536	1 US-07-820-011A-4	Sequence 4, Appl
2	2778.5	97.2	536	2 US-08-426-509A-13	Sequence 13, Appl
3	2778.5	97.2	536	2 US-08-232-545-13	Sequence 13, Appl
4	2778.5	97.2	536	2 US-08-444-711A-2	Sequence 2, Appl
5	2778.5	97.2	536	2 US-09-929-266-10	Sequence 10, Appl
6	2778.5	97.2	536	2 US-09-977-261-13	Sequence 13, Appl
7	2778.5	97.2	536	5 PCT-US93-00445-4	Sequence 4, Appl
8	2778.5	97.2	536	5 PCT-US95-05008-13	Sequence 13, Appl
9	2778.5	97.2	537	2 US-09-949-016-10282	Sequence 10282, A
10	2745.5	96.0	530	2 US-09-444-711A-4	Sequence 4, Appl
11	2645	92.5	533	2 US-07-820-011A-2	Sequence 2, Appl
12	2642	92.4	533	1 US-07-820-011A-2	Sequence 2, Appl
13	2642	92.4	533	5 PCT-US93-00445-2	Sequence 2, Appl
14	2111	73.8	543	2 US-08-426-509A-14	Sequence 14, Appl
15	2111	73.8	543	2 US-08-232-545-14	Sequence 14, Appl
16	2111	73.8	543	2 US-09-470-881-8	Sequence 8, Appl
17	2111	73.8	543	2 US-09-538-092-870	Sequence 870, App
18	2111	73.8	543	2 US-09-977-261-14	Sequence 14, Appl
19	2111	73.8	543	5 PCT-US95-05008-14	Sequence 14, Appl
20	2103	73.6	541	2 US-09-864-291-20	Sequence 20, Appl
21	1931.5	67.6	532	1 US-08-594-447-1	Sequence 1, Appl
22	1931.5	67.5	532	1 US-08-665-647-1	Sequence 1, Appl
23	1929.5	67.5	536	2 US-08-426-509A-12	Sequence 12, Appl
24	1929.5	67.5	536	2 US-08-232-545-12	Sequence 12, Appl
25	1929.5	67.5	536	2 US-09-977-261-12	Sequence 12, Appl
26	1929.5	67.5	536	5 PCT-US95-05008-12	Sequence 12, Appl

27	1928	67.4	537	2 US-08-426-509A-11	Sequence 11, Appl
28	1928	67.4	537	2 US-08-232-545-11	Sequence 11, Appl
29	1928	67.4	537	2 US-09-977-261-11	Sequence 11, Appl
30	1928	67.4	537	5 PCT-US95-05008-11	Sequence 11, Appl
31	1923	67.3	536	2 US-09-538-092-859	Sequence 859, App
32	1920	67.2	537	2 US-09-771-161A-212	Sequence 212, App
33	1920	67.2	537	2 US-09-771-161A-213	Sequence 213, App
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35	1847.5	64.6	529	2 US-08-232-545-15	Sequence 15, Appl
36	1847.5	64.6	529	2 US-09-538-092-885	Sequence 885, App
37	1847.5	64.6	529	2 US-09-977-261-15	Sequence 15, Appl
38	1847.5	64.6	529	5 PCT-US95-05008-15	Sequence 15, Appl
39	1744	61.0	485	2 US-10-094-749-2726	Sequence 2726, Ap
40	1520.5	53.2	573	2 US-09-949-016-10415	Sequence 10415, A
41	1520	53.2	505	2 US-08-426-509A-17	Sequence 17, Appl
42	1520	53.2	505	2 US-08-232-545-17	Sequence 17, Appl
43	1520	53.2	505	2 US-09-977-261-17	Sequence 17, Appl
44	1520	53.2	505	5 PCT-US95-05008-17	Sequence 17, Appl
45	1462.5	51.2	512	2 US-08-426-509A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-07-820-011A-4
Sequence 4, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.

/ AUTHORS: Gibbs, Carol P.
 / AUTHORS: Tanaka, Akio
 / AUTHORS: Kung, Heing-jien
 / AUTHORS: Fujita, Donald J.
 / TITLE: Human Cellular src Gene:
 / TITLE: Nucleotide Sequence and Derived Amino
 / TITLE: Acid Sequence of the Region Coding for
 / TITLE: the Carboxy-Terminal Two-Thirds of
 / TITLE: pp60c-src
 / JOURNAL: Molecular and Cellular Biology
 / VOLUME: 5
 / ISSUE: 5
 / PAGES: 1122-1129
 / DATE: May, 1985
 / PUBLICATION INFORMATION:
 / AUTHORS: Tanaka, Akio
 / AUTHORS: Gibbs, Carol P.
 / AUTHORS: Arthur, Richard R.
 / AUTHORS: Anderson, Stephen K.
 / AUTHORS: Kung, Heing-jien
 / AUTHORS: Fujita, Donald J.
 / TITLE: DNA Sequence Encoding the
 / TITLE: Amino-Terminal Region of the Human c-src
 / TITLE: Protein: Implications of Sequence
 / TITLE: Divergence among src-Type Kinase
 / TITLE: Oncogenes
 / JOURNAL: Molecular and Cellular Biology
 / VOLUME: 7
 / ISSUE: 5
 / PAGES: 1978-1983
 / DATE: May, 1987
 / US-07-820-011A-4

Query Match 97.2%; Score 2778.5; DB 1; Length 536;
 Best Local Similarity 97.6%; Pred. No. 2.6e-214;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 540 NL 541
 DB 535 NL 536

RESULT 2
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 / Sequence 13, Application US/08426509A
 / Patent No. 6326469
 / GENERAL INFORMATION:
 / APPLICANT: Ullrich, Axel
 / APPLICANT: Glehizky, Mikhail
 / APPLICANT: Sures, Imran G.
 / TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
 / TITLE OF INVENTION: TYROSINE KINASES
 / NUMBER OF SEQUENCES: 21
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Pennie & Edmonds
 / STREET: 1155 Avenue of the Americas
 / CITY: New York,
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10036-2711
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/426,509A
 / FILING DATE: 21-APR-1995
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/232,545
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Coruzzi, Laura A
 / REGISTRATION NUMBER: 30,742
 / REFERENCE/DOCKET NUMBER: 7683-0074-999
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 212-790-9090
 / TELEFAX: 212-869-9741
 / TELEX: 66141 PENNIE
 / INFORMATION FOR SEQ ID NO: 13:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 536 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: unknown
 / TOPOLOGY: unknown
 / MOLECULE TYPE: No. 6326469e
 / US-08-426-509A-13

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
 Best Local Similarity 97.6%; Pred. No. 2.6e-214;
 Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MGSNKSXPDAOSRRSLSPSENNVHGA-GGAPASOTPSKPSADGHRPSAFAVPRAE 59
 DB 1 MGSNKSXPDAOSRRSLSPSENNVHGA-GGAPASOTPSKPSADGHRPSAFAVPRAE 60
 QY 60 PKLFGFNSDVTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKY 119
 DB 61 PKLFGFNSDVTYSPORAGALAGVTTFVALYDYESRTETDLSFKKGERLQIVNTRKY 117
 QY 120 DVREGDWMLAHSLSGTGTGTPSNVYAPSDSIQAEEMVFGKITRRSEERLLNAENPRGT 179
 DB 118 --BGDWMLAHSLSGTGTGTPSNVYAPSDSIQAEEMVFGKITRRSEERLLNAENPRGT 174
 QY 180 FLVRESEETTKGAYCISVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAYYS 239
 DB 175 FLVRESEETTKGAYCISVSPFDNAKGLNVKHYKIRKLDGSGFYITSTRQFNSLQOLVAYYS 234
 QY 240 KHAADGLCHRLTTCPTSKPTQGLAKDAWEIPRESRLRLEVKLGQSGFGEVWMTNNGTTR 299

Db 235 KHADELCHRLTTVCPTSPKPTQGLAKDAMEIPRESLRLVYLGGCGCFGEVMMGTWGTTR 294
Qy 300 VAIKTLKPGTMSPEAFIQEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNKKSLLDFLK 359
Db 295 VAIKTLKPGTMSPEAFIQEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNKKSLLDFLK 354
Qy 360 GETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLPAANTLVGENLVCKYADFGLARLI 419
Db 355 GETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLPAANTLVGENLVCKYADFGLARLI 414
Qy 420 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVVPQGMVREV 479
Db 415 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVVPQGMVREV 474
Qy 480 LDQVGRGYRMPCEPCEPSLHDLMCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 539
Db 475 LDQVGRGYRMPCEPCEPSLHDLMCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 3
US-08-232-545-13
; Sequence 13, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Gishizsky, Mikhail
; APPLICANT: Sures, Iman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Penile & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-232-545-13

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 59

Db 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 60
Qy 60 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDSERTETDLSFKGGERLQIVNTRKV 119
Db 61 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDSERTETDLSFKGGERLQIVNTRKV 117
Qy 120 DVREGBMWLAHSLSTGQTYTIPSNYVAPSPDSIQAEENYFGKITRSEBRLLNENPCT 179
Db 118 ---BGDWMLAHSLSLTGQTYTIPSNYVAPSPDSIQAEENYFGKITRSEBRLLNENPCT 174
Qy 180 FLVRESSTTGAYCLASDSDPNAGKLVKHYKIKLDSGGFYITSRTQFNSLQOLVAYYS 239
Db 175 FLVRESSTTGAYCLASDSDPNAGKLVKHYKIKLDSGGFYITSRTQFNSLQOLVAYYS 234
Qy 240 KHADELCHRLTTVCPTSPKPTQGLAKDAMEIPRESLRLVYLGGCGCFGEVMMGTWGTTR 299
Db 235 KHADELCHRLTTVCPTSPKPTQGLAKDAMEIPRESLRLVYLGGCGCFGEVMMGTWGTTR 294
Qy 300 VAIKTLKPGTMSPEAFIQEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNKKSLLDFLK 359
Db 295 VAIKTLKPGTMSPEAFIQEAQVMKKLRHEKLVOLYAVVSEBPIYIVTEYNKKSLLDFLK 354
Qy 360 GETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLPAANTLVGENLVCKYADFGLARLI 419
Db 355 GETGKYLRLPOLVDMASQIASGMAYVERMNYVHRDLPAANTLVGENLVCKYADFGLARLI 414
Qy 420 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVVPQGMVREV 479
Db 415 EDNEYTAROGAKFPFKMTAPEALYGRFTIKSDVMSFGILLTELTTKGRVVPQGMVREV 474
Qy 480 LDQVGRGYRMPCEPCEPSLHDLMCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 539
Db 475 LDQVGRGYRMPCEPCEPSLHDLMCQCKRKEBERPTEFYLAQLEDFYFTSTEPQYQGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 4
US-09-444-711A-2
; Sequence 2, Application US/09444711A
; Patent No. 6764633
; GENERAL INFORMATION:
; APPLICANT: Yeatman, Timothy J.
; APPLICANT: Itby, Rosalyn B.
; TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
; FILE REFERENCE: USF-1136
; CURRENT APPLICATION NUMBER: US/09/444,711A
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(536)
; OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
; OTHER INFORMATION: by the normal c-Src coding region
US-09-444-711A-2

Query Match 97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 59
Db 1 MGSNKSXPKQASQRRRLSEPSENVHGA-GGAFPASQTPSPKPSADGHRGSPAAAFVPPAAE 60

Qy 60 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDSERTETDLSFKGGERLQIVNTRKV 119

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Db      61 PKLFGFNSSDVTYTSQRAAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
Qy      120 DVREGDWMIAHLSISTGQTGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 179
Db      118 ---EGDMMWLAHLSISTGQTGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 174
Qy      180 FLVRESEETTKGAYCLASVSPFDNAKGLNVGHYKIRKLDGSGGFYITSTRTOFNSLQOLVAAYS 239
Db      175 FLVRESEETTKGAYCLASVSPFDNAKGLNVGHYKIRKLDGSGGFYITSTRTOFNSLQOLVAAYS 234
Qy      240 KHADGICHLITTVCPYTSKPTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 239
Db      235 KHADGICHLITTVCPYTSKPTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 234
Qy      300 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLK 359
Db      295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLK 354
Qy      360 GETGKYLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADPGLARLI 419
Db      355 GETGKYLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADPGLARLI 414
Qy      420 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTTELTKGRVPPGMVNRREV 479
Db      415 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTTELTKGRVPPGMVNRREV 474
Qy      480 LDQVERGYMPCBPCEPESLHDMCQWKPEBERPTEFYLOAFLEDYFTSTEPQYOPGB 539
Db      475 LDQVERGYMPCBPCEPESLHDMCQWKPEBERPTEFYLOAFLEDYFTSTEPQYOPGB 534
Qy      540 NL 541
Db      535 NL 536

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RESULT 5

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US-09-929-266-10
; Sequence 10, Application US/09929266
; Patent No. 6824981
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Lattimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershner
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Kevin J. McConnell
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10

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Query Match      97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
Qy      1 MGSNKSXPDAQORRRSLSESENVHGA-GGAPPASQTPSKPASADGHRGSAFVPPAAE 59
Db      1 MGSNKSXPDAQORRRSLSESENVHGA-GGAPPASQTPSKPASADGHRGSAFVPPAAE 60

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Qy      60 PKLFGFNSSDVTYTSQRAAGALAGVTTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 119
Db      61 PKLFGFNSSDVTYTSQRAAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
Qy      120 DVREGDWMIAHLSISTGQTGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 179
Db      118 ---EGDMMWLAHLSISTGQTGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 174
Qy      180 FLVRESEETTKGAYCLASVSPFDNAKGLNVGHYKIRKLDGSGGFYITSTRTOFNSLQOLVAAYS 239
Db      175 FLVRESEETTKGAYCLASVSPFDNAKGLNVGHYKIRKLDGSGGFYITSTRTOFNSLQOLVAAYS 234
Qy      240 KHADGICHLITTVCPYTSKPTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 239
Db      235 KHADGICHLITTVCPYTSKPTQGLANDAMEIPRESLRLEVKLGQCGFGEVWMTGNQTTT 234
Qy      300 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLK 359
Db      295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEBPIYIYTEYMSKSLDPLK 354
Qy      360 GETGKYLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADPGLARLI 419
Db      355 GETGKYLRLPOLVDMASQIASGMAYVERMYVHRDLRAANILVGENLVCKVADPGLARLI 414
Qy      420 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTTELTKGRVPPGMVNRREV 479
Db      415 EDNEYTAROGAKPPIKMTAPEALYGRFTIKSDVMSFGILLTTELTKGRVPPGMVNRREV 474
Qy      480 LDQVERGYMPCBPCEPESLHDMCQWKPEBERPTEFYLOAFLEDYFTSTEPQYOPGB 539
Db      475 LDQVERGYMPCBPCEPESLHDMCQWKPEBERPTEFYLOAFLEDYFTSTEPQYOPGB 534
Qy      540 NL 541
Db      535 NL 536

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RESULT 6

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US-09-977-261-13
; Sequence 13, Application US/09977261
; Patent No. 6908984
; GENERAL INFORMATION:
; APPLICANT: ULIRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-13

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Query Match      97.2%; Score 2778.5; DB 2; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
Qy      1 MGSNKSXPDAQORRRSLSESENVHGA-GGAPPASQTPSKPASADGHRGSAFVPPAAE 59
Db      1 MGSNKSXPDAQORRRSLSESENVHGA-GGAPPASQTPSKPASADGHRGSAFVPPAAE 60
Qy      60 PKLFGFNSSDVTYTSQRAAGALAGVTTTFVALYDYSRTETDLSFKKGERLQIVNNTKV 119
Db      61 PKLFGFNSSDVTYTSQRAAGPLAGGVTTFVALYDYSRTETDLSFKKGERLQIVNNT --- 117
Qy      120 DVREGDWMIAHLSISTGQTGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 179

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Db 118 ---BGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEEMVFGKITRSESRLLLNANENRG 174
QY 180 FLVRESEETTKGAYCLSYSDPDNAKGLNVKHYKIRKLDSCGFYITSRTQFNSLQOLVAYYS 239
Db 175 FLVRESEETTKGAYCLSYSDPDNAKGLNVKHYKIRKLDSCGFYITSRTQFNSLQOLVAYYS 234
QY 240 KHAADGLCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLGGCCGCEGVMGTMNGTTR 299
Db 235 KHAADGLCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLGGCCGCEGVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 354
QY 360 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLPAANILVGENIVCKVADFGRLRI 419
Db 355 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLPAANILVGENIVCKVADFGRLRI 414
QY 420 EDNEYTARQGAKEPIKMTAPBAALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 479
Db 415 EDNEYTARQGAKEPIKMTAPBAALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEYLOAFLEBYFTSTEPQYQPG 539
Db 475 LDQVERGYRMPCEPCESLHDLMCQCKRKEPERPTEYLOAFLEBYFTSTEPQYQPG 534
QY 540 NL 541
Db 535 NL 536

RESULT 7
PCT-US93-00445-4
; Sequence 4, Application PC/TUS9300445
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 760 Kb storage
; COMPUTER: DELL 486/50
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00445
; FILING DATE: 19930105
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/820, 011
; FILING DATE: 06-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-101PCT
; TELEPHONE: (203) 253 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear

MOLECULE TYPE: Protein
HYPOTHETICAL: No
FRAGMENT TYPE: Complete Sequence
ORIGINAL SOURCE:
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 5
PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
PCT-US93-00445-4
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
QY 1 MGSNKSXPKQASQRRSLSESENVGA-GGAFPASQTPSKPASADGHRGSAFVPPAAE 59
Db 1 MGSNKSXPKQASQRRSLSESENVGA-GGAFPASQTPSKPASADGHRGSAFVPPAAE 60
QY 60 PKLFGFNSSDYTSPPQAGALAGVTTFVALYDYESRTERDLSFKGGERLQIYNNTRKV 119
Db 61 PKLFGFNSSDYTSPPQAGALAGVTTFVALYDYESRTERDLSFKGGERLQIYNNTRKV 117
QY 120 DVREGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEEMVFGKITRSESRLLLNANENRG 179
Db 118 ---BGDMWLAHSLSTGQGYIIPSNYVAPSDSIQAEEMVFGKITRSESRLLLNANENRG 174
QY 180 FLVRESEETTKGAYCLSYSDPDNAKGLNVKHYKIRKLDSCGFYITSRTQFNSLQOLVAYYS 239
Db 175 FLVRESEETTKGAYCLSYSDPDNAKGLNVKHYKIRKLDSCGFYITSRTQFNSLQOLVAYYS 234
QY 240 KHAADGLCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLGGCCGCEGVMGTMNGTTR 299
Db 235 KHAADGLCHRLITTVCPSTKPTQGLAKDAMEIPRESLLEVLGGCCGCEGVMGTMNGTTR 294
QY 300 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIOEAQVMKGLRHEKLVOLYAVVSEEPYIVTEYNNKSGSLDPLK 354
QY 360 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLPAANILVGENIVCKVADFGRLRI 419
Db 355 GETGKYLRPLQVLVDMASQIASGMAVVERMNVYHRDLPAANILVGENIVCKVADFGRLRI 414
QY 420 EDNEYTARQGAKEPIKMTAPBAALYGRFTIKSDVMSFGILLTTLTGKRVYPGMNVREV 479

Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLETITTKGRVPIPGMVNREV 474
Qy 480 LDQVGRGYMPCPEPCESLHDLIMCQCKRKEBERPTEFYLOAFLEDYFTSTBPQOPGE 539
Db 475 LDQVGRGYMPCPEPCESLHDLIMCQCKRKEBERPTEFYLOAFLEDYFTSTBPQOPGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 8
PCT-US95-05008-13
Sequence 13, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Misenbachten E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-13

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPDAQORRSLSPESENVHGA-CGAFPASQTPSPKASADGHRGSAAFVPPAAE 59
Db 1 MGSNKSXPDAQORRSLSPESENVHGA-CGAFPASQTPSPKASADGHRGSAAFVPPAAE 60
Qy 60 PKLFGGFNSSDVTYTSQBRAGALAGVTTFTVALYDYSRTETDLSFKKGERLQIVNNTKRV 119
Db 60 PKLFGGFNSSDVTYTSQBRAGALAGVTTFTVALYDYSRTETDLSFKKGERLQIVNNTKRV 119

Db 61 PKLFGGFNSSDVTYTSQBRAGALAGVTTFTVALYDYSRTETDLSFKKGERLQIVNNTKRV 117
Qy 120 DVREGDWMLAHSLSSTQGTGYIPSNVYAPSDSIQAEEMYGKTIIRRESSELLINAEPRGT 179
Db 118 --EGDWMLAHSLSSTQGTGYIPSNVYAPSDSIQAEEMYGKTIIRRESSELLINAEPRGT 174
Qy 180 FLVRESEETTKGAYCALSVDSPDNAKGLNAGVYKLRKLDGSGFYITSTRTOFNSLQQLVAAYYS 239
Db 175 FLVRESEETTKGAYCALSVDSPDNAKGLNAGVYKLRKLDGSGFYITSTRTOFNSLQQLVAAYYS 234
Qy 240 KHAADGLCHRLTYTCPTSKPOTQGLANDAMEIPRESLRLEVKLGQCGFGEVMGTNGTTR 299
Db 235 KHAADGLCHRLTYTCPTSKPOTQGLANDAMEIPRESLRLEVKLGQCGFGEVMGTNGTTR 294
Qy 300 VAIKTLKPGTMSPEALQEAQVWKLRHKKLVOLYAVSEEPYIYTEMNKSGSLDFLK 359
Db 295 VAIKTLKPGTMSPEALQEAQVWKLRHKKLVOLYAVSEEPYIYTEMNKSGSLDFLK 354
Qy 360 GETGKYLRLPOLVDMSAOLASGMAVYERANVYHRDLRANILVGENLVCKVADFGIARLI 419
Db 355 GETGKYLRLPOLVDMSAOLASGMAVYERANVYHRDLRANILVGENLVCKVADFGIARLI 414
Qy 420 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLETITTKGRVPIPGMVNREV 479
Db 415 EDNEYTARQAKPFIKMTAPEALYGRFTIKSDVMSGILLETITTKGRVPIPGMVNREV 474
Qy 480 LDQVGRGYMPCPEPCESLHDLIMCQCKRKEBERPTEFYLOAFLEDYFTSTBPQOPGE 539
Db 475 LDQVGRGYMPCPEPCESLHDLIMCQCKRKEBERPTEFYLOAFLEDYFTSTBPQOPGE 534
Qy 540 NL 541
Db 535 NL 536

RESULT 9
US-09-949-016-10282
Sequence 10282, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10282
LENGTH: 537
TYPE: PRT
ORGANISM: Human
US-09-949-016-10282

Query Match 97.2%; Score 2778.5; DB 2; Length 537;
Best Local Similarity 97.6%; Pred. No. 2.6e-214;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

Qy 1 MGSNKSXPDAQORRSLSPESENVHGA-CGAFPASQTPSPKASADGHRGSAAFVPPAAE 59
Db 2 MGSNKSXPDAQORRSLSPESENVHGA-CGAFPASQTPSPKASADGHRGSAAFVPPAAE 61
Qy 60 PKLFGGFNSSDVTYTSQBRAGALAGVTTFTVALYDYSRTETDLSFKKGERLQIVNNTKRV 119
Db 62 PKLFGGFNSSDVTYTSQBRAGALAGVTTFTVALYDYSRTETDLSFKKGERLQIVNNTKRV 118


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Oy 301 AIKTLKPTMSSEALQEAQWKKLHKKLVOLYAVVSEEPITYIYEMNKGSLDFPKG 360
Db 293 AIKTLKPTMSSEALQEAQWKKLHKKLVOLYAVVSEEPITYIYEMNKGSLDFPKG 352
Oy 361 ETGKTLRLPOLVDMSAQISGAAVYERMMYVHHDLPANILVGNLVCRAVDGLRLIE 420
Db 353 EMGKTLRLPOLVDMAAQISGAAVYERMMYVHHDLPANILVGNLVCRAVDGLRLIE 412
Oy 421 DNEYTARQAKRPIMTAPREALYGRFTIKSDVMSFGILLTTLTGGRVPPPMNREYL 480
Db 413 DNEYTARQAKRPIMTAPREALYGRFTIKSDVMSFGILLTTLTGGRVPPPMNREYL 472
Oy 481 DVERGYMPCCPECPESLHDMCOCMKRKEPERPFVEYLQAFJADYFTSTEPQYGEN 540
Db 473 DVERGYMPCCPECPESLHDMCOCMKRDRDPERPFVEYLQAFJADYFTSTEPQYGEN 532
Oy 541 L 541
Db 533 L 533

RESULT 12
US-07-820-011A-2
; Sequence 2, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madril, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; TITLE OF INVENTION: and Plasmidogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820.011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; HYPOTHEetical: No
; FRAGMENT TYPE: Complete Sequence
; ORIGINAL SOURCE:
; ORGANISM: Gallus, gallus
; PUBLICATION INFORMATION:
; AUTHORS: Takeya, Tatsuo
; AUTHORS: Hanafusa, Hidesaburo
; TITLE: Structure and Sequence of the

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/ TITLE: Cellular Gene Homologous to the RSV src
/ TITLE: Gene and the Mechanism for Generating the
/ TITLE: Transforming Virus
/ JOURNAL: Cell
/ VOLUME: 32
/ PAGES: 881-890
/ DATE: March, 1983
/ US-07-820-011A-2

Query Match          92.4%; Score 2642; DB 1; Length 533;
Best Local Similarity 92.8%; Pred. No. 2.3e-203;
Matches 502; Conservative 14; Mismatches 17; Indels 8; Gaps 2;

OY 1 MGSNKSXPXKASORRRSLSEPEENVHAGGAPASQTSQSPASADQHGPSAAFPPPAAEP 60
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 1 MGSSKSPKXSDQSRRLSEPPDSTH--HGCPASQTPKXAPATHTRPPSPSGTVATEP 58
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 61 KLFGSPNSSDPVTSPORAGALAGVTTFVALVDYESTRETDLSFKKGERLOIVNTRKYD 120
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 59 KLPGFNTSDPVTSPORAGALAGVTTFVALVDYESTRETDLSFKKGERLOIVNNT---- 114
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 121 VREGDWMVLAHSLSTGQTGYIPSNVAPSDSIQAEEMYPGKITRRESERLLMAENPCTP 180
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 115 --EGDWMVLAHSLTGTGYIPSNVAPSDSIQAEEMYPGKITRRESERLLNPNPCTP 172
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 181 LVRSSETTKGAYCISVDFDNKAKLANKYKIRKLDGSGFYITRTQPNLSIQOLVAYYSK 240
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 173 LVRSSETTKGAYCISVDFDNKAKLANKYKIRKLDGSGFYITRTQPNLSIQOLVAYYSK 232
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 241 HADGICRLTFVCPCTSPKPTQGLAKDAWEIPRESLRLEVKLGQSGCFGEVMMGTNQTTRV 300
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 233 HADGICRLTNVCTSPKPTQGLAKDAWEIPRESLRLEVKLGQSGCFGEVMMGTNQTTRV 292
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 301 AIKTLKQTPMSPEAFLOBAQVMKKLRHEKLVQLVAVVSEBPIYIVTEYMNKGLLDPKLG 360
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 293 AIKTLKQTPMSPEAFLOBAQVMKKLRHEKLVQLVAVVSEBPIYIVTEYMNKGLLDPKLG 352
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 361 ETGKTLPLPOLVDMASQIASMAVVERMNYVHRDLRANLIVGENLVCKVADPGLALIE 420
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 353 EMGKTYLPLPOLVDMAAQIASMAVVERMNYVHRDLRANLIVGENLVCKVADPGLALIE 412
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 421 DNEVTAROGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVPYRGVNNREVL 480
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 413 DNEVTAROGAKFPKMTAPBAALYGRFTIKSDVMSFGILLTELTKGRVPYRGVNNREVL 472
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 481 DOVERGYRMPCEPCPSLHDLMQCCKRKEBERPTEYLOAFLEDYFTSTEPQYQGEN 540
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 473 DOVERGYRMPCEPCPSLHDLMQCCKRKEBERPTEYLOAFLEDYFTSTEPQYQGEN 532
   |||||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 541 L 541
   |||:|||||:|||||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 533 L 533

RESULT 13
PCT-US93-00445-2
/ Sequence 2, Application PC/TUS9300445
/ GENERAL INFORMATION:
/ APPLICANT: Bell, Leonard
/ APPLICANT: Madri, Joseph A.
/ APPLICANT: Warren, Stephen L.
/ APPLICANT: Luthringer, Daniel J.
/ TITLE OF INVENTION: Genetically Engineered
/ TITLE OF INVENTION: Endothelial Cells
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Maurice M. Klee
/ STREET: 1951 Burr Street
/ CITY: Fairfield
/ STATE: Connecticut
/ COUNTRY: USA
/ ZIP: 06430
/ COMPUTER READABLE FORM:

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MEDIUM TYPE: 3.5 inch, 760 kb storage
 COMPUTER: DELL 486/50
 OPERATING SYSTEM: DOS 5.0
 SOFTWARE: Displaywrite 3
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/00445
 FILING DATE: 19930105
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/820, 011
 FILING DATE: 06-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-101PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255 1400
 TELEFAX: (203) 254 1101
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 533 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: No
 FRAGMENT TYPE: Complete Sequence
 ORIGINAL SOURCE:
 ORGANISM: Gallus, gallus
 PUBLICATION INFORMATION:
 AUTHORS: Takeya, Tatsuo
 TITLES: Structure and Sequence of the
 TITLE: Cellular Gene Homologous to the RSV SRC
 TITLE: Gene and the Mechanism for Generating the
 JOURNAL: Cell
 VOLUME: 32
 PAGES: 881-890
 DATE: March, 1983

Query Match	92.4%	Score 2642	DB 5	Length 533
Best Local Similarity	92.8%	Pred. No. 2.3e+203		
Matches 502	Conservative 14	Mismatches 17	Indels 8	Gaps 2
QY	1	MGSNKRKPKASQRRRLSEPEENVGAGCAPPAQTPPKPSADHRGPSAFAVYPAAP	60	
DB	1	MGSSKSRKPKDPSQRRRLSEPPDSTH--HGCFPASGTPKMTAAPDHRTPSPSFCVIAHEP	58	
QY	61	KLPGFNSSDTVTYSQPRAGALAGGYTFVALYDIESRTETDLSFKKGERLQIVNTRKVD	120	
DB	59	KLPGFNPSTDTVTSPORAGALAGGYTFVALYDYESRRETDLSPFKKGERLQIVNNT---	114	
QY	121	VREEDMWLHLSLNGQGYTIPSNVYAPSDLSQAEWYFGKLTTRRESEKLLNAENRGTF	180	
DB	115	--BEDMWLHLSLTGGQGYTIPSNVYAPSDLSQAEWYFGKLTTRRESEKLLNAPENRGTF	172	
QY	181	LVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRQENSLQOLVAAYYSK	240	
DB	173	LVRESETTKGAAYCLSVSPFDNAKGLNVGHYKIRKLDGSGFYITSRQENSLQOLVAAYYSK	232	
QY	241	HADSLCHRLTIVGPTSKRQTOGLAKDAWEIPRESRLREVKLGQCGFGEVWMTANGTTRV	300	
DB	233	HADSLCHRLTIVGPTSKRQTOGLAKDAWEIPRESRLREVKLGQCGFGEVWMTANGTTRV	292	
QY	301	AIKTLKCGTMSPEAPLOEAQYMKLHREKLVOLVYVSEEPYIYVTEYMNKSLDLPFKG	360	
DB	293	AIKTLKCGTMSPEAPLOEAQYMKLHREKLVOLVYVSEEPYIYVTEYMNKSLDLPFKG	352	
QY	361	ETGKYRLRLPOLVDMSAQIASGMAVYERNNVYHRDLRAANILVGNLVCKVADFGIARLIE	420	
DB	353	EMGKYRLRLPOLVDMAAQIASGMAVYERNNVYHRDLRAANILVGNLVCKVADFGIARLIE	412	

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QY 421 NENEYARCGAKPPIKMTAPEALYGRFTKSPVMSFGILLTETTKGRVPYPMNAREVL 480
Db 413 DNEYIARCGAFPIKMTAPEALYGRFTKSPVMSFGILLTETTKGRVPYPMNAREVL 472
QY 481 DQVERGYMPCBPBECPESLHDLMCQCMRKSPERPFFBYLQAFLEDYFTSTBPOYGEN 540
Db 473 DQVERGYMPCBPBECPESLHDLMCQCMRKDPERPFFBYLQAFLEDYFTSTBPEYGEN 532
QY 541 L 541
Db 533 L 533
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	Query Match	73.8%	Score 2111	DB 2	Length 543
	Best Local Similarity	72.8%	Pred. No. 8,8e-161		
	Matches	405	Conservative	49	Mismatches 74; Indels 28; Gaps 4
QY	1	MGSNKS-----PKDASORRSLSPESENHGAGCAPASQTPSKSPASADGHR-----	47		
DB	1	MGCISKENKSPAIRYPBNTPEPVSTVSXHGAEPTTSPCCSSAKGTAVNFFSLSM	60		
QY	48	--GPSAAFPVPAABEKLFCGFENSSDPTVTSPPQAGALAGVTFVALYDYESRFTDLSFK	105		
DB	61	PPGSSSGVTP-----FGAASSSSVSPSSIPAGLTGVTTFVALYDYEARFTDLSFK	113		
QY	106	KGERLQIVNNTRKVDVREGDWMLAHSLSGTGTGYLPSNVVAPSDSIQAEWYFGKITRRR	165		

Db 114 KGERFQIINN-----EGDWEARSIAIGKNGIIPSNVYAPADSIOAEWYFGKMGKRD 167
Qy 166 SERLLLAENPRGTFIVRESEETTKGAYCISVSDPNAKGLNVHYKIRKLDGSGFYITSR 225
Db 168 AERLLINPGNQRIIFLVRESEETTKGAYSLIRDMDEIRGDNVHYKIRKLDNGGYITTR 227
Qy 226 TQNSIQOLVAVYYSKADGICHRLTTCPTSKPOTQGLADAMEIPRESIRLEVKGQGC 265
Db 228 AQPDTLQKLVKHYTHADGICHRLTTCPTVKPQTQGLADAMEIPRESIRLEVKGQGC 287
Qy 286 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEBPIYIV 345
Db 288 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEBPIYIV 347
Qy 346 TEYMNKGSLLDPLKSGTGYLRPLQVDMSAQIASGMAVYERNVYHRDLRAANIIVGEN 405
Db 348 TEYMNKGSLLDPLKSGTGYLRPLQVDMSAQIASGMAVYERNVYHRDLRAANIIVGEN 407
Qy 406 LVCKVADFGIARLIENNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 465
Db 408 LVCKVADFGIARLIENNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 467
Qy 466 KGRVYPGMVNRREVLDOVERGYRMPCCPESLHDLMOCKWKEPERPTEFYLOAFLE 525
Db 468 KGRVYPGMVNRREVLDOVERGYRMPCCPESLHDLMOCKWKEPERPTEFYLOAFLE 527
Qy 526 DYTSTTEPOYQGENL 541
Db 528 DYTSTTEPOYQGENL 543

RESULT 15
US-08-232-545-14
; Sequence 14, Application US/08232545
; Patent No. 6506578
; GENERAL INFORMATION:

; APPLICANT: Ulrich, Axel
; APPLICANT: Glisheky, Mikhail
; APPLICANT: Sures, Iman G.
; TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,545
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

; MOLECULE TYPE: protein
US-08-232-545-14

Query Match 73.8%; Score 2111; DB 2; Length 543;
Best Local Similarity 72.8%; Pred. No. 8.8e-161;
Matches 405; Conservative 49; Mismatches 74; Indels 28; Gaps 4;

Qy 1 MGSNKR-----PDAQQRRLSEPSNENAGAGAPFASQTPSPAPADGHR----- 47
Db 1 MGCIRKKNKSPAIKRYRPENTPEPVSTSVHYGAEPITVSPCSSSAKGAIVNPFSSLSMT 60
Qy 48 --GPSAFAVPPAEPKLFGEFNSSDVTSPQRAAGALAGVTFVALYDRESRTETLSFK 105
Db 61 FPGSSGVTP-----FGASSSFVSVSSYRAGLTGCTTIFVALYDYEARTEDLSFK 113
Qy 106 KGERLOIVNTRKVDVBEQDWMIAHSLSTGQGYIPSNVYAPADSIOAEWYFGKTRRE 165
Db 114 KGERFQIINN-----EGDWEARSIAIGKNGIIPSNVYAPADSIOAEWYFGKMGKRD 167
Qy 166 SERLLLAENPRGTFIVRESEETTKGAYCISVSDPNAKGLNVHYKIRKLDGSGFYITSR 225
Db 168 AERLLINPGNQRIIFLVRESEETTKGAYSLIRDMDEIRGDNVHYKIRKLDNGGYITTR 227
Qy 226 TQNSIQOLVAVYYSKADGICHRLTTCPTSKPOTQGLADAMEIPRESIRLEVKGQGC 285
Db 228 AQPDTLQKLVKHYTHADGICHRLTTCPTVKPQTQGLADAMEIPRESIRLEVKGQGC 287
Qy 286 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEBPIYIV 345
Db 288 FGEVMMGTWNGTTRVAIKTLKPGTMSPEAFLOEAQVKKLRHEKLVOLYAVVSEBPIYIV 347
Qy 346 TEYMNKGSLLDPLKSGTGYLRPLQVDMSAQIASGMAVYERNVYHRDLRAANIIVGEN 405
Db 348 TEYMNKGSLLDPLKSGTGYLRPLQVDMSAQIASGMAVYERNVYHRDLRAANIIVGEN 407
Qy 406 LVCKVADFGIARLIENNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 465
Db 408 LVCKVADFGIARLIENNEYTARQAKFPIKMTAPEALYGRFTIKSDVMSFGILLTELTT 467
Qy 466 KGRVYPGMVNRREVLDOVERGYRMPCCPESLHDLMOCKWKEPERPTEFYLOAFLE 525
Db 468 KGRVYPGMVNRREVLDOVERGYRMPCCPESLHDLMOCKWKEPERPTEFYLOAFLE 527
Qy 526 DYTSTTEPOYQGENL 541
Db 528 DYTSTTEPOYQGENL 543

Search completed: June 5, 2006, 17:18:17
Job time : 32.0766 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:14 ; Search time 108.267 Seconds
(without alignments)
2314.645 Million cell updates/sec

Title: US-10-691-079-3

Perfect score: 2859

Sequence: 1 MGSNKSXPDAASQRRSLR.....AFLEDYFTSTPEYQPGENL 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
 - 2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
 - 3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
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 - 6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2859	100.0	541	4 US-10-691-079-3	Sequence 3, Appli
2	2837.5	99.2	542	5 US-10-732-923-13447	Sequence 13447, A
3	2820.5	98.7	542	4 US-10-691-079-1	Sequence 1, Appli
4	2778.5	97.2	536	3 US-09-977-260-13	Sequence 11, Appl
5	2778.5	97.2	536	3 US-09-929-266-10	Sequence 10, Appl
6	2778.5	97.2	536	3 US-09-977-261-13	Sequence 13, Appl
7	2778.5	97.2	536	4 US-10-691-079-2	Sequence 2, Appli
8	2778.5	97.2	536	5 US-10-887-588-2	Sequence 2, Appli
9	2778.5	97.2	536	5 US-10-487-641-2	Sequence 2, Appli
10	2778.5	97.2	536	5 US-10-825-568-10	Sequence 10, Appl
11	2778.5	97.2	536	5 US-10-821-231C-1	Sequence 1, Appli
12	2778.5	97.2	536	5 US-10-469-469-273	Sequence 24, Appl
13	2778.5	97.2	536	6 US-11-233-510-24	Sequence 56, Appl
14	2773.5	97.0	535	4 US-10-394-132A-56	Sequence 56, Appl
15	2773.5	97.0	535	5 US-10-814-109-4	Sequence 4, Appli
16	2745.5	96.0	530	5 US-10-887-588-4	Sequence 4, Appli
17	2711.5	94.8	533	4 US-10-330-773-749	Sequence 749, App
18	2648	92.6	533	4 US-10-276-633-1	Sequence 1, Appli
19	2648	92.6	533	5 US-10-732-923-13652	Sequence 13652, A
20	2645	92.5	533	5 US-10-732-923-13654	Sequence 13654, A
21	2645	92.5	533	6 US-11-230-995-3	Sequence 3, Appli
22	2643	92.4	533	4 US-10-732-923-13650	Sequence 13650, A
23	2623	91.7	533	4 US-10-276-633-2	Sequence 2, Appli
24	2603	91.0	587	5 US-10-732-923-13472	Sequence 13472, A
25	2596	90.8	568	5 US-10-732-923-13474	Sequence 13474, A
26	2590	90.6	587	5 US-10-732-923-13469	Sequence 13469, A
27	2581	90.3	557	5 US-10-732-923-13475	Sequence 13475, A

28	2515	88.0	526	5 US-10-732-923-13499	Sequence 13499, A
29	2498	87.4	526	5 US-10-732-923-13484	Sequence 13484, A
30	2498	87.4	772	5 US-10-732-923-13485	Sequence 13485, A
31	2479	86.7	526	5 US-10-732-923-13483	Sequence 13483, A
32	2473	86.5	526	5 US-10-732-923-13497	Sequence 13497, A
33	2468	86.3	537	5 US-10-732-923-13636	Sequence 13636, A
34	2467	86.3	526	5 US-10-732-923-13493	Sequence 13493, A
35	2467	86.3	526	5 US-10-732-923-13498	Sequence 13498, A
36	2466	86.3	526	5 US-10-732-923-13489	Sequence 13489, A
37	2465	86.2	526	5 US-10-732-923-13486	Sequence 13486, A
38	2463.5	86.2	523	5 US-10-732-923-13488	Sequence 13488, A
39	2463.5	86.2	535	5 US-10-732-923-13495	Sequence 13495, A
40	2463	86.1	526	5 US-10-732-923-13491	Sequence 13491, A
41	2452	85.8	526	5 US-10-732-923-13487	Sequence 13487, A
42	2448	85.6	526	5 US-10-732-923-13482	Sequence 13482, A
43	2444.5	85.5	532	5 US-10-732-923-13633	Sequence 13633, A
44	2442.5	85.4	532	5 US-10-732-923-13635	Sequence 13635, A
45	2439.5	85.3	532	5 US-10-732-923-13637	Sequence 13637, A

ALIGNMENTS

RESULT 1
US-10-691-079-3

Sequence 3, Application US/10691079
Publication No. US2004017631A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: PRAV002/0030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 541
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-691-079-3

Query Match 100.0%; Score 2859; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 4e-177;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSNKSXPDAASQRRSLRSEENVHAGAFPAASQTPSPKPSADGHRGSAFVPPAEP	60
DB	1	MGSNKSXPDAASQRRSLRSEENVHAGAFPAASQTPSPKPSADGHRGSAFVPPAEP	60
QY	61	KLFGGNSSTVTTSPPQAGALAGVTFVALYDSESTETDLSFKKGERLQIVNTRKVD	120
DB	61	KLFGGNSSTVTTSPPQAGALAGVTFVALYDSESTETDLSFKKGERLQIVNTRKVD	120
QY	121	VRESDWMLAHSITGQGYIPSNYVAPSDSIQAEEMVFGKITRRESRLTLMAENPGTF	180
DB	121	VRESDWMLAHSITGQGYIPSNYVAPSDSIQAEEMVFGKITRRESRLTLMAENPGTF	180
QY	181	LVESEETTKAYCISVSPDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQOLVAYYSK	240
DB	181	LVESEETTKAYCISVSPDNAGLVNKHKIRKLDGSGFYITSRTQFNSLQOLVAYYSK	240
QY	241	HADGLCHRLTTCVPTSPQOTGLAKDAWEIPRESLRLEVTLGGCCGCFGEVWNGTTRV	300
DB	241	HADGLCHRLTTCVPTSPQOTGLAKDAWEIPRESLRLEVTLGGCCGCFGEVWNGTTRV	300
QY	301	AITTKRGTMSPAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYMEVYMGSLDPLKG	360
DB	301	AITTKRGTMSPAPLOEAQVMKKLRHEKLVOLYAVVSEEPITYMEVYMGSLDPLKG	360
QY	361	ETGKYRLPOLVMSAQIASGMAVVERMNVVHDLRAANILVGBNLCVKVADFGLABIE	420
DB	361	ETGKYRLPOLVMSAQIASGMAVVERMNVVHDLRAANILVGBNLCVKVADFGLABIE	420

QY 421 DNEVTAAGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 480
 DB 421 DNEVTAAGAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 480
 QY 481 DQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 DB 481 DQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 QY 541 L 541
 DB 541 L 541
 RESULT 2
 US-10-732-923-13447
 ; Sequence 13447, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ. ID NOS: 24149
 ; SEQ. ID NO 13447
 ; LENGTH: 542
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-732-923-13447

Query Match 99.2%; Score 2837.5; DB 5; Length 542;
 Best Local Similarity 99.3%; Pred. No. 1e-175;
 Matches 538; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MGSNKSXPDAQRRRLSEPSENVHAGAFAPASQTPSPKPSADGHRGSAFAVP-ALAE 59
 DB 1 MGSNKSXPDAQRRRLSEPSENVHAGAFAPASQTPSPKPSADGHRGSAFAVP-ALAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDYSRTETDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDYSRTETDLSFKKGERLQIVNNTKRV 120
 QY 120 DVEEGMWLAHSISTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 179
 DB 121 DVEEGMWLAHSISTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 180
 QY 180 FLVRESETTKGAAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRQFNSLQOLVAAYS 239
 DB 181 FLVRESETTKGAAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
 QY 240 KHAHGLCHRLTTYCPTSPKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNGTTR 299
 DB 241 KHAHGLCHRLTTYCPTSPKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNGTTR 300
 QY 300 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEEPYIYTEYMNKSLDDFLK 359
 DB 301 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEEPYIYTEYMNKSLDDFLK 360
 QY 360 GETGKTLRLPOLVDMASQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 419
 DB 361 GETGKTLRLPOLVDMASQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
 QY 420 EDNEVTAARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 479
 DB 421 EDNEVTAARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 480
 QY 480 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 539
 DB 481 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 - QY 540 NL 541

DB 541 NL 542
 RESULT 3
 US-10-691-079-1
 ; Sequence 1, Application US/10691079
 ; Publication No. US2004016313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMA S.A.
 ; TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
 ; FILE REFERENCE: FRAV2002/0030
 ; CURRENT APPLICATION NUMBER: US/10/691,079
 ; CURRENT FILING DATE: 2003-10-22
 ; NUMBER OF SEQ. ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ. ID NO 1
 ; LENGTH: 542
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-691-079-1

Query Match 98.7%; Score 2820.5; DB 4; Length 542;
 Best Local Similarity 98.7%; Pred. No. 1.3e-174;
 Matches 535; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MGSNKSXPDAQRRRLSEPSENVHGA-GAPASQTPSPKPSADGHRGSAFAVP-ALAE 59
 DB 1 MGSNKSXPDAQRRRLSEPSENVHAGAGAFAPASQTPSPKPSADGHRGSAFAVP-ALAE 60
 QY 60 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDYSRTETDLSFKKGERLQIVNNTKRV 119
 DB 61 PKLFGFNSSDVTYSPQAGALAGVTTFYALYDYSRTETDLSFKKGERLQIVNNTKRV 120
 QY 120 DVEEGMWLAHSISTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 179
 DB 121 DVEEGMWLAHSISTGQGYIPSNVYAPSDSIQAEEMVFGKITRRESERLLNAENPRGT 180
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 DB 181 FLVRESETTKGAAYCLSVSPDNAGKLVNKHVKIRKLDGSGFYITSTRQFNSLQOLVAAYS 240
 QY 240 KHAHGLCHRLTTYCPTSPKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNGTTR 299
 DB 241 KHAHGLCHRLTTYCPTSPKQTOGLADAMEIPRESLRLEVKLGQCGFGEVMMGTNGTTR 300
 QY 300 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEEPYIYTEYMNKSLDDFLK 359
 DB 301 VALKTLPKGTMSPEAFLOBAQVWKLRHEKLVOLYAVVSEEPYIYTEYMNKSLDDFLK 360
 QY 360 GETGKTLRLPOLVDMASQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 419
 DB 361 GETGKTLRLPOLVDMASQIASGMAVYERMYVHRDLRAANIIVGENLVCKVADFGIARLI 420
 QY 420 EDNEVTAARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 479
 DB 421 EDNEVTAARQAKFPKMTAPEALYGRFTIKSDVMSFGILLTELTKGRVYPGMVNRVL 480
 QY 480 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 539
 DB 481 LDQVERGYRMPCCPECPESLHDLMCQWRKEBERPTEFYLAFLDYFTSTEPQYQGEN 540
 QY 540 NL 541
 DB 541 NL 542
 RESULT 4
 US-09-977-260-13
 ; Sequence 13, Application US/09977260
 ; Publication No. US20020192790A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ULLRICH, AXEL

```

; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-260-13

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Query Match      97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKRPASADGHRGSPSAFVPPAAE 59
DB 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKRPASADGHRGSPSAFVPPAAE 60
QY 60 PKLPGFNSSDVTYSPQACALAGVTTFVALVDYESTRTDLSFKKGERLQIVNNTKRV 119
DB 61 PKLPGFNSSDVTYSPQACALAGVTTFVALVDYESTRTDLSFKKGERLQIVNNTKRV 117
QY 120 DVEBGDWMLHSLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESEERLLNENRGT 179
DB 118 ---BGDWMLHSLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESEERLLNENRGT 174
QY 180 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
DB 175 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
QY 240 KHADGLCHRLTTYCPTSKPQTQGLAKDAWEIPRESLLEVKLGCGCGEYVWMTGNCTTR 299
DB 235 KHADGLCHRLTTYCPTSKPQTQGLAKDAWEIPRESLLEVKLGCGCGEYVWMTGNCTTR 294
QY 300 VALKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYITEYNNKSGSLDPLK 359
DB 295 VALKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYITEYNNKSGSLDPLK 354
QY 360 GETGKYRLPOLYDMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLI 419
DB 355 GETGKYRLPOLYDMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLI 414
QY 420 EDNEYTRARQAKPPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTGKRPVYPMVNRREV 479
DB 415 EDNEYTRARQAKPPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTGKRPVYPMVNRREV 474
QY 480 LDVERGYRMPCEPCESLHDLWCOCWRKEPERPFEEYLOAFLEDFYFSTEPQYQGE 539
DB 475 LDVERGYRMPCEPCESLHDLWCOCWRKEPERPFEEYLOAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536

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RESULT 5
US-09-929-266-10
; Sequence 10, Application US/09929266
; Publication No. US20030045694A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Letimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kershnar
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matthesich

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```

; APPLICANT: Kevin J. McConnell
; APPLICANT: ULTRA-SENSITIVE DETECTION SYSTEMS
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.0003U2
; CURRENT APPLICATION NUMBER: US/09/929,266
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-266-10

```

```

Query Match      97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

```

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QY 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKRPASADGHRGSPSAFVPPAAE 59
DB 1 MGSNKSXPXKASQRRRLSEPSENVHGA-GGAFPASQTPSKRPASADGHRGSPSAFVPPAAE 60
QY 60 PKLPGFNSSDVTYSPQACALAGVTTFVALVDYESTRTDLSFKKGERLQIVNNTKRV 119
DB 61 PKLPGFNSSDVTYSPQACALAGVTTFVALVDYESTRTDLSFKKGERLQIVNNTKRV 117
QY 120 DVEBGDWMLHSLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESEERLLNENRGT 179
DB 118 ---BGDWMLHSLSTGQGYIPSNYVAPSDSIQAEVYFGKITRRESEERLLNENRGT 174
QY 180 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 239
DB 175 FLVRESEETTGAYCLSVSDPDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQQLVAYYS 234
QY 240 KHADGLCHRLTTYCPTSKPQTQGLAKDAWEIPRESLLEVKLGCGCGEYVWMTGNCTTR 299
DB 235 KHADGLCHRLTTYCPTSKPQTQGLAKDAWEIPRESLLEVKLGCGCGEYVWMTGNCTTR 294
QY 300 VALKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYITEYNNKSGSLDPLK 359
DB 295 VALKTLKPGTMSPEAFLOEAQVWKKLRHEKLVOLYAVVSEPIYITEYNNKSGSLDPLK 354
QY 360 GETGKYRLPOLYDMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLI 419
DB 355 GETGKYRLPOLYDMSAQIASGMAVYERMYVHRDLPAANILVGENLVCKVADGRLRLI 414
QY 420 EDNEYTRARQAKPPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTGKRPVYPMVNRREV 479
DB 415 EDNEYTRARQAKPPIKMTAPBAALYGRFTIKSDVMSFGILLTELTTGKRPVYPMVNRREV 474
QY 480 LDVERGYRMPCEPCESLHDLWCOCWRKEPERPFEEYLOAFLEDFYFSTEPQYQGE 539
DB 475 LDVERGYRMPCEPCESLHDLWCOCWRKEPERPFEEYLOAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536

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RESULT 6
US-09-977-261-13
; Sequence 13, Application US/0977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULTRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261

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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 536
TYPE: PRF
ORGANISM: Homo sapiens
US-09-977-261-13

Query Match 97.2%; Score 2778.5; DB 3; Length 536;
Best Local Similarity 97.6%; Pred. No. 6,6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 MGSNKSXPDAQSRRLSPSENVHGA-GGAFPASQTPSKPASADGHRPSAFAVPAAE 59
    |||
DB 1 MGSNKSXPDAQSRRLSPSENVHGA-GGAFPASQTPSKPASADGHRPSAFAVPAAE 60
    |||
QY 60 PKLFGFNSDVTSPQRAAGALAGVTTFVALYDYESRTEPDLSPFKGGERLQIVNNTKRY 119
    |||
DB 61 PKLFGFNSDVTSPQRAAGALAGVTTFVALYDYESRTEPDLSPFKGGERLQIVNNT--- 117
    |||
QY 120 DVREGDWMLAHSLSTQOTGYIPSNVYAPSDSIQAEEMYGKTRRESEBLLNAENPRGT 179
    |||
DB 118 ---EGDWMLAHSLSTQOTGYIPSNVYAPSDSIQAEEMYGKTRRESEBLLNAENPRGT 174
    |||
QY 180 FLVRESETTKGAICLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQQLVAYYS 239
    |||
DB 175 FLVRESETTKGAICLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQQLVAYYS 234
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QY 240 KPADGICHLITVCPTSKPQTQGLAKDAWEIPRESIRLEVKLGOGCGFGEVMWGTVNGTTR 299
    |||
DB 235 KPADGICHLITVCPTSKPQTQGLAKDAWEIPRESIRLEVKLGOGCGFGEVMWGTVNGTTR 294
    |||
QY 300 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEPIYIYTEYMNKSLDLDFLK 359
    |||
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEPIYIYTEYMNKSLDLDFLK 354
    |||
QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 419
    |||
DB 355 GETGKYLRLPOLVDMSAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 414
    |||
QY 420 EDNETYARQAGAPPIKMTAPEALYGRPTIKSDVMSFGILLTELTKGRVPPYGMVNRREV 479
    |||
DB 415 EDNETYARQAGAPPIKMTAPEALYGRPTIKSDVMSFGILLTELTKGRVPPYGMVNRREV 474
    |||
QY 480 LQOVERGYMPCPECPESLHDLMCQMKPEBERPTFEYLOAFLEDYFTSTEPYQOPGE 539
    |||
DB 475 LQOVERGYMPCPECPESLHDLMCQMKPEBERPTFEYLOAFLEDYFTSTEPYQOPGE 534
    |||
QY 540 NL 541
    ||
DB 535 NL 536
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RESULT 7
US-10-691-079-2
Sequence 2, Application US/10691079
Publication No. US20040176313A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMA S.A.
TITLE OF INVENTION: Inhibitors of SRC kinase for use in Alzheimer's disease
FILE REFERENCE: FRAV2002/0030
CURRENT APPLICATION NUMBER: US/10/691,079
CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRF
ORGANISM: Homo sapiens
US-10-691-079-2

Query Match 97.2%; Score 2778.5; DB 4; Length 536;
Best Local Similarity 97.6%; Pred. No. 6,6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 MGSNKSXPDAQSRRLSPSENVHGA-GGAFPASQTPSKPASADGHRPSAFAVPAAE 59
    |||
DB 1 MGSNKSXPDAQSRRLSPSENVHGA-GGAFPASQTPSKPASADGHRPSAFAVPAAE 60
    |||
QY 60 PKLFGFNSDVTSPQRAAGALAGVTTFVALYDYESRTEPDLSPFKGGERLQIVNNTKRY 119
    |||
DB 61 PKLFGFNSDVTSPQRAAGALAGVTTFVALYDYESRTEPDLSPFKGGERLQIVNNT--- 117
    |||
QY 120 DVREGDWMLAHSLSTQOTGYIPSNVYAPSDSIQAEEMYGKTRRESEBLLNAENPRGT 179
    |||
DB 118 ---EGDWMLAHSLSTQOTGYIPSNVYAPSDSIQAEEMYGKTRRESEBLLNAENPRGT 174
    |||
QY 180 FLVRESETTKGAICLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQQLVAYYS 239
    |||
DB 175 FLVRESETTKGAICLSVSDFDNAKGLNVGKIRKLDSCGFYITSTRQFNSLQQLVAYYS 234
    |||
QY 240 KPADGICHLITVCPTSKPQTQGLAKDAWEIPRESIRLEVKLGOGCGFGEVMWGTVNGTTR 299
    |||
DB 235 KPADGICHLITVCPTSKPQTQGLAKDAWEIPRESIRLEVKLGOGCGFGEVMWGTVNGTTR 294
    |||
QY 300 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEPIYIYTEYMNKSLDLDFLK 359
    |||
DB 295 VAIKTLKPGTMSPEAFLOEAQVWKLRHEKLVQLYAVVSEPIYIYTEYMNKSLDLDFLK 354
    |||
QY 360 GETGKYLRLPOLVDMSAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 419
    |||
DB 355 GETGKYLRLPOLVDMSAQIASGMAVYERNNYVHRDLRAANILVGENLVCKVADFGIARLI 414
    |||
QY 420 EDNETYARQAGAPPIKMTAPEALYGRPTIKSDVMSFGILLTELTKGRVPPYGMVNRREV 479
    |||
DB 415 EDNETYARQAGAPPIKMTAPEALYGRPTIKSDVMSFGILLTELTKGRVPPYGMVNRREV 474
    |||
QY 480 LQOVERGYMPCPECPESLHDLMCQMKPEBERPTFEYLOAFLEDYFTSTEPYQOPGE 539
    |||
DB 475 LQOVERGYMPCPECPESLHDLMCQMKPEBERPTFEYLOAFLEDYFTSTEPYQOPGE 534
    |||
QY 540 NL 541
    ||
DB 535 NL 536
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RESULT 8
US-10-887-588-2
Sequence 2, Application US/10887588
Publication No. US20040261142A1
GENERAL INFORMATION:
APPLICANT: Yeaman, Timothy J.
APPLICANT: Itby, Rosalyn B.
TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods
FILE REFERENCE: USF-T136
CURRENT APPLICATION NUMBER: US/10/887,588
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US/09/444,711
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 536
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)_(536)
OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
by the normal c-Src coding region
US-10-887-588-2

Query Match 97.2%; Score 2778.5; DB 5; Length 536;

Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 MGSNKSFKDASQRRSLSEPSENVHGA-GGAFPASQTPSKASADGHRGSPAATVPAAE 59
DB 1 MGSNKSFKDASQRRSLSEPSENVHGAAGGAFPASQTPSKASADGHRGSPAATVPAAE 60
QY PKLFGFNSSDVTYSPOBAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTKV 119
DB PKLFGFNSSDVTYSPOBAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTKV 117
QY 120 DVREBGMWLAHSLSTGQGYI PSNYVA PSDSIQAEWYFGKITRRESERLLNENPRGT 179
DB 118 ---BGDWMLHSLSTGQGYI PSNYVA PSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 239
DB 175 FLVRESSTTGAYCLSYSDPDNAGLVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEI PRESLEVLVKGCGCEGVMGTWGTTR 299
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEI PRESLEVLVKGCGCEGVMGTWGTTR 294
QY 300 VAIKTLKPGTMSPEAFIQEAOVMKGLRHEKLVOLYAVVSEPIYIVTEYNSKSLDLFLK 359
DB 295 VAIKTLKPGTMSPEAFIQEAOVMKGLRHEKLVOLYAVVSEPIYIVTEYNSKSLDLFLK 354
QY 360 GETSKYRLPOLVDMSAQISGMA YVERMNYVHRDLRAANILVGENLVCKVADGGLARLI 419
DB 355 GETSKYRLPOLVDMSAQISGMA YVERMNYVHRDLRAANILVGENLVCKVADGGLARLI 414
QY 420 EDNETYARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTETTTGKRVYPGMVNREV 479
DB 415 EDNETYARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTETTTGKRVYPGMVNREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDYFTSTEPQYQGE 539
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDYFTSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 9
US-10-497-641-2
; Sequence 2, Application US/10497641
; Publication No. US20050037446A1
; GENERAL INFORMATION:
; APPLICANT: Schmitt and Stork
; TITLE OF INVENTION: AGENTS THAT RECOGNIZE SRC WHEN PHOSPHORYLATED AT SERINE 17
; FILE REFERENCE: 65064-02
; CURRENT APPLICATION NUMBER: US/10/497,641
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/US02/41564
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/345,888
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-641-2

Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
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QY 60 PKLFGFNSSDVTYSPOBAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTKV 119
DB 61 PKLFGFNSSDVTYSPOBAGLAGVTTFFVALYDESRTETDLSFKKGERLOIVNNTKV 117
QY 120 DVREBGMWLAHSLSTGQGYI PSNYVA PSDSIQAEWYFGKITRRESERLLNENPRGT 179
DB 118 ---BGDWMLHSLSTGQGYI PSNYVA PSDSIQAEWYFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 239
DB 175 FLVRESSTTGAYCLSYSDPDNAGLVKHYKIRKLDGSGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEI PRESLEVLVKGCGCEGVMGTWGTTR 299
DB 235 KHADGLCHRLTTVCPTSKPOTQGLAKDAMEI PRESLEVLVKGCGCEGVMGTWGTTR 294
QY 300 VAIKTLKPGTMSPEAFIQEAOVMKGLRHEKLVOLYAVVSEPIYIVTEYNSKSLDLFLK 359
DB 295 VAIKTLKPGTMSPEAFIQEAOVMKGLRHEKLVOLYAVVSEPIYIVTEYNSKSLDLFLK 354
QY 360 GETSKYRLPOLVDMSAQISGMA YVERMNYVHRDLRAANILVGENLVCKVADGGLARLI 419
DB 355 GETSKYRLPOLVDMSAQISGMA YVERMNYVHRDLRAANILVGENLVCKVADGGLARLI 414
QY 420 EDNETYARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTETTTGKRVYPGMVNREV 479
DB 415 EDNETYARQAKFPIKMTAPBAALYGRFTIKSDVMSFGILLTETTTGKRVYPGMVNREV 474
QY 480 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDYFTSTEPQYQGE 539
DB 475 LDQVERGYRMPCEPCESLHDLMCQCRKEPEERPFTEYLOAFLEDYFTSTEPQYQGE 534
QY 540 NL 541
DB 535 NL 536
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RESULT 10
US-10-825-568-10
; Sequence 10, Application US/10825568
; Publication No. US20050069916A1
; GENERAL INFORMATION:
; APPLICANT: Brian T. Chait
; APPLICANT: Darin R. Latimer
; APPLICANT: Paul M. Lizardi
; APPLICANT: Eric R. Kerehnar
; APPLICANT: Jon S. Morrow
; APPLICANT: Matthew E. Roth
; APPLICANT: Martin J. Matcovich
; TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
; FILE REFERENCE: 01173.000302
; CURRENT APPLICATION NUMBER: US/10/825,568
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/929,266
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/224,939
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/283,498
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-568-10
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Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

QY 1 MSGNSKPKDASQRRSLSEPVNHA-GGAPASQTPSKPASADHGRPSAAFPVPAE 59
DB 1 MSGNSKPKDASQRRSLSEPVNHA-GGAPASQTPSKPASADHGRPSAAFPVPAE 60
QY 60 PKLFGFNSDVTTSFORAGALAGVTTVALYDYSRTTDLSPFKGGERLQIVNTRKY 119
DB 61 PKLFGFNSDVTTSFORAGALAGVTTVALYDYSRTTDLSPFKGGERLQIVNTRKY 117
QY 120 DVREGMMLAHSLSTGOTGYIPSNVYAPSDIOAEEMYGKTRRSEERLLNAENPRGT 179
DB 118 ---EGMMLAHSLSTGOTGYIPSNVYAPSDIOAEEMYGKTRRSEERLLNAENPRGT 174
QY 180 FLVRESETTKGAACLSVSDFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAACLSVSDFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 234
QY 240 KHAADGLCHRLTVCPYSPKQTOGLADAMEIPRESLRLEVKLGQCGCFGEVWMTNGTTR 299
DB 235 KHAADGLCHRLTVCPYSPKQTOGLADAMEIPRESLRLEVKLGQCGCFGEVWMTNGTTR 294
QY 300 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYITEYMNKSGSLDLPLK 359
DB 295 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYITEYMNKSGSLDLPLK 354
QY 360 GETGKTLRLPOLVDMASQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKTLRLPOLVDMASQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNEYTARQAKFPIKMTAPEALYGRFTIKSDVWSFGILTLTKGRVPYGMVNRREV 479
DB 415 EDNEYTARQAKFPIKMTAPEALYGRFTIKSDVWSFGILTLTKGRVPYGMVNRREV 474
QY 480 LQOVERGYMPCBPCEBSLHDMCQMKRKEBERPFEYLOAFLEDYFTSTBPQOPGE 539
DB 475 LQOVERGYMPCBPCEBSLHDMCQMKRKEBERPFEYLOAFLEDYFTSTBPQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 11
US-10-821-231C-1
; Sequence 1, Application US/10821231C
; Publication No. US20050275837A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Dongmiao
; APPLICANT: Ben-Amotz, Dor
; APPLICANT: Xie, Yong
; APPLICANT: Davila, Vincent J.
; APPLICANT: Mrozek, Melissa
; APPLICANT: Ortiz, Cora
; TITLE OF INVENTION: PROCESS AND APPARATUS FOR SEGREGATION AND TESTING BY SPECTRAL
; FILE REFERENCE: 12264/17
; CURRENT APPLICATION NUMBER: US/10/821,231C
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/462,083
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/462,472
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 60/490,057
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/554,701
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/551,311
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-821-231C-1
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;
QY 1 MSGNSKPKDASQRRSLSEPVNHA-GGAPASQTPSKPASADHGRPSAAFPVPAE 59
DB 1 MSGNSKPKDASQRRSLSEPVNHA-GGAPASQTPSKPASADHGRPSAAFPVPAE 60
QY 60 PKLFGFNSDVTTSFORAGALAGVTTVALYDYSRTTDLSPFKGGERLQIVNTRKY 119
DB 61 PKLFGFNSDVTTSFORAGALAGVTTVALYDYSRTTDLSPFKGGERLQIVNTRKY 117
QY 120 DVREGMMLAHSLSTGOTGYIPSNVYAPSDIOAEEMYGKTRRSEERLLNAENPRGT 179
DB 118 ---EGMMLAHSLSTGOTGYIPSNVYAPSDIOAEEMYGKTRRSEERLLNAENPRGT 174
QY 180 FLVRESETTKGAACLSVSDFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 239
DB 175 FLVRESETTKGAACLSVSDFDNAKGLNVKHYKIRKLDGSGFYITSRTQFNSLQOLVAAYS 234
QY 240 KHAADGLCHRLTVCPYSPKQTOGLADAMEIPRESLRLEVKLGQCGCFGEVWMTNGTTR 299
DB 235 KHAADGLCHRLTVCPYSPKQTOGLADAMEIPRESLRLEVKLGQCGCFGEVWMTNGTTR 294
QY 300 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYITEYMNKSGSLDLPLK 359
DB 295 VAIKTLKPGTMSPEALQEAQVWKLRHEKLVOLYAVSEEPYIYITEYMNKSGSLDLPLK 354
QY 360 GETGKTLRLPOLVDMASQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 419
DB 355 GETGKTLRLPOLVDMASQIASGMAVYERNVYHRDLRAANILVGENLVCKVADFGIARLI 414
QY 420 EDNEYTARQAKFPIKMTAPEALYGRFTIKSDVWSFGILTLTKGRVPYGMVNRREV 479
DB 415 EDNEYTARQAKFPIKMTAPEALYGRFTIKSDVWSFGILTLTKGRVPYGMVNRREV 474
QY 480 LQOVERGYMPCBPCEBSLHDMCQMKRKEBERPFEYLOAFLEDYFTSTBPQOPGE 539
DB 475 LQOVERGYMPCBPCEBSLHDMCQMKRKEBERPFEYLOAFLEDYFTSTBPQOPGE 534
QY 540 NL 541
DB 535 NL 536

RESULT 12
US-10-469-469-273
; Sequence 273, Application US/10469469
; Publication No. US20060079493A1
; GENERAL INFORMATION:
; APPLICANT: FRITZ, LAWRENCE C.
; APPLICANT: BURROWS, FRANCIS J.
; TITLE OF INVENTION: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
; FILE REFERENCE: CON-0010-USN
; CURRENT APPLICATION NUMBER: US/10/469,469
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06518
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/272,751
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 273
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-469-469-273
Query Match 97.2%; Score 2778.5; DB 5; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;

Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 GSNKSKPKDASQRRRSLEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAPVPAAE 59
Db 1 GSNKSKPKDASQRRRSLEPSENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
QY 60 PKLFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNTRKV 119
Db 61 PKLFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDWMLAHSLSTGCTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 179
Db 118 ---EGDWMLAHSLSTGCTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRLDSGGFYITSRQFNSLQOLVAYYS 239
Db 175 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRLDSGGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPPTSPTQGLAKDAMEIPRESLREVLKGGCGEVMGTMGTTR 299
Db 235 KHADGLCHRLTTVCPPTSPTQGLAKDAMEIPRESLREVLKGGCGEVMGTMGTTR 294
QY 300 VAIKTLKPGTMSPEAFIQEAQVMKCLRHEKLVQLYAVVSEEPYIYITEYMSKSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIQEAQVMKCLRHEKLVQLYAVVSEEPYIYITEYMSKSLDPLK 354
QY 360 GETGKYRLPOLVDMASQIASGMAVVERMYVHRDLRAANILVGENLVCKVADGLARLI 419
Db 355 GETGKYRLPOLVDMASQIASGMAVVERMYVHRDLRAANILVGENLVCKVADGLARLI 414
QY 420 EDNETYAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVAREV 479
Db 415 EDNETYAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVAREV 474
QY 480 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
Db 535 NL 536
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RESULT 13

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US-11-233-510-24
; Sequence 24, Application US/11233510
; Publication No. US20060063190A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Whitehead, Clark M.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Marcello, Raphael
; APPLICANT: Morel, Didier
; TITLE OF INVENTION: Methods and Compositions for Evaluating
; TITLE OF INVENTION: Breast Cancer Prognosis
; FILE REFERENCE: 46143/296738
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 60/612,073
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/611,965
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-233-510-24
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Query Match 97.2%; Score 2778.5; DB 6; Length 536;
Best Local Similarity 97.6%; Pred. No. 6.6e-172;
Matches 529; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 1 GSNKSKPKDASQRRRSLEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAPVPAAE 59
Db 1 GSNKSKPKDASQRRRSLEPSENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
QY 60 PKLFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNTRKV 119
Db 61 PKLFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNT--- 117
QY 120 DVREGDWMLAHSLSTGCTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 179
Db 118 ---EGDWMLAHSLSTGCTGYIPSNYVAPSDSIQAEEMVFGKITRRESERLLNENPRGT 174
QY 180 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRLDSGGFYITSRQFNSLQOLVAYYS 239
Db 175 FLVRESSTTGAYCLSYSDPDNAGLVKVKYIKRLDSGGFYITSRQFNSLQOLVAYYS 234
QY 240 KHADGLCHRLTTVCPPTSPTQGLAKDAMEIPRESLREVLKGGCGEVMGTMGTTR 299
Db 235 KHADGLCHRLTTVCPPTSPTQGLAKDAMEIPRESLREVLKGGCGEVMGTMGTTR 294
QY 300 VAIKTLKPGTMSPEAFIQEAQVMKCLRHEKLVQLYAVVSEEPYIYITEYMSKSLDPLK 359
Db 295 VAIKTLKPGTMSPEAFIQEAQVMKCLRHEKLVQLYAVVSEEPYIYITEYMSKSLDPLK 354
QY 360 GETGKYRLPOLVDMASQIASGMAVVERMYVHRDLRAANILVGENLVCKVADGLARLI 419
Db 355 GETGKYRLPOLVDMASQIASGMAVVERMYVHRDLRAANILVGENLVCKVADGLARLI 414
QY 420 EDNETYAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVAREV 479
Db 415 EDNETYAROGAKKPEIKMTAPPAALYGRFTIKSDVMSFGILLTELTTKGRVYVPGVAREV 474
QY 480 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYQGE 539
Db 475 LDQVERGYRMPCEPCEBSLHDLMCQCRKEPEERPTFEYLQAFLEDFYFSTEPQYQGE 534
QY 540 NL 541
Db 535 NL 536
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RESULT 14

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US-10-394-322A-56
; Sequence 56, Application US/10394322A
; Publication No. US2003023391A1
; GENERAL INFORMATION:
; APPLICANT: Sunesis Pharmaceuticals, Inc.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-56
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Query Match 97.0%; Score 2773.5; DB 4; Length 535;
Best Local Similarity 97.6%; Pred. No. 1.4e-171;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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QY 2 GSNKSKPKDASQRRRSLEPSENVHGA-GGAFPASQTPSKPASADGHRGSAAPVPAAE 60
Db 1 GSNKSKPKDASQRRRSLEPSENVHGAAGGAFPASQTPSKPASADGHRGSAAPVPAAE 60
QY 61 KLRGFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNTRKVD 120
Db 61 KLRGFGFNSSDVTYVSPORAGLAGGVTTFVALYDRESRTETDLSFKKGERLQIVNNTRKVD 120
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Db      61 KLFEGFNSSPTVTS PQRAEPLAGVTT FVALYDYESRTEETDLSFKKGERLQIVNNT---- 116
Qy      121 VREGDMMLAHSLSTGQTGYIPSNYVAPSDSIQAEEMYPGKITRRESERLLINAEENRGT 180
Db      117 --EGDMMLAHSLSTGQTGYIPSNYVAPSDSIQAEEMYPGKITRRESERLLINAEENRGT 174
Qy      181 LVRESSETTKGAYCLSYSDFDNAGLVNKHKIRKLDGCGFYITSRTQFNSLQOLVAVYSK 240
Db      175 LVRESSETTKGAYCLSYSDFDNAGLVNKHKIRKLDGCGFYITSRTQFNSLQOLVAVYSK 234
Qy      241 HADGLCHRLTTVCPTSPQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 300
Db      235 HADGLCHRLTTVCPTSPQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 294
Qy      301 AITLKPCTMSPEAPFLOEAQVMKKLRHEKLVOLYAVVSEEPITYITEYNKSGSLDPLKG 360
Db      295 AITLKPCTMSPEAPFLOEAQVMKKLRHEKLVOLYAVVSEEPITYITEYNKSGSLDPLKG 354
Qy      361 ETGKYLRRLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRLIE 420
Db      355 ETGKYLRRLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRLIE 414
Qy      421 DNEYTAROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVL 480
Db      415 DNEYTAROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVL 474
Qy      481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPTEYLQAFLEDYFTSTEBQYQGEN 540
Db      475 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPTEYLQAFLEDYFTSTEBQYQGEN 534
Qy      541 L 541
Db      535 L 535

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RESULT 15
US-10-814-109-4
; Sequence 4, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; APPLICANT: Gangrich, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of S
; FILE REFERENCE: 2560.004
; CURRENT APPLICATION NUMBER: US/10/814,109
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-814-109-4

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Query Match      97.0%; Score 2773.5; DB 5; Length 535;
Best Local Similarity 97.6%; Pred. No. 1.4e-171;
Matches 528; Conservative 3; Mismatches 3; Indels 7; Gaps 2;

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Qy      2 GSNKSKPKDASQRRSLSEPSENVHGA-GGAFPAQSQTSPSKPASADGHRGSPAAFPVPAAP 60
Db      1 GSNKSKPKDASQRRSLSEPAENVHGAAGGAFPAQSQTSPSKPASADGHRGSPAAFPVPAAP 60
Qy      61 KLFEGFNSSPTVTS PQRAEPLAGVTT FVALYDYESRTEETDLSFKKGERLQIVNNT 120
Db      61 KLFEGFNSSPTVTS PQRAEPLAGVTT FVALYDYESRTEETDLSFKKGERLQIVNNT 116
Qy      121 VREGDMMLAHSLSTGQTGYIPSNYVAPSDSIQAEEMYPGKITRRESERLLINAEENRGT 180
Db      117 --EGDMMLAHSLSTGQTGYIPSNYVAPSDSIQAEEMYPGKITRRESERLLINAEENRGT 174
Qy      181 LVRESSETTKGAYCLSYSDFDNAGLVNKHKIRKLDGCGFYITSRTQFNSLQOLVAVYSK 240
Db      175 LVRESSETTKGAYCLSYSDFDNAGLVNKHKIRKLDGCGFYITSRTQFNSLQOLVAVYSK 234

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Qy      241 HADGLCHRLTTVCPTSPQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 300
Db      235 HADGLCHRLTTVCPTSPQTOGLAKDAWEIPRESLRLEVKLGCGCFGEVMMGTNGTTRV 294
Qy      301 AITLKPCTMSPEAPFLOEAQVMKKLRHEKLVOLYAVVSEEPITYITEYNKSGSLDPLKG 360
Db      295 AITLKPCTMSPEAPFLOEAQVMKKLRHEKLVOLYAVVSEEPITYITEYNKSGSLDPLKG 354
Qy      361 ETGKYLRRLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRLIE 420
Db      355 ETGKYLRRLPOLVDMASQIASGMAVYERMMYVHRDLRAANILVGENLVCKVADFGRLRLIE 414
Qy      421 DNEYTAROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVL 480
Db      415 DNEYTAROGAKFPIKWTAPAEALYGRFTIKSDVMSFGILLTELTTKGRVPYPGMVRREVL 474
Qy      481 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPTEYLQAFLEDYFTSTEBQYQGEN 540
Db      475 DOVERGYRMPCEPCEPSLHDLMCQCKRKEPERPTEYLQAFLEDYFTSTEBQYQGEN 534
Qy      541 L 541
Db      535 L 535

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Search completed: June 5, 2006, 17:43:01
Job time : 109.267 secs

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OM protein - protein search, using sw model

Run on: June 5, 2006, 17:37:49 ; Search time 7.01729 Seconds
(without alignments)
891.618 Million cell updates/sec

Title: US-10-691-079-3
Perfect score: 2859
Sequence: 1 MGSNKSXPXKASQRRSLRP.....AFLEDYFTSTPEYQYQENL 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1520	53.2	505	US-10-511-937-2991	Sequence 2991, App
2	1462.5	51.2	512	US-10-505-928-353	Sequence 353, App
3	1462.5	51.2	512	US-10-511-937-2492	Sequence 2492, App
4	1452	50.8	509	US-10-511-937-2467	Sequence 2467, App
5	832	29.1	631	US-11-312-958-60	Sequence 60, Appl
6	822	28.8	659	US-10-511-937-2593	Sequence 2593, App
7	795	27.8	620	US-10-511-937-2959	Sequence 2959, App
8	589.5	20.6	983	US-11-302-678-2	Sequence 2, Appl
9	577	20.2	994	US-11-303-935-12	Sequence 12, Appl
10	575	20.1	998	US-11-303-935-2	Sequence 2, Appl
11	572.5	20.0	993	US-11-303-935-11	Sequence 11, Appl
12	556.5	19.5	1130	US-11-312-958-52	Sequence 52, Appl
13	488	17.1	894	US-11-251-465-21	Sequence 21, Appl
14	483	16.9	343	US-11-251-465-67	Sequence 67, Appl
15	481.5	16.8	885	US-10-505-928-432	Sequence 432, App
16	481.5	16.8	885	US-11-251-465-20	Sequence 20, Appl
17	478.5	16.7	346	US-11-255-147-4	Sequence 4, Appl
18	478.5	16.7	348	US-11-255-147-2	Sequence 2, Appl
19	476.5	16.7	422	US-11-251-465-67	Sequence 67, Appl
20	476.5	16.7	422	US-11-251-465-70	Sequence 70, Appl
21	475	16.6	806	US-11-251-465-22	Sequence 22, Appl
22	470	16.4	972	US-11-255-147-8	Sequence 8, Appl
23	457	15.0	1308	US-11-248-122-2	Sequence 2, Appl
24	451	15.8	999	US-10-196-749-434	Sequence 434, App
25	440	15.4	391	US-11-223-945-38	Sequence 38, Appl

26	440	15.4	1259	7	US-11-223-945-40	Sequence 40, Appl
27	439	15.4	550	6	US-10-538-066-757	Sequence 757, App
28	439	15.4	1255	6	US-10-538-066-364	Sequence 364, App
29	439	15.4	1255	7	US-11-223-945-43	Sequence 43, Appl
30	434	15.2	993	6	US-10-511-937-2463	Sequence 2463, App
31	433	15.1	976	6	US-10-511-937-2423	Sequence 2423, App
32	433	15.1	1006	6	US-10-511-937-2425	Sequence 2425, App
33	420.5	14.7	1338	6	US-10-505-928-634	Sequence 634, App
34	420.5	14.7	1338	6	US-10-505-928-857	Sequence 857, App
35	411.5	14.4	1298	7	US-10-505-928-274	Sequence 274, App
36	407	14.2	953	7	US-11-312-958-56	Sequence 56, Appl
37	400	14.0	369	6	US-10-953-349-3910	Sequence 3910, App
38	400	14.0	374	6	US-10-953-349-3909	Sequence 3909, App
39	400	14.0	412	6	US-10-953-349-3908	Sequence 3908, App
40	394	13.8	344	6	US-10-511-814-2	Sequence 2, Appl
41	394	13.8	648	6	US-10-511-814-14	Sequence 14, Appl
42	364.5	12.7	272	6	US-10-370-959-27	Sequence 27, Appl
43	364.5	12.7	278	6	US-10-370-959-17	Sequence 17, Appl
44	364.5	12.7	278	6	US-10-370-959-31	Sequence 31, Appl
45	364	12.7	247	7	US-11-251-465-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-511-937-2991
Sequence 2991, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wollgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2991
LENGTH: 505
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2991
Query Match 53.2%; Score 1520; DB 6; Length 505;
Best Local Similarity 55.7%; Pred. No. 2.7e-75;
Matches 299; Conservative 85; Mismatches 117; Indels 36; Gaps 6;
QY 1 MGSNKSXPXKASQRRSLRPSENVHAGAPFAPSQTPSKPASADGHRGPSAAFYPPAAEP 60
DB 1 MGSNKSXPXKASQRRSLRPSENVHAGAPFAPSQTPSKPASADGHRGPSAAFYPPAAEP 60
QY KLFGRFSSDTVYSPQAGALAGVTFV-VALDYBERTTDLSFKRGRLQIYNNTRKV 119
DB 41 ---GPNSHSNTPGIRE---AGSEDIIVVALDYEAIIHHEDLSFGQDQVVLSESS--- 90
QY 120 DVREGDWMLHSLSTGQGYIPSNVYVAPSDISQAEVYFGKITRRESERLLTNENRGT 179
DB 91 ---GEMWKAISLATRKEGIIIPSNVYVAPSDISQAEVYFGKITRRESERLLTNENRGT 146

[illegible]

RESULT 2
US-10-505-928--353
? Sequence 353, Application US/10505928
? Publication No. US20060088532A1
? GENERAL INFORMATION:
? APPLICANT: Ludwig Institute for Cancer Research et al
? TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
? FILE REFERENCE: 28967/39178
? CURRENT APPLICATION NUMBER: US/10/505,928
? CURRENT FILING DATE: 2004-08-27
? PRIOR APPLICATION NUMBER: US 60/363,019
? PRIOR FILING DATE: 2002-03-07
? NUMBER OF SEQ ID NOS: 866
? SOFTWARE: PatentIn 3.2
? SEQ ID NO 353
? LENGTH: 512
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-505-928--353

Query Match	51.2%	Score 1462.5;	DB 6;	Length 512;
Best Local Similarly	53.1%	Prod. No. 3.3e-72;		
Matches 291; Conservative	86;	Mismatches 120;	Indels 51;	Gaps 10;

QY 1 MSMSKSPDA-----SQRRLSLEPSENVHAGAPASQTPSPKAPNADQHRPSA 51
Db 1 MGCTSKSGKADSLSDGVDLKTQPVKXTERETIIVR-----PTSKQKAP----- 44
QY 52 AAVPPAAEPKLPFG--FNSSDVTVTSPPQAGALAGVTFVALYDYESRTETDLSFKKGR 109
Db 45 --VP---ESQLLPGRGFOTKD-----PEEGSDIV-----VALYPDGIHPDILSFFKGEK 89
QY 110 LQIVNNTRKYDVBEGGMWLAHSLSTGGYVPSNVAAPSDSIAQEWYFGKITRSEERL 169
Db 90 MKYLE-----EHGEWMAKSLILTKGEGFIPSNVVALQNTLIEBWFMDITKDMERQ 142
QY 170 LINAENPQTPVLRSEETTKGAYCULSVSDPDNAKLANVKAHKIRLDSGGEYITSRTQFN 229
Db 143 LLAFGNSAGAFILIRESEETLKGSFSLSYVDPFVHGDVIAKHKISLNDGSGYISPRITFP 202
QY 230 SLQGLAAVYSSKADGLCHRLTLTVCTSPKQTOGLAKDAMEIPRESRLREYVLDGGCGEYV 289
Db 203 CISDMTKHQQKADGLCRRLKCAKCSIPKQ-KPMDKDMELPRESIKULYKRLGAGCGEV 261
QY 290 WNGTANGTRVAIKTLKPGTMSPEAPLODPAQWKKDLRHEKLVQIYAAYS-BEPIYIVTEY 348
Db 262 WNGYVNNSTKVAIVKTLKPGTMSVQAFLEBANIMTKLTQHDKLVRIYAAVTRREPIYIITEY 321

Qy	349	MNKGSLDPLDKETKTYLRLPOLYMSQAIASGMAVYERMMYHRRDLRAANILVGENLYC	408
Db	322	MANGSLDPLDKDDEGGKVLPLPLDPSQAIDBGMAVIERKNYIHRDLRAANVLVSESLMC	381
Qy	409	KVADFGIARLIEDNETYARQCAKFPFIKMTAPEALYGRFTIKSDVMSFGILLTELVTYKGR	468
Db	382	KIADFGIARVIDNETYAREGAKFPFIKMTAPEALINFGCFITIKSDVMSFGILLVYIVTYGK	441
Qy	469	VVPYKGNVREVLDOYERGYRMPCCPECCESLHDLMOQMRKEPERPTFYELQAFLEDYF	528
Db	442	IPYRGNTNADVMTALISQGYRMPRVENCPEDELVDIMKMCWEKAEERPTFDYLSVLDDFY	501
Qy	529	TSTREPOYO	536
Db	502	TATEGOYQ	509

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RESULT 3
US-10-511-937--2492
; Sequence 2492, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2492
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937--2492

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Query Match	51.28;	Score 1462.5;	DB 6;	Length 512;
Best Local Similarity	53.14;	Pred. No. 3.3e-72;		
Matches 291;	Conservative	86;	Mismatches 120;	Indels 51; Gaps 10;
QY	1	MGNSKSPKDA-----SQRRLSPSENNHAGAGAPASOTPSKPAADGHRGSA	51	
Db	1	MGCIKSKGKDSLDDGVDLTKIQPVNRNERTIYYVD-----FTSNKQORP-----	44	
QY	52	AFVPAAPPLFEG--FNSSDTVTPSRACAGAGVTTVALYVYEGRTETDLSFFKGER	109	
Db	45	--VF--ESQLPGRQFQTKD-----PEEGQDIV-----VALYVYDGIHPDLSFFKGER	89	
QY	110	LQIVNTRKVDVREGDWLHLSLSTGTQGYIPSNVYAPSDSIQAEVYFGKITRESERL	169	
Db	90	MKYLE-----EHGEWMAKASLLTKKEGFIPISNVYAKLNTLLEBEMVFFQKITRKDAERQ	142	
QY	170	LNAENRGTFIVRESEETTGAYCLASDPMNAQMLVKKYIKIKLDSGGGYIRTSQTQN	229	
Db	143	LIRAGSAGAFIRESLTLKGSFSLSRDDPYNHGVYIKYIKIRSLDNGGYISPIRTTFP	202	
QY	230	SLQQLVAYYSKADGLCHRLTTCVPTSKPOTQGLAKDAMEIPRESLRLEVLGGQCGEIV	289	
Db	203	CISIMIRHYGKQADGLCRRLKAKISKPP--KPMDDKAMEIPRESIKLVKRLAGQFQEV	261	

QY	290	WMGTNGTTRVAVIKULKPEPTMSBEALIOBAOWKKLRHETLYOVAVVVS-EEPIYIVTEY	348
Db	262	WMGYNNSTKVAIVKILPKPEPTMSVOALEEKNLAKTKLQHDLYVAVVAVVKEEPIYIITEY	321
QY	349	WKKSGILDLFLKGETGKYTLR.POLVDMNSAQIASGMAYVERMNVYHRLDRAANIIIVGENTVC	408
Db	322	MAKSGILDLFLKDEGGKVVLPKLIIDESAQIAEGMAYIERKNYIHRDLRAANVIVSESLMC	361
QY	409	KVADSGIARLIEDNNEYTAROGAKFPIKXMTAPRALVGRFPIKSDWVSFGILLTELTKGR	466
Db	382	KIADGILKAVIEDNETAREGAKFPIKXMTAPRALVINGCFPIKSDWVSFGILLLEIVYGG	441
QY	469	VVPYPMVAVREVLDOVERGYRMPCPPECPESLHLMCOQMKBEERPTFEYLQAFLEDYF	528
Db	442	IIPYERTNADVMTALSSQGYRMPREVNCPDELYDIMGMCKEKABERNPTFDLYSDVDYF	501
QY	529	TSTEFQYQ	536
Db	502	TATEGYQ	509

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? RESULT 4
? US-10-511-937-2467
? Sequence 2467, Application US/10511937
? Publication No. US20060088836A1
? GENERAL INFORMATION:
? APPLICANT: EXPRESSION DIAGNOSTICS, INC.
? APPLICANT: Wohlgenuth, Jay
? APPLICANT: Fry, Kirk
? APPLICANT: Woodward, Robert
? APPLICANT: Ly, Ngoc
? APPLICANT: Prentice, James
? APPLICANT: Morris, MacDonald
? APPLICANT: Rosenberg, Steven
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
? TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
? FILE REFERENCE: 506612000104
? CURRENT APPLICATION NUMBER: US/10/511,937
? CURRENT FILING DATE: 2004-10-19
? PRIOR APPLICATION NUMBER: PCT/US2003/012946
? PRIOR FILING DATE: 2003-04-24
? PRIOR APPLICATION NUMBER: US 10/131,831
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: US 10/325,899
? PRIOR FILING DATE: 2002-12-20
? NUMBER OF SEQ ID NOS: 3117
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 2467
? LENGTH: 509
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-511-937-2467

```

Query Match	50.8%	Score 1452	DB 6	Length 509
Best Local Similarity	59.7%	Pred. No. 1.2e-71		
Matches 268	Conservative 80	Mismatches 93	Indels 8	Gaps 2
Qy	89	VALVDYESRRTDLSFFKGGKRLQIVNNNRKRVADREGDMWMLAHSLSTGTGTGYPISNYYAPS	148	
Db	67	IAMSYPSESHDODLGFKEKGEPRLRIE-----QGGEWKKQKSLTTGGEGFIPFVFKVA	119	
Qy	149	DSIAQAEVYFGKIKTRRESESERLILNAENRGRGFLVARESETTGAYGLASISDPDNKAGLVNK	208	
Db	120	NSLEPEPMPFNKLSKDKAERQLAPAGNTHGSFLIRESESTGVSFSLSRDPDQNGEVYK	179	
Qy	209	HYKIRKLDGSGGYIYSRTQFNLSLOOLVAVYVSGHADGLCHRLITTVVPTSPKPTOGSLAKDAM	268	
Db	180	HYKIRKLDNGSGFYISPRITTFPEHMLVAVHTYMASGGLCTRLSRPQOTQKPC-KPMWDEBM	238	
Qy	269	EIPRESRLVAVLGGQCGCFGEVWMTGNCSTTRVAITLKPGTMSPEAPLOEQAQVMKKLREH	328	
Db	239	EVPEPTTLKLVIRLGLGQCGEYVWMTGYNCHTKVAVYSLKQSGMSPPAFIAEINLMKQLOHQ	298	

Qy	329	KLVLQYLVAVSEBPIYIVLWENXKSLBLPEIKSETGYLRLPOLVDBSADIIASMAVVERN	368
Db	299	RLVRLVYAVVTOBPIITLITHEWENSLVLPDLKPPSGIKLTIINKLDMAAQIABSMATIEER	358
Qy	389	NYVHRDLTPAANIIVGSENVCKVADGGLRLIEDNEYTAQAGKFPKMTAPBAALVGRFT	448
Db	359	NYIHRDLTPAANIIVASDLSCKIADPGLRLIEDNEYTAAGAKFPIKMTAPBAALVNGTFT	418
Qy	449	IKSDVMSFGIILITBELTYKGRVPYPGWVNRFEVLDOYERGRYMPCPPECPSLHLMCOQNR	508
Db	419	IKSDVMSFGIILITBELTYHGRIPYPMQMTPEVQLNBERGYRMYRPNDCPEELYOLMLCMK	478
Qy	509	KEPEBRPFEEYQLANLEDYFTSTEROYOP	537
Db	479	ERPEBRPFEDYLRSVLEDFPTATSGOYOP	507

```

US-11-312-958-60
RESULT 5
Sequence 60, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millenium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Sllios-santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47114, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13424 MOLECULES
FILE REFERENCE: MP102-027P1RNONMIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 631
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-60
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	Query Match	29.1%	Score 832,	DB 7,	Length 611,
	Best Local Similarity	37.9%	Pred. No. 2.9e-38;		
	Matches 186,	Conservative 92;	GMSD Matches 169;	Indels 44;	Gaps 13;
Cy	VPAAABK-----LFGGFSNDPTYSQGRAGALAGVTTVALDYAESRRETIDLSF	104			
	:::::	:::::	:::::	:::::	
Dd	LPPAPETKKRRPPIPLEEEDNSEEV-----VAATDFQAACHDIRL	200			
	:	:	:	:	:
Cy	KKGRLGIIVNNTRKYDRREGDMWLAHSLISTGTSYIPSNYYA--PSDSIQAEWYFKGIT	162			
	:::::	:::::	:::::	:::::	

Db 201 ERGCEYLIL---EKNDVH---MMWRARD-KYGENEGYIPSNVYTGKSNLDOYEWYCRNMN 253
Qy 163 RRESEULLNANENRGFTLVRESEETTKGAYCLSV--SDFDNAKGLNVGHYKIRKLDSC--G 219
Db 254 RSTAEQ-LRSEKEGGEFWRDS--SOPGLYTVSLYTFEGEGSGGFHRYHKETTSPPK 311
Qy 220 FYTSTRQFNSLOOLVAAYYSKHAIDGLCHRL---TTVCPTSKPOTQGLAKAMEIPRESLR 276
Db 312 YVLAEGHAFPSIEIIEYHGNMAGLVTRLRFPYSVGNKAPPTAGSYEKMEINPELRT 371
Qy 277 LEVKGOGGCEGVWVGWGTNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLHEKLVOLYAV 336
Db 372 FMBELSGFLGVVRLGKRAQYKVAIKAIIEGAMCEBDFIEAKVMKLTNPKLVOLYGV 431
Qy 337 VSEB-PIIYTERWNGSLDDPLKGEYKTLRLPOLVDMNAQIASGAAVYERNAVYRDL 335
Db 432 CTQOKPIIYTEMERGCLNLFROGHSFR--DVLISMCOOVCEGNEYLERNSFIHRDL 490
Qy 396 RAANIVGENLVCKVADFGFLARLIEDNEYTAROGAKPEPIKMTAPEALYGRFTIKSDVMS 455
Db 491 AARNCVSEAGVYKVDGFMARFLDDQYTSSSGAKFPVMKCPREVNYSRFSKSDVMS 550
Qy 456 FGILLTELTTKGVPYPGMVNREVLDQVERGYMPCPECPESLHDLMOQCMRKEPERP 515
Db 551 FGVLMVEVFTEGRMPEKTYNTEVVMVTRGHRLYQKCLASNYVEVWLRCMQEKPEGRP 610
Qy 516 TPEYLOAFLED 526
Db 611 SFEDLRTIDE 621

RESULT 6

US-10-511-937-2593
Sequence 2593, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2593
LENGTH: 659
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2593

Query Match 28.8%; Score 822; DB 6; Length 659;
Best Local Similarity 36.4%; Pred. No. 1e-37;
Matches 181; Conservative 94; Mismatches 194; Indels 28; Gaps 13;
Qy 39 KPASADGHHGSAFAFPRAEPKLFQGFNSSDVTVTSPPQAGALAGVTTTFVALYDYESRT 98
Db 176 KGGSS--HKTKTKPLPPTPEBDIL---KKPLPPEPAAAPVSTSEKKVVALYDTPKMN 229
Qy 99 ETDLSFKGGERLQIVNTRKVDVREBGMWMLAHSLSGTGCTGYPISNVAAP--DSIOAEWY 157

Db 230 ANDLQLRKGEYFIEESNL-----PMWRARD-KNGQEGYIPSNVYTEAEDSIEMEWY 282
Qy 158 FGKTRRESERILLNANENRGFTLVRESEETTKGAYCLSV--SDFDNAKGLNVGHYKIRKLD 215
Db 283 SKMTTISOAEQ-LKQEGKEGGEFWRDS--SKAGKYTVSVFAKSTGDPQGV-IRHYVVCST 339
Qy 216 DSGGFYTRTOPNSLOOLVAAYYSKHAIDGLCHRLTTVCPTSK-----POTQGLAKAMEI 270
Db 340 PQOQYVLAEGHAFPSIEIIEYHGNMAGLVTRLRFPYSVGNKAPPTAGSYEKMEINPELRT 397
Qy 271 PRESRLLEVKGOGGCEGVWVGWGTNGTTRVAIKTLKPGTMSPEAFLOEAOVMKRLHEKLV 330
Db 398 DPDLTFKLKELGTGCGGVYKRGQYDVAKIMIKEGSMBDFIEAKVMKLTNPKLVOLYGV 457
Qy 331 VOLYAVSEB-PIIYTERWNGSLDDPLKGEYKTLRLPOLVDMNAQIASGAAVYERNAVYRDL 339
Db 458 VOLYGVCTQOKPIIYTEMERGCLNLFROGHSFR--EKRHRFQOOLLEMKDKVCEABEYLESQ 516
Qy 390 YVHRDLRAANIVGENLVCKVADFGFLARLIEDNEYTAROGAKPEPIKMTAPEALYGRFTI 449
Db 517 FLHRDLAARNCVSEAGVYKVDGFMARFLDDQYTSSSGAKFPVMKCPREVNYSRFSKSDVMS 576
Qy 450 KSDVMSFGILLTELTTKGVPYPGMVNREVLDQVERGYMPCPECPESLHDLMOQCMRKEPERP 509
Db 577 KSDIMAFGVLMVEVFTEGRMPEKTYNTEVVMVTRGHRLYQKCLASNYVEVWLRCMQEKPEGRP 636
Qy 510 EPERPTPEYLOAFLED 526
Db 637 KADERPTFKILLSNILD 653

RESULT 7

US-10-511-937-2959
Sequence 2959, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2959
LENGTH: 620
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2959

Query Match 27.8%; Score 795; DB 6; Length 620;
Best Local Similarity 34.8%; Pred. No. 2.7e-36;
Matches 179; Conservative 90; Mismatches 181; Indels 64; Gaps 15;
Qy 19 ESEENVHAGAGFAPASQTSKPSASDGHGSPSAFAFPRAEPKLFQGFNSSDVTVTSPPQRA 78
Db 147 DPTKN-----ASKKPLPPTPEBNRR-----PLMBDB----- 172
Qy 79 GALAGVTTTFVALYDYESRTETDLSFKGGERLQIVNTRKVDVREBGMWMLAHSLSGTGCTG 138

Db 173 -----ETVYIALYDQTNDFQELALRNREYCL-----LDSEIHMMRVQD-RNGHEG 219
Qy 139 YIYSNVAAPS--DSIOABEWYFGKITRRESRLILNANPNPGTFLVARESETTKAYCLSV 196
Db 220 YPSSSYLVEKSPNNLEFYEWYTKNSISRDKAEKLLDTR-GKEGAFWVDSRTA-GTYTVSV 277
Qy 197 SDPQNA-----KGLVKKYKIRKLDG--GFYTSRTQFNSLQOLVAAYYSKHAQDGLCHRLT 250
Db 278 --FTKAVVSENPNFCIKYHIKEDNDPKRYVAEKYVFDISPLILNHONGGGLVTRLR 335
Qy 251 -TVC--FTSKPQTQGLAKDAWEIPRESLRLEVKLGQCGFGEVMMGTNGTTRVAIKTLKP 307
Db 336 YPVCFGKQKAPVTAAGLRYGKKVVIDPSELTFQVIGSGQFGLVHLGYMLNKKOKVAKITRE 395
Qy 308 GTMSPEAFLOBAQVMKLRHEKLYQLYAVVSE--PIYIVTEYNNKGLSLDPLKSETGKYL 366
Db 396 GANSEDFEIEBAEYMWMLSPKLVQLYGVCLQAPICLVEFMEHGCISDILRTORGIF- 454
Qy 367 RLDPQVMSAQIYSGMAVVERMNVVHRDLRAANILVGENLVCKVADFGALRIEDNEXTA 426
Db 455 AAEITLGMCLDVCGMAYLEBACVYHRDLAARNCVGENOVYIKVSDFGMTRFVLDDQTS 514
Qy 427 ROGAKPEIKWTAPBALYGRFTIKSDVMSFGILLTETTKGRVYPGMVNRVLDQYERG 486
Db 515 STGKRFVVKASPEVFSFSRYSSKSDVMSFGVLMVEVFSBGKIPYENRNSSEVEDISTG 574
Qy 487 YRMPCEPCEBSLHDLMCQCKRKEPERPTEYIL 520
Db 575 FRLYKPRLASTHYQIMNHCWKERPEDRPAFSRL 608
RESULT 8
US-11-302-678-2
Sequence 2, Application US/11302678
Publication No. US20060088881A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MP102-012P1NM, OMNI
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-12-14
PRIOR APPLICATION NUMBER: US/10/345,680
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FaSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 983
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-302-678-2

Query Match 20.6%; Score 589.5; DB 7; Length 983;
Best Local Similarity 31.0%; Pred. No. 4.7e-25;
Matches 173; Conservative 82; Mismatches 166; Indels 137; Gaps 20;
Qy 49 PSAAFVPPAEPKLFGGFNSSDVTYSFORAGALAGVTTFVALYDYESRTETDLSFKKGE 108
Db 378 PNRVFL-----PRFGILNTTVIT-----D 398
Qy 109 RLQIVNTRKVDRESGMWMLAHSLSGTQGY----IPSNVYAPDSIOAEWYFGKITR 164
Db 399 LIAHTNYTFEIDAVNG-----VSELSSPPROFAAVSITTNQAPAPVTLIKK---DRSRN 451
Qy 165 ESERLLNANPNQTF-----VRESSTGAYCLSDPDNAGLVK-----H 209
Db 452 SISLSWQEPHPNGIILDYVKYKYEKOQETSYTL-----RANGINVTLSLKPDTIYV 506
Qy 210 YKIRKLDGSGFYITSRT-QFNS-----LQQ 233
Db 507 FQIRPRTAGYGTNSRKFEFTSPDSISGSSQVMMIAISAVAILLTVIYVILGR 566
Qy 234 LVAYSRH-AD-----GLCHRLTVCP-TSKPQTQGLAKDAWEIPRESLR 277
Db 567 FCGYKSGHGADEKRLHFGNGHLKLPGL---RTYVDPTHYEDPTQAVHEFAKELDATYISI 623
Qy 278 EVKLGGCGFGEVMMGTNGTTR-----VAITLKGTMSPEA--FLOBAQVMKLRHEKLY 331
Db 624 DKVWAGEFGEVSGRLKLPKKEISVAITLKGYTEKRRDPLGSRASIGQDPHPIT 683
Qy 332 QLYAVSE-PIYIVTEYNNKGLSLDPLKSETGKYLRLPOLVDMASQIYSGMAVVERMNV 390
Db 684 RLEGVTTKSKPWIVITMYENGSLDSFLRKHDAQFYI-QLVGLRGIASGMKLSMGY 742
Qy 391 VHRDLRAANILVGENLVCKVADFGALRIEDN--EYTAQGAKEPIKWTAPBALYGRF 447
Db 743 VHRDLAARNILINSNLVCKVSDFCLSRVLEDDPEAYTTR-GGKIPIRMTSPBAIARKE 801
Qy 448 TISDWSFGILLTETTKGRVYPGMVNRVLDQYERGTRMPPEPCPESLHDLMCQW 507
Db 802 TSASDWSYGIIVMEWVSYGEPYEMSNODVIRKAVDEGYRLPPMCCPALYQILMLDCW 861
Qy 508 RKPEERPTFEYLOAFLE 525
Db 862 QKDRNRPKEQIVSILD 879
RESULT 9
US-11-303-935-12
Sequence 12, Application US/11303935
Publication No. US20060099708A1
GENERAL INFORMATION:
APPLICANT: Cloesek, Thomas
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDKI
SIGNAL TRANSDUCTION
DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

QY 75 -----PORAGALAGVTTFFVAL-----YDYESRT 98
DB 358 GGRNDVTYRLCKRCSEGECEVPCGSNIGMPOQTGLEDNYVTVMOLLAHANTFFVEA 417
QY 99 ETDLS-FKKGERLQIVNNTRKVDVREGDWMILASLSTGQTGYIPSNVAPS--DSIOAEE 155
DB 418 VNGVSDLSRSQRL-----FAAVSITTTQ-----AAPSQVSGWKKE- 452
QY 156 WYFKITRRESERILLNAENPRG-----TFVRESETTGACVCLASVD 198
DB 453 -----RVLQRSVQLSMQEPHPNGVITEYEIKYEKQDERTYSTLKTKSTS-----AS 501
QY 199 FDNAKGLNVHVKYIKRKLDSGGF-YITSRTQNSLQQLVAVYSKADGLCHRLTTY----- 252
DB 502 INNLKPGTVYVFOIRAVTAAGYGNYSRPLDVATLEE-----ASGMFEATVVSSEQN 553
QY 253 -----CPTSKPQTQ-----LAKDA 267
DB 554 PVIIIVAVVAAGTIIIVFWVPGFIIGRRHCGYSKADQEGDEBELYFHKFPQTKTYIDPET 613
QY 268 WEIIPRES-----LRLVYKLGQCGCFGEVWVG-----TWNGTTRVALIKTLKPGTMS 311
DB 614 YEDPNRAVHQPAKELDASCIKIERVIGAGEGECGRLKLPQORDVAVAIKTLKVGYTE 673
QY 312 PEA--FLQEAQVMKKLHREKLVQYAVVSE-EPYIYTEYMNKSLDPLKGETGKTLRL 368
DB 674 KORRDFICEASIMQGFPHPNVHLEGVTRCKPVMYIIEFMENALDAPFKHDGQFVI 733
QY 369 POLVDMSAQJASGAAYVERMYVHRDLRAANIIVGENLVCKVADFGIARLIEDNE---YT 425
DB 734 -QLVGMRLGIAAGKRYLADNGYVHRDLAARKIIVNSNLVCKVSDFGLSRVIEDDPEAVYT 792
QY 426 ARQAKPEPIKATBAALYGRFTIKSDVMSFGIILTELTTRGARVPYPMVNRVLDYVER 485
DB 793 T-TGGKLPVMTAEALQYRKFTSASDVMSYGIWMEWMSYGERPYDMSNOVIKAIIE 851
QY 486 GYRMPCEPCESLHDLMOQCKRKEBERPTEFYLOAFLE 525
DB 852 GYRLPAPMDCPAGLHQLMLDCMQKDRAPERKFEQIVGILD 891

RESULT 11
US-11-303-935-11
; Sequence 11, Application US/11303935
; Publication No. US20060099708A1
; GENERAL INFORMATION:
; APPLICANT: Cioseek, Thomas
; Ullrich, Axel
; Millauner, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
AND TREATMENT OF MDK1
; SIGNAL TRANSDUCTION
DISORDERS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
; COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/303,935
FILING DATE: 19-Dec-2005
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/073,064
FILING DATE: 12-Feb-2002
APPLICATION NUMBER: US/08/438,265
FILING DATE: MAY 9, 1995
APPLICATION NUMBER: US/08/368,776
FILING DATE: January 3, 1995
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-303-935-11
Query Match 20.0%; Score 572.5; DB 7; Length 993;
Best Local Similarity 28.5%; Pred. No. 3,96-24;
Matches 179; Conservative 85; Mismatches 192; Indels 171; Gaps 23;
30 AAPSQTPSPKPSASDQ-HRQPS-----AATVPRAAEKLRGCFNSSDTVTS----- 74
DB 300 SFSDBRESSCCECEDGYRAPSDPPYVACTRPSPAPQNL--FVINQTVVLSLEMSPPADN 357
QY 75 -----PORAGALAGVTTFFVAL-----YDYESRT 98
DB 358 GGRNDVTYRLCKRCSEGECEVPCGSNIGMPOQTGLEDNYVTVMOLLAHANTFFVEA 417
QY 99 ETDLS-FKKGERLQIVNNTRKVDVREGDWMILASLSTGQTGYIPSNVAPS--DSIOAEE 155
DB 418 VNGVSDLSRSQRL-----FAAVSITTTQ-----AAPSQVSGWKKE- 452
QY 156 WYFKITRRESERILLNAENPRG-----TFVRESETTGACVCLASVD 198
DB 453 -----RVLQRSVQLSMQEPHPNGVITEYEIKYEKQDERTYSTLKTKSTS-----AS 501
QY 199 FDNAKGLNVHVKYIKRKLDSGGF-YITSRTQNSLQQLVAVYSKADGLCHRLTTY--- 252
DB 502 INNLKPGTVYVFOIRAVTAAGYGNYSRPLDVATLEEASATVVSSEQNPIIIIVAVVAGT 561
QY 253 -----CPTSKPQTQ-----LAKDAWEIIPRES----- 274
DB 562 IIVFWVPGFIIGRRHCGYSKADQEGDEBELYFHKFPQTKTYIDPETYEDPNRAVHQPAK 621
QY 275 -----LRLVYKLGQCGCFGEVWVG-----TWNGTTRVALIKTLKPGTMSPEA--FLQEAQVM 322
DB 622 ELDA SCIKIERVIGAGEGECGRLKLPQORDVAVAIKTLKVGYTEKORRDFICEASIM 681
QY 323 KKLREHLVQLYAVVSE-EPYIYTEYMNKSLDPLKGETGKTLRLPOLVDMSAQJASG 381
DB 682 GQFDHPVNVHLEGVTRCKPVMYIIEFMENALDAPFKHDGQFVI--QLVGMRLGIAAG 740
QY 382 MAYERNANVYHRDLRAANIIVGENLVCKVADFGIARLIEDNE---YTARQAKPEPIKTA 438
DB 741 MRYLADMGYVHRDLAARNIIVNSNLVCKVSDFGLSRVIEDDPEAVYTT-TGGKLPVMTA 799
QY 439 PEALYGRFTIKSDVMSFGIILTELTTRGARVPYPMVNRVLDYVERGYRMPCEPCEBS 498
DB 800 PEAQYRKFTSASDVMSYGIWMEWMSYGERPYDMSNOVIKAIIEBGYRLPAPMDCPAG 859
QY 499 LHDLMCOCKRKEBERPTEFYLOAFLE 525
DB 860 LHQMLDCMQKDRAPERKFEQIVGILD 886

```
RESULT 12
US-11-312-958-52
/ Sequence 52, Application US/11312958
/ Publication No. US20060100152A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Rosenfeld, Julie Beth
/ APPLICANT: Siles-Santiago, Immaculada
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
/ TITLE OF INVENTION: 27410, 33360, 619, 15985, 69112, 2158, 224, 615, 44373,
/ TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
/ TITLE OF INVENTION: 13424 MOLECULES
/ FILE REFERENCE: MPIO2-027P1RNONIM
/ CURRENT APPLICATION NUMBER: US/11/312,958
/ CURRENT FILING DATE: 2005-12-20
/ PRIOR APPLICATION NUMBER: US/10/369,022
/ PRIOR FILING DATE: 2003-02-19
/ PRIOR APPLICATION NUMBER: US 60/360,495
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/370,121
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/373,010
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/373,908
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/377,717
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US 60/379,949
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US 60/382,409
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/385,280
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 60/386,879
/ PRIOR FILING DATE: 2002-06-06
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FaalSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 1130
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-312-958-52

Query Match      19.5%, Score 556.5; DB 7; Length 1130;
Best Local Similarity 30.0%; Pred. No. 3,2e-23;
Matches 176; Conservative 68; Mismatches 178; Indels 165; Gaps 20;

OY 60 PRLFGFNSSDTYSQORAGALAGVTTFYALYDSRTETDLSFKKGERLQIVNTRKY 119
DB 522 PKPF-----FAIVTTTQDAPSLIG-----VVRKDMASONSIALS----- 556
OY 120 DVREGDMWLAHSLSTGQGYIPSNVAVPSDSIOAEWYFGK-----ITRESERLL 171
DB 557 -----WQAPAPASNAI-----LDYEIKYKEKEHQULTYSTRSKASV 596
OY 172 NAEPRGTFLVSESETTKGAYCLSVDF-----DNAKGLNVKHYKTRKIDS--GG--- 219
DB 597 TGLKPTKTVPHIRVATATGYSYSGQKFERETGDETSDMAABEGQLVATAVAGGF 656
OY 220 -----FYTTSRTQF-----NSLQQLVAYYSKHA--DGLCHRLTTPCP--TSK 257
DB 657 VILLTFLITGRCQWYIKAKMKSEKRRHMLQ-----NGHLFPPI--KTYIDDTYE 707
OY 258 PQTGLAKAWMPRESLLEVLVGLGCGFGEVWMTGNTR-----VAITKLKPGTMSB 313
DB 708 DPSLAHBEPAKEDPSRIRIERVITGAGEGECVSGRLKTPGKKEIPVALIKTLKGHMD 767
OY 314 A--FLQEAQVMKKLRHEKLVQLYAVVSE----- 339
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DB 768 RRDFLAEASIMGQFDHPNIIIRLEGVTKRSFPAIGVEAFCPSPFLRAGFLNSIQAPHPVG 827
OY 340 -----BEIYIVTERYMNKSGSLDDFLKSTGTXYLLPOLVMSAQIAGMAVERM 388
DB 828 GGSLLPPIRIPRAGRWMLVIVYMENGSLDSFLRKIDGHFTYI--QLVGNLRLGIASGMKYLSDM 886
OY 389 NYVHRDLRANILVGENLVCKVADFGIARLIEDNEYTA--ROGAKPPIKMTAPEALYGR 446
DB 887 GYVHRDLARNILVNSNLVCKVSDPGLSRVLEDDPPAAVTTTGKPIRMTAPEALAYRK 946
OY 447 FTIKSDVMSFGILIELTTKGRVPYGMVNRVLDQVBERGYRMPCEPCEPSLHIMCQC 506
DB 947 FSSASDAMSYGIVMEVMSGERPYWEMGNQDVIILSIEEGYRLPAPMCGCPASIHQLMLHC 1006
OY 507 WKREPEREPFEYLOAF-----EDYFTSRNPQVQGE 539
DB 1007 WQKERNHRKPFDTDIVSFLDKLIRNPSALHTLVEDIIMPE---SPGE 1050
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RESULT 13
US-11-251-465-21
/ Sequence 21, Application US/11251465
/ Publication No. US20060094061A1
/ GENERAL INFORMATION:
/ APPLICANT: Brys, Reginald
/ APPLICANT: Vandeghinste, Nick
/ APPLICANT: Tonne, Peter
/ TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
/ TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
/ FILE REFERENCE: P30, 172-A USA
/ CURRENT APPLICATION NUMBER: US/11/251,465
/ CURRENT FILING DATE: 2005-10-14
/ PRIOR APPLICATION NUMBER: 60/619,384
/ PRIOR FILING DATE: 2004-10-15
/ NUMBER OF SEQ ID NOS: 880
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 21
/ LENGTH: 894
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-251-465-21

Query Match      17.1%, Score 488; DB 7; Length 894;
Best Local Similarity 28.4%; Pred. No. 1.2e-19;
Matches 170; Conservative 71; Mismatches 215; Indels 142; Gaps 23;
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OY 14 RRRSLPESENMGAGGAPFASQTPSK-----PASADGHRGSAAFV-- 54
DB 295 RLGSLHPHTPPYH--IRVACTSSQGPSWTWMLFEVTPREGVPLGPPEPISATRNGSOAFVIM 353
OY 55 -PPAA--EPKLFQ--GFNSSDT-----VTSFORAGALAGVTTFYALYDES 96
DB 354 QEPRAPLQGTLLGYRLAYGQDTPREVLIDGRQEVTLLELQGDGSVSNLTVCAAY---- 409
OY 97 RTETDLSFKKGERLQIVNTRKVDVREGDMWLAHSLSTGQGYI--PSNVVAASDSIOABE 155
DB 410 -----TAAGDGPWSLPPVLEAWRPQAOQPVHQLVKEPTSPAS 447
OY 156 W-----YFGKTRRESERLLNAENPRGTFV--RESSETTKGAYCLSVDFPNKAGLVNK 208
DB 448 WPMWYVLGAVVAACVLL-----ALFLVHRKKKEIRYG-----EVEFPEYVERGELVY 496
OY 209 HYKIRLDSGFGFYITSRTQFNSLQQLVAVYSKADGLCHRLTTPVCPSPQOTGLAKDAM 268
DB 497 RYRVKRSYSRR--TTBATLNSL-----GISEELK 523
OY 269 E-----IPRESLRLEVLVGLGCGFGEVWMTGN-----GTTTVAIKTLKPG--TMSP--EATL 316
DB 524 EKLRDVMDVRHKLVALGKTLGEBGFAGVMEGQINODDSILKVAVKTMKIAICTRSBLEDFL 583
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QY      317  SEAOYMKLRLHKLKLVQLYAVV---SEEPY-----IYTEVYNNKSLDPL-----KGEQKY 365
Db      564  SEAVCMKEKEDHNHYMKLIGVCFQGSERSESPFAVAVLIPFKHGDLSFLYSKRLGDQPVY 643
QY      366  LRLPOLVDMSAOIASGMAYVERNNVYHDLRAANILVGENLVCKVADFGIARLIENDEYT 425
Db      644  LPTQWLIVKFMADIASGMEYLSTKRPFIRDLAARNCLNEMSVCAVDFGLSKITVNGDY- 702
QY      426  ARQG--AKFPYKMTAPEALYGRFTIKSDYWSGILITLTTTKGRVPYFGMVRREVLDQV 483
Db      703  YRQRIAKAPVYKMIIESLADRYTTSKSDWSGVTWMEVATATGQTPYPEVENSEIYDYL 762
QY      484  BRGYMPCPECEPESLHDIACQCRKEPERPFEEYLQALIEBYPFSTSEYOQGEUL 541
Db      763  RQGNRLKQPADCDIGLYALMSRCWEALNPQDRPSEFTELREULENTYKALPAPQADETIL 820

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RESULT 14

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: Sequence 6 Application US/11255147
: Publication No. US20060094081A1
: GENERAL INFORMATION:
: APPLICANT: SCHUBERT, CARSTEN
: APPLICANT: SPRINGER, BARRY A.
: APPLICANT: DECKMAN, INGRID
: APPLICANT: PATCH, RAYMOND J.
: APPLICANT: STRUBLE, GEOFFREY T.
: APPLICANT: WA, HONGCHANG
: APPLICANT: SCHALK-HIHI, CELINE
: APPLICANT: BRANDT, BENJAMIN M.
: APPLICANT: PERROUNIA, IOANNA
: TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE C-FMS KINASE DOMAIN:
: TITLE OF INVENTION: APPLICATIONS AND USE OF HETEROLOGOUS SUBSTITUTIONS OF
: TITLE OF INVENTION: KINASE INSERT DOMAINS FOR CRYSTALLIZATION
: FILE REFERENCE: PRD2389USNP
: CURRENT APPLICATION NUMBER: US/11/255,147
: CURRENT FILING DATE: 2005-10-20
: PRIOR APPLICATION NUMBER: 60/620,698
: PRIOR FILING DATE: 2004-10-22
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 6
: LENGTH: 343
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-11-255-147-6

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Query Match	16.9%	Score 483	DB 7	Length 343
Best Local Similarity	35.9%	Pred. No. 8	2e-20	
Matches	107	Conservative	60	Mismatches 105, Indels 26, Gaps 8

QY	250	TTVCTSTSPQTOGLAKDAWEITRESRLRLVETKGGCCFGEV-----WMTGNNGTTRVAIK	303
DB	41	TFIDTOLPY-----NEKKEPFRNNLQFGKTLGDAFKEVBEATAFGEGKEADAVLKAVK	95
QY	304	TLKPTSTMS--PEAFLOEAQVMKCL-RHEKTLVOLY-AVNSEEPITYIVTEEMNGKSLIDFLK	359
DB	96	MUKSTRAHDEKRALMSLSKIMSHLGQHEINIVALLDACHGGGVLLVITTECCCGDDLNTLR	155
QY	360	GET-----GKTLRLPOLVDMSAQIASGMAYVERNNYVHRDI-RAANILVGENLVCKV	410
DB	156	RKSLRPEAENNNGRPPTRDILLHFSSOVAQGAFLASKNCICHRDVAARVLLLTNGHVAKI	215
QY	411	ADFGIAR-LIEDNEXTARQGAKEPIKMTAPAEALTYGREFITSDVMSFGILLTELTTKKRV	469
DB	216	GDFGLARDIMDSNNTIVKGNARLPLVXMAAPESIPFCVYTVGSDVMSXYGLIMEISLGIN	275
QY	470	PYRG-MVNRVULDOYRGTRMPCPECCESLHDMCCCKRKEPERPPTVEYQATLED	526
DB	276	PPPGILVNSKFKVLVDGYQMAOPAFAPKNITISINQACMALEPTRHPFOOICSTLQE	333

RESULT 15

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US-10-505-928-432
; Sequence 432, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 432
; LENGTH: 885
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-505-928-432

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Query Match

[illegible]

Search completed: June 5, 2006, 17:43:28
Job time : 8.01729 secs

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